

# **Repatriation of Guadalupe Bass in the Blanco River, Texas: A Case Study in the Opportunistic Use of Drought as a Fisheries Management Tool**

**STEPHAN MAGNELIA\***, **GORDON LINAM**, **RYAN MCGILLICUDDY**,  
**KEN SAUNDERS**, AND **MELISSA PARKER**  
*Texas Parks and Wildlife Department*  
*Post Office Box 1685, San Marcos, Texas 78667, USA*

**TIMOTHY BIRDSONG**  
*Texas Parks and Wildlife Department*  
*4200 Smith School Road, Austin, Texas 78744, USA*

**DIJAR LUTZ-CARRILLO**, **JÁNAYE WILLIAMSON**  
*Texas Parks and Wildlife Department*  
*505 Staples Road, San Marcos, Texas 78666, USA*

**RACHAEL LINDSEY RANFT<sup>1</sup>**  
*The Nature Conservancy*  
*23345 Bat Cave Road, San Antonio, Texas, 78266, USA*

**TIMOTHY BONNER**  
*Texas State University, Department of Biology/Aquatic Station*  
*601 University Drive, San Marcos, Texas 78666, USA*

---

\*Corresponding author: [stephan.magnelia@tpwd.texas.gov](mailto:stephan.magnelia@tpwd.texas.gov)

<sup>1</sup>Current address: Eco-vative Associates  
223 Paisano Drive, Victoria, TX 77904, USA

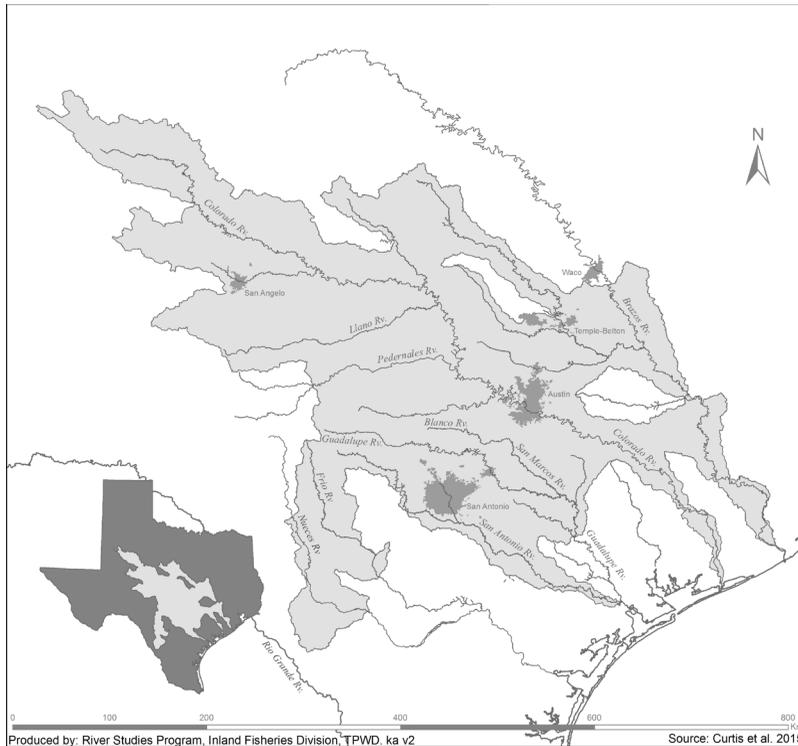
**Abstract.**—Repatriation of Guadalupe Bass *Micropterus treculii* was undertaken in the Blanco River, Texas, after extirpation due to hybridization with non-native, introduced Smallmouth Bass *Micropterus dolomieu*. In summer 2011, much of the river was reduced to a series of disconnected, enduring pools due to severe drought. Electrofishing and seines were used to remove Smallmouth Bass from fifty-two enduring pools in a 24-km reach of the river upstream of a natural fish passage barrier. After the removal effort was completed, stockings of non-introgressed, hatchery-produced Guadalupe Bass fingerlings ( $n = 316,016$ ) were initiated in spring 2012 when river flows returned. Successful recruitment of wild, naturally-produced Guadalupe Bass was documented in fall 2014 and 2015. In the reach where Smallmouth Bass were removed, only Guadalupe Bass were detected, despite a historic flood event in spring 2015, which provided an opportunity for upstream movement of Smallmouth Bass and Guadalupe Bass x Smallmouth Bass hybrids past the barrier.

## Introduction

Guadalupe Bass (GB), the official state fish of Texas, is endemic to streams that originate in the Edwards Plateau ecoregion of central Texas, including portions of the Brazos, Colorado, Guadalupe and San Antonio river basins (Figure 1; Curtis et al. 2015). They inhabit spring-fed streams, with larger individuals associated with moderate depths (1.0 m) and slow current velocities ( $<0.05$  m/s) downstream from riffles with instream cover such as log complexes, boulders, and undercut banks (Edwards 1980; Perkin et al. 2010; Curtis et al. 2015). Juveniles initially seek swift habitats, but transition to deeper depths and moderately flowing eddies as they near age-1 (Edwards 1980; Curtis et al. 2015). They are a highly sought after sport fish for river anglers (Thomas et al. 2015) and also a species of conservation concern (Hubbs et al. 2008; Texas Parks and Wildlife Department 2012) due to decreased stream flow (Hurst et al. 1975), reservoir construction (Edwards 1978), habitat degradation, and hybridization with nonnative Smallmouth Bass (SMB) (Edwards 1980). Extirpation of GB has occurred in portions of their historical range as

a result of hypolimnetic dam releases (Edwards 1978) and hybridization with SMB (Littrell et al. 2007; Bean et al. 2013). Since 1990, Texas Parks and Wildlife Department (TPWD) restoration efforts have included a genetic refuge restoration strategy (Araguas et al. 2008, 2009; Caudron et al. 2011), where SMB are not stocked in any location that provides it access to GB populations whose genetic purity is to be maintained or restored (Garrett 1991). Despite this effort, the proportion of SMB and GB x SMB hybrids (hybrids) within some streams has been shown to continually increase until Guadalupe Bass are extirpated (Littrell et al. 2007; Bean et al. 2013; Fleming et al. 2015). In response to the threat of additional extirpations of GB populations, TPWD initiated the Guadalupe Bass Restoration Initiative (GBRI) (Birdsong et al. 2010; Garrett et al. 2015) in 2010.

The Blanco River is located along the eastern edge of the Edwards Plateau ecoregion in south-central Texas in an area commonly referred to as the Texas Hill Country. The watershed (Figure 1) is within the historical range of GB and is of high ecological importance given that it hosts 36 species of conservation concern including five species



**Figure 1.** Distribution of Guadalupe Bass including historical and introduced populations. Map adapted from Curtis et al. 2015.

of fish (TPWD 2012). The watershed is also a priority for conservation investments by The Nature Conservancy (TNC) who has established relationships with a network of landowners interested in wildlife conservation (TNC 2016). Furthermore, the Blanco River is at high risk for habitat alteration due to its location just west of the Austin-San Antonio urban corridor (Crawford et al. 2016). These factors would have otherwise propelled the Blanco River to be considered as a priority for the GBRI; however, stockings of SMB in the Blanco River in 1977 and 1980 resulted in GB  $\times$  SMB hybridization and genetic introgression (Garrett 1991). By 1991, 30% of the micropterids collected from the Blanco River were genetically identified as GB  $\times$  SMB hybrids (Morizot et al. 1991). Supplemental stockings of 80,014 genetically pure GB fingerlings occurred in the Blanco River in 1994 and 1995, a conservation strategy that was

initiated in the Guadalupe River headwaters in 1992 intended to reduce hybridization and genetic introgression of wild populations of GB (Fleming et al. 2015); however, because of state fish hatchery production resource constraints, supplemental stocking of GB in the Blanco River was abandoned after 1995 (G. Garrett, TPWD retired, personal communication), and the apparent extirpation of GB from the Blanco River was subsequently documented in 2005 (Littrell et al. 2007).

The continued persistence of SMB and hybrids in the Blanco River following GB extirpation provided evidence of the suitability of stream habitats to support SMB in the long-term. Bean et al. (2013) observed variable levels of GB  $\times$  SMB hybridization in streams where nonnative SMB had been introduced, with the highest levels of hybridization found in streams where SMB persisted long-term. Fisheries managers believed

that supplemental stockings of GB, such as those made in the Guadalupe River (Fleming et al. 2015), would likely be an ineffective repatriation approach in the Blanco River in the absence of SMB removal. Furthermore, a large-scale removal program for SMB and hybrids did not seem feasible, so efforts to repatriate GB to the Blanco River were deemed futile.

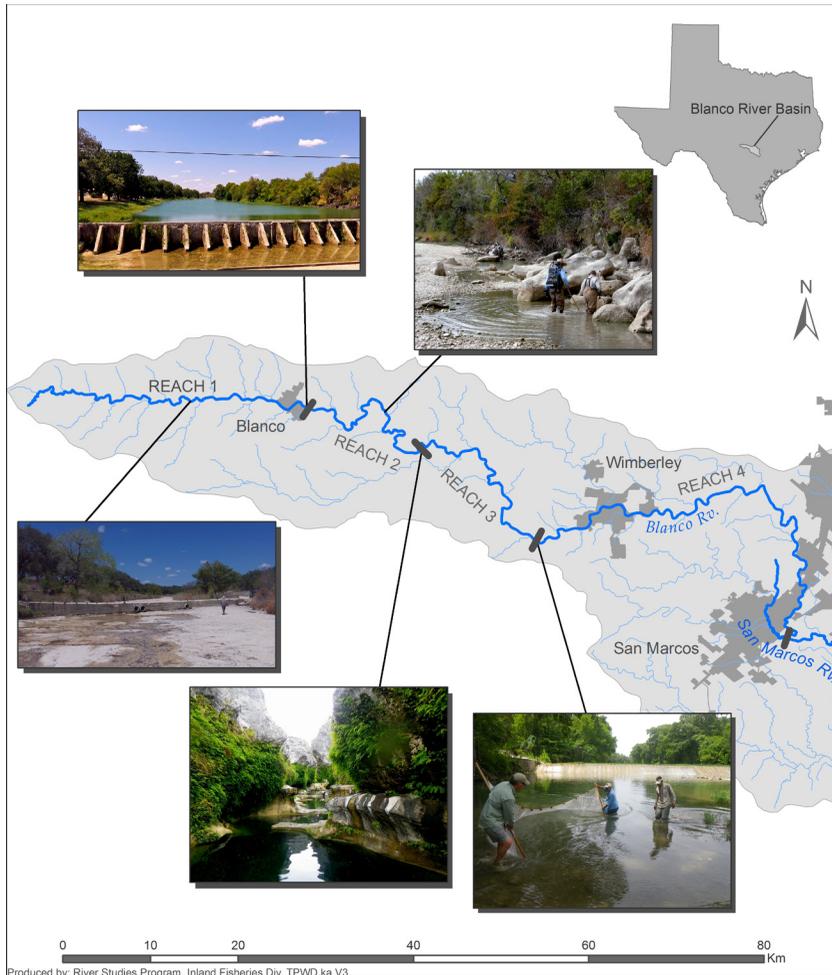
This perspective changed in 2011, a time during which most of Texas experienced exceptional drought conditions (National Drought Mitigation Center et al. 2016). Record high temperatures from June through August combined with minimal precipitation contributed to record low stream flows throughout much of the State (Winters 2013). The Blanco River was reduced to a series of disconnected enduring pools. Conditions appeared to offer an opportunity for the targeted removal of SMB and hybrids seeking refuge in those pools. Opportunistic removal of invasive fish species that aggregate as a result of weather conditions has been suggested as an effective population control strategy (Shepard et al. 2014; Koizumi et al. 2017). A limitation of this strategy for the Blanco River was a constant source of SMB and hybrids known to persist within the San Marcos River, a spring-fed river that had stable flows throughout the 2011 drought. The Blanco River is a tributary of the San Marcos River (Figure 1), and in the absence of an effective barrier to upstream fish movement, we believed that SMB and hybrids would eventually move upstream and recolonize upon the return of normal flows. However, data from past fish collections revealed a discontinuity in the Blanco River fish assemblage upstream from a gorge containing a series of waterfalls (Texas Game and Fish Commission 1957; Bean et al. 2007). It was thought this natural feature might provide an effective barrier to upstream movement of SMB and hybrids and the area upstream from this to the headwaters would be a reach where removal ef-

forts might be effective. The objective of this project was to implement an isolation management strategy (Novinger and Rahel 2003) and establish a self-sustaining population of pure GB upstream of the barrier, through removal of SMB and hybrids, and repatriation of GB through stocking.

## Repatriation Area Description

The Blanco River is intermittently fed by shallow springs and seeps, and in some reaches the channel gains water, while in others water is lost to the aquifer through the karst landscape (Slade et al. 2002; Wierman et al. 2010). Although streamflow was absent during the summer of 2011, these springs as well as approximately 90 low-head dams and low-water crossings influenced the amount of water (i.e., number of enduring pools and depth of those pools) that remained. While the entirety of the Blanco River and its tributaries were considered for the repatriation effort, for planning purposes the river was divided into four distinct reaches (Figure 2).

Reach 1 was the upper 38 km of the mainstem Blanco River and tributaries from the headwaters to a low-head dam just downstream from the city of Blanco (Figure 2). This reach was highly fragmented with 37 low-head dams and 17 low-water crossings. It also contained 36 main channel small impoundments, many of which still held large areas of water during summer 2011. The lower 6 km of this reach entering and in the city of Blanco was characterized by a series of 10 consecutive impoundments. While some of these were dry others had as much as 2–3 ha of water remaining (Figure 2). The lower portion of this reach is reported to be a gaining reach (Wierman et al. 2010), likely due to the influence of springs such as Koch Springs (Brune 1975), which enters the river at one of the lower reservoirs and was flowing during the project. Portions of this reach not imme-



**Figure 2.** Location of Reaches 1 through 4 for the Blanco River, TX Guadalupe Bass repatriation project. Photographs (starting at top left and proceeding clockwise) are of: 1) A large enduring pool upstream of a low-head dam at the lower portion of Reach 1 in summer 2011, 2) A small enduring pool in Reach 2 in summer 2011, 3) The dam at the lower end of Reach 3 in fall 2014, 4) The bottom of the gorge looking upstream in fall 2014, 5) A dewatered portion of Reach 1 in summer 2011.

diately upstream of a dam or crossing were largely dewatered in summer 2011 (Figure 2).

Reach 2 was the 24 km of the main-stem Blanco River and tributaries from the low-water dam located just upstream of the FM 165 bridge crossing to a 0.4-km long in-channel narrow gorge bordered by 23-m high cliffs (Texas State Historical Association 2016) located at approximately river

km 62. In the most upstream portion of the gorge was a series of five consecutive natural waterfalls ranging in height from 0.6 to 3.3 m in height (Figure 2). Unlike the numerous low-head dams and low-water crossings on the Blanco River the gorge was suspected to be an effective fish passage barrier at least among small fishes (e.g., percids; Bean et al. 2007), but its effectiveness as a barrier to larger and more mobile fishes (e.g., black

basses) was unknown. Fifty-two enduring pools were identified, and while this reach contained seven dams and seven low-water crossings, all but one of the enduring pools were small ( $\leq 0.1$  ha), and all but three were shallow ( $< 1$  m) (Figure 2). The one large pool was located at the very upper portion of the reach and covered approximately 1.6 ha. Approximately 8 km of this area was reported as a losing reach (Wierman et al. 2010), which likely contributed to the lack of water under the severe drought conditions. At least one of the larger and deeper pools was reported by the landowner to have held water even during the 1950s drought of record for Texas, which is likely due to the influence of an undescribed seep or spring.

Reach 3 was the Blanco River and tributaries from the gorge to an in-channel dam at approximately river km 85 (Figure 2). Most of this stretch is a gaining reach (Wierman et al. 2010) influenced not only by springs, but also a major tributary, the Little Blanco River. Thirty-two enduring pools were identified, with the largest being an impoundment that covered approximately 6.5 ha located at the very downstream boundary. A number of the other pools were between 2 and 3 ha.

Reach 4 consisted of the remaining 56 km of the Blanco River to the confluence with the San Marcos River. The approximate upper half of this portion is a gaining reach, influenced by input from a major spring, Jacobs Well (Brune 1975), which feeds the Blanco River tributary Cypress Creek (Wierman et al. 2010). While we did not enumerate or measure the size of enduring pools in this reach, on-the-ground observations from public access points indicated the upper half contained many large and deep pools while the lower portion (a losing reach) was predominately dry.

## Detection of Smallmouth Bass and Hybrids

In summer 2011 seining, backpack electrofishing, and boat electrofishing were used in a targeted collection of micropterids for the purpose of detecting the presence of SMB and hybrids within each of the four reaches. All fish were identified to species in the field and released, except a pelvic fin clip was taken for genetic analysis to confirm species identification of small fish ( $< 75$  mm) for which identification was inconclusive. Fin clips were preserved in 95% nondenatured ethanol, processed to isolate genomic DNA (Lutz-Carrillo et al. 2015), and then evaluated for taxonomic status using a 10-locus subset of taxa-informative microsatellite loci (MPX4, MPX5, MPX6, and MPX17; Lutz-Carrillo et al. 2015). The detection of SMB and hybrids in Reach 1 would have likely ended the repatriation effort, as we felt removal efforts would have been futile due to the relatively large amount of water remaining in impoundments, and downstream movement of SMB and hybrids was likely. More than 400 micropterids were collected from 16 locations within Reach 1 in an effort to detect the presence of SMB and hybrids. Locations included all private lands accessible by TNC staff, including small impoundments in the headwaters, and all public bridge and low-water crossings, where water remained. All micropterids from this reach were identified either visually in the field, or through genetic analysis ( $n = 55$ ) as Largemouth Bass *Micropterus salmoides* (LMB). This finding was consistent with previous collections of micropterids in this reach between 2003 and 2005 (Bean et al. 2007). Smallmouth Bass and hybrids were encountered in surveys of Reaches 2, 3, and 4.

## Reach-Specific Repatriation Strategies

Although SMB and hybrids were not detected in Reach 1, affording a seemingly simple opportunity for repatriation of GB, the number of impoundments in this reach made it appear habitat was more suitable for LMB than GB. There was also concern that high levels of predation from LMB, which were prevalent in this reach, could occur on stocked GB fingerlings. We were unsure if GB could persist in this reach long-term and it was not initially considered for the repatriation effort.

Reach 2 afforded what appeared to be the highest likelihood for successful removal of SMB and hybrids. Almost all the enduring pools in this reach were relatively small ( $\leq 0.1$  ha) and it was thought electrofishing and seining would be effective removal techniques. If removal of SMB and hybrids was successful in Reach 2, we believed the risk of SMB recolonization from downstream of the gorge would be minimized. It was also thought habitat in this reach was conducive for establishing a naturally reproducing population of pure GB. The decision was made to conduct georeferenced aerial mapping of enduring pools in Reach 2 and then send removal crews to each of the pools.

Reaches 3 and 4 lacked a significant barrier to prevent upstream migration of SMB and hybrids from the San Marcos River. Given the large enduring pools in these reaches we also believed that removal of SMB and hybrids would be nearly impossible and as such determined that efforts to repatriate GB to these reaches would be limited to supplemental stockings similar to GB restoration efforts in the upper Guadalupe River (Fleming et al. 2015).

## Mapping of Enduring Pools

To increase efficiency of ground crews for removal efforts, we collected georeferenced imagery of the river channel using an unmanned aerial system (UAS). The specific UAS platform, data collection, and image processing techniques are described by Birdsong et al. (2015). The UAS mapping produced a 20-cm georeferenced photomosaic of the river channel of Reaches 2 and 3. Nine enduring pools in Reach 2 were encountered in the field that were not visible in the UAS imagery because of obstruction by tree canopy or shadows. Pools visible in the photomosaic were delineated in Google Earth Pro (Google Inc., Mountain View, CA, USA).

## Removal of Smallmouth Bass and Hybrids

Pulsed direct current boat, barge (Smith Root pulsator model GPP-5.0), and backpack electrofishing (Smith Root model 12-B POW), as well as seines, were used to target SMB and hybrids from enduring pools in Reach 2. Boat and barge pulsators were set to the low voltage range (50–500 V), 60 Hz, and voltage increased until fish were stunned (approximately 10–15 amps). The backpack shocker was set to 60 Hz, 6 micro seconds pulse width (setting I5) and an output voltage of 300. Electrofishing has been reported to be a successful technique for eradicating (Shepard et al. 2014), or reducing the number of nonnative salmonids in small streams during genetic restoration projects (Caudron and Champigneulle 2011). Seines were comprised of delta weave mesh and had double lead weights to help maintain contact with the bottom. Seine sizes were: 4.6 m x 1.8 m with 4.8-mm mesh and 9.1 m x 1.8 m with 6.4-mm mesh. The 9.1-m seine was also used as a block net when deemed appropriate.

Each pool was examined on-site, the sampling gear(s) best suited for the situation determined, and repeated sampling conducted until we were satisfied the pool had been adequately sampled, and no SMB or hybrids were caught. Approximately 270 h were spent seining and electrofishing the fifty-two enduring pools in Reach 2. Individuals identified or suspected to be a SMB or hybrid were removed. A pelvic fin-clip was preserved in ethanol, and species identification determined with genetic analysis, using the methodology previously described in the detection sampling portion of the project. Nontarget species were not dipped while electrofishing, and those collected in seines were released back into the pool.

A total of 45 micropterids were removed from enduring pools in Reach 2. Of those, 25 were genetically identified as SMB (mean length = 181.5 mm; range = 135–460 mm) while the remainder were identified as LMB. No hybrids were collected. Thousands of fishes, including many species previously collected in this portion of the Blanco River (Bean et al. 2007) and common to central Texas, were collected and returned to enduring pools, suggesting removal methods were effective. We were surprised by the small number of SMB collected, given the relatively large number of other species in pools, and surmised their abundance had been reduced as a result of the drought and low flow conditions, and/or they were not particularly abundant in Reach 2. A previous study indicated relative abundance of GB and SMB in the overall fish assemblage of the Blanco River was <1% (Bean et al. 2007). At the conclusion of the fish removal portion of the project, we were confident that all pools in Reach 2 had been located and sampled.

## Repatriation of Guadalupe Bass

By spring 2012, drought conditions had subsided throughout much of Texas and typical flow conditions returned to the Blanco River. Guadalupe Bass fingerlings cultured at the TPWD A.E. Wood State Fish Hatchery were stocked in spring 2012 ( $n = 102,616$ ; mean length = 40 mm; range = 35–51 mm), 2013 ( $n = 133,817$ ; mean length = 39 mm; range = 35–48 mm), 2015 ( $n = 23,805$ ; mean length = 40 mm; range = 35–51 mm) and 2016 ( $n = 55,778$ ; mean length = 46 mm; range = 36–58 mm). Broodstock used for production of fingerlings were acquired from the wild (South Llano River, TX) and were supplemented annually with additional wild fish from the same source. Each year approximately 100 pairs of broodfish were penned for spawning with nearly half of penned fish participating in spawning based on genetic analysis of production fingerlings (Lutz-Carrillo et al. 2015; TPWD, unpublished data).

In 2012 and 2013, 72% of the fingerlings were stocked at 8 sites located in Reach 2 where removal efforts were conducted. The remaining fingerlings were stocked at three sites located in Reach 3, and one site in Reach 4 to see if supplemental stocking might reduce introgression without removal of SMB and hybrids, similar to results reported from the upper Guadalupe River (Fleming et al. 2015). No fish were stocked in spring 2014 as we were interested in documenting if natural reproduction from the 2012 and/or 2013 stockings had occurred. Guadalupe Bass are reported to attain sexual maturity at Age 1 (Edwards 1980). All GB produced in 2015 and 2016 were stocked in Reach 1. While the habitat in Reach 1 appeared more conducive to LMB, lotic habitat was present under higher flow conditions and we were interested to see if this area might also sustain a population of GB.

## Post-Stocking Monitoring

In fall 2014 and 2015, micropterids appearing to be GB, SMB, or hybrids were collected using seines and boat and backpack electrofishing for genetic analysis. An effort was made in both years to collect 100 fish for analysis. Seine and electrofishing specifications/settings previously described for removal efforts were also used for monitoring collections. A total of 119 seine hauls covering 1.45 river km, and 1.9 h of boat and backpack electrofishing effort were expended for both monitoring collections. A pelvic fin clip was removed and preserved in 95% nondenatured ethanol for genetic analysis to confirm species identification. In fall 2014, individuals were collected from six sites in Reach 2 ( $n = 69$ ) and two sites in Reach 4 ( $n = 31$ ). In fall 2015, individuals were collected from four sites in Reach 2 ( $n = 59$ ) and a total of five sites in Reaches 3 and 4 ( $n = 32$ ).

Each post-stocking sample was first genotyped using the taxa-specific marker panel previously described to verify species status. In order to verify the origins of recovered fish, potential parental broodfish and wild collected individuals were genotyped at 22 microsatellite loci (Table 1; Lutz-Carrillo et al. 2008; Seyoum et al. 2013). Reactions were performed as multiplexes in 10- $\mu$ L volumes with Platinum Multiplex PCR Master Mix (1X), equimolar amounts of labeled and unlabeled primer pairs (0.02–0.15  $\mu$ M), and 50 ng template DNA (Table 1). Polymerase chain reaction (PCR) conditions were 95°C (120 s) followed by 28 cycles of 95°C (30 s), annealing (55.6–57.9°C) for 90 s, and 72°C (90 s), ending with a 60°C final extension (30 min). Products from each reaction were diluted in formamide and resolved on an ABI 3500 genetic analyzer (ThermoFisher Scientific). Allele sizes were quantified using GeneMapper Software 5 (ThermoFisher Scientific).

Hatchery broodfish were then assigned or excluded as potential parents using the likelihood approach implemented in CER-VUS v.3.0.3 (Marshall et al. 1998; Kalinowski et al. 2007). Simulations (parent-pair, sexes known), assuming 85% of candidate parents were sampled, to allow for documentation errors and typing errors of 1%, were used to determine critical logarithm of odds (LOD) thresholds. The LOD threshold value was then used to assign parentage with 95% and then 80% confidence. Mismatches can arise due to a true parent missing from the parent pool, mis-assigned genders, de novo mutations in the fingerlings, scoring errors, or failed PCRs (Araki and Blouin 2005), thus prior to final assignments any trio of offspring and parental pair with mismatches but a positive LOD score were also visually inspected. Individuals excluded as offspring of all hatchery parent pairs were classified as having wild origins. Individuals assigned to a hatchery parent pair were classified as having primary hatchery origins. Using the measured total lengths of recovered samples, annual pen assignments for broodfish, and detected spawning pairs (based on pre-stocking fingerling sampling and genotyping; Lutz-Carrillo et al. 2015) these individuals were further classified to year-class.

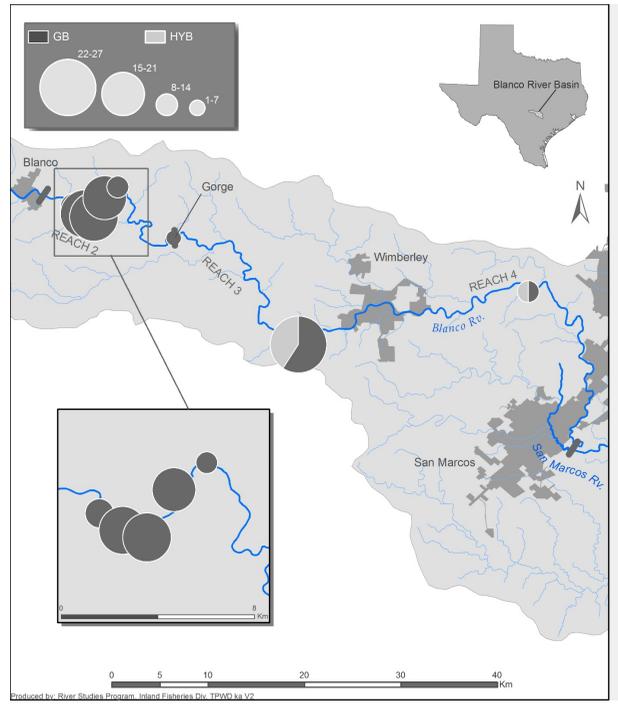
During the first post-stocking collection (fall 2014) genetic analyses resolved 86 GB, 13 hybrids, and a single LMB. Ignoring the LMB (not a target species), all fish (100%) recovered from Reach 2 ( $n = 68$ ) were identified as GB and 32% recovered downstream of the gorge were identified as GB ( $n = 10$ ) (Figure 3). Among the GB recovered, 28% ( $n = 13$ ) had primary hatchery origins. All of these were recovered from Reach 2 (Figure 4). Among individuals identified as having primary hatchery origins, 15% ( $n = 2$ ) were stocked in 2012 and 85% ( $n = 11$ ) were stocked in 2013. The remaining GB ( $n = 33$ ), including all GB collected in Reach 3 ( $n = 10$ ), were not assigned to hatchery parents.

**Table 1.** Parentage marker panel. Primer sequences, concentrations ( $\mu\text{M}$ ), labels (5'-mod), multiplex groups (rxn), and annealing temperatures ( $T_a$ ). 5'-PIG tail additions to promote 3'-A-addition are denoted by lower case bases.

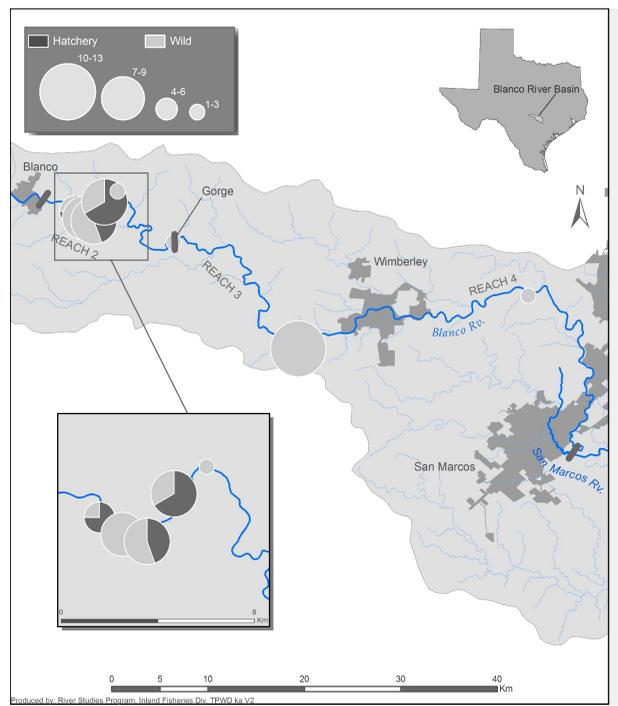
Primer	Primer Sequence (5'-3')	$\mu\text{M}$	5'-mod	rxn	$T_a$
TPW130f	GTCTCACCTGTGCCAATGTGA	0.05		1	57.9
TPW130r	TAGGAGTTGGGGTCACTTGCTT		6FAM	1	
TPW38f	ACATTCAAACCACTTTCCCACA	0.1	6FAM	1	
TPW38r	gtttGTGACAGACTTTGTTGTCCCAT			1	
TPW51f	gttTCATTGCAACACAACACAGAGA	0.05		1	
TPW51r	ATGGGACTATAGGCATCACACA		6FAM	1	
TPW70f	ATATCCACTTCGGTGATCCAGT0.15	VIC	1		
TPW70r	gtttCAGGAGTATGTTTCCCTCATGC			1	
TPW11f	ACCTTGCAACCCAAAGGTTATT	0.08	PET	2	57.1
TPW11r	gttTCTGCCTCAGAGACACAACATA			2	
TPW12f	GTAGGGTTGTTCCCCATGAATC	0.05		2	
TPW12r	TGCTCGCTGTCTCTATCTCTTC	6FAM	2		
TPW55f	CAGCAAGATGTCAACCAGGTAA	0.05	VIC	2	
TPW55r	gttTCCTGAGATACTGAATTAGGGGT			2	
TPW90f	CGATGTTCAAGAAGATGCCAGA	0.03	VIC	2	
TPW90r	gtttCATTTCCCTGTTCCCACTTACC			2	
Msaf14f	GAAAGAAAGGTCCAGTCATGTAGAA	0.1		2	
Msaf14r	ATGTTATTGAGTAGATCCCAATGGA		6FAM	2	
TPW173f	AACCACACAGTGACACAAACTG	0.05	NED	2	
TPW173r	gttTCTTACAGAGGGCAATAGGGAC			2	
Msaf10f	CACACTTCACTCAATCCCGTC	0.05	VIC	3	57.9
Msaf10r	gtttACAGCTGTAAAGATTTTGGGCA			3	
Msaf32f	gttTGCCTCACATCCTCTTATCCAT	0.1		3	
Msaf32r	CCTGTCTCACAAGTCTCACAAG		6FAM	3	
TPW96f	gTTGTGTTTGATTGAGCGAAGGA	0.05		3	
TPW96r	GCATAAAGACTGGGAACAGAGG		6FAM	3	
TPW62f	gtttATGCTTTCTGCTGAAGTGC	0.05		3	
TPW62r	TCCCTTTTGGAAGTAGAAGT		PET	3	
TPW107f	gtttACCTTGTTGGCCTGATGTTGGAGC	0.05		3	
TPW107r	AAGGGGTAAATCCATCTGTCCACC		VIC	3	
TPW112f	GTCCACCAGAGACAACCTGCGT	0.05		3	
TPW112r	CTAGTGCGACCCAGAGAACG		6FAM	3	
TPW132f	TCAGCAAAGTTTCTCCAGTGGAAC	0.05	NED	3	
TPW132r	GCATCTCTGAGCCAGGACAT			3	
Msaf22f	GCAGCAGGAGAGGGCAAG	0.02	NED	4	55.6
Msaf22r	gttTGTCTGAAGAGCAGTGACA			4	
TPW25f	CCTGCACCCACATACGT	0.05	VIC	4	
TPW25r	gtttACCTTTGTGCTGTTCTGTC			4	
TPW50f	gttTGGCAGGTCGTAATGTATG	0.04		4	
TPW50r	GATTTGAGCTTCTACTTTACG		VIC	4	
TPW68f	CATCAACTTTAATGCAAATACAG	0.05	6FAM	4	
TPW68r	gtttAAGAGGAGGATGCAACTAAG			4	
TPW76f	ACACAGTGTCTAGTTCTGCA	0.05	PET	4	
TPW76r	GTGAATACCTCAGCAAGCAT			4	

\*TPW prefix indicates primers taken directly or modified from Lutz-Carrillo et al. 2008.

Msaf prefix indicates primers taken directly or modified from Seyoum et al. 2013.



**Figure 3.** Guadalupe Bass (GB) and Smallmouth Bass or hybrids (HYB) detected in fall 2014 at Blanco River, TX sampling sites in the post-stocking monitoring effort upstream and downstream of the gorge barrier. Circles are scaled by sample size.



**Figure 4.** Stocked fish (HATCHERY) and wild fish (WILD) detected among Guadalupe Bass in fall 2014 at Blanco River, TX sampling sites in the post-stocking monitoring effort upstream and downstream of the gorge barrier. Circles are scaled by sample size.

On May 24, 2015, the Blanco River rose approximately 12.2 m above the base flow stage of 1.5 m (U.S. Geological Survey 2016). As a reference, the National Weather Service flood stage is 3.96 m. Floodwaters spread into the riparian area at the gorge (C. Furl, Edwards Aquifer Authority, personal communication) making it possible for SMB or hybrids to have moved upstream from Reach 3 into Reach 2.

During the second post-stocking collection (Fall 2015), 91 micropterids were collected. Genetic analyses resolved 72 GB and 19 hybrids. All fish recovered from Reach 2 ( $n = 59$ ) were again GB and 41% recovered from downstream of the gorge were GB ( $n = 13$ ) (Figure 5). Among GB recovered, 4% had primary hatchery origins ( $n = 3$ ) with one of these fish recovered from Reach 3 (Figure 6). Among individuals identified as having primary hatchery origins, two were from the 2013 stocking and one was from the 2015 stocking. The remaining GB ( $n = 69$ ) were not assigned to hatchery parents.

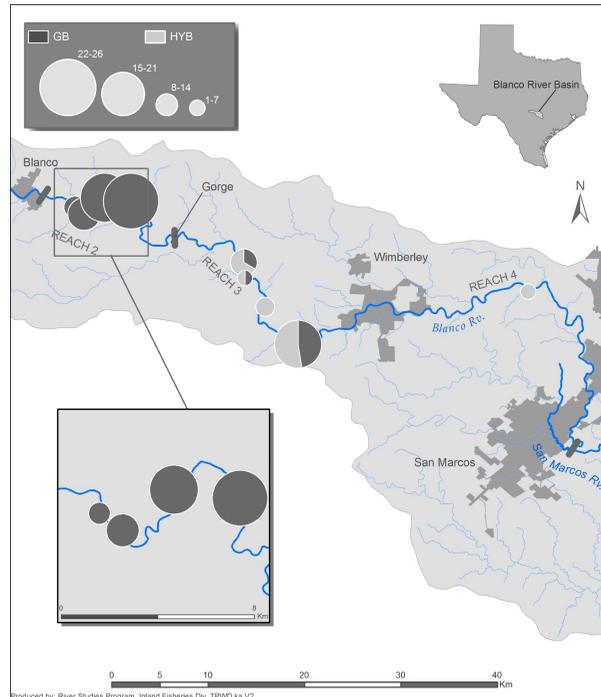
## Discussion

Following extirpation of GB from the Blanco River (Littrell et al. 2007) and failure to detect GB in our pre-stocking sampling, the detection of only nonintrogressed GB in post-stocking collections from the target reach in 2014 suggested that both the target species removal and GB repatriation efforts were successful. It also appeared the gorge fish passage barrier was effective in preventing upstream movement of SMB and hybrids to the newly established GB population in Reach 2. The detection of only nonintrogressed GB in this reach in 2015, following a historic flood event, reinforced these conclusions. The detection of some nonintrogressed GB downstream of the barrier was also encouraging, but a more tentative result, as these individuals are expected to be more susceptible to hybridization than those up-

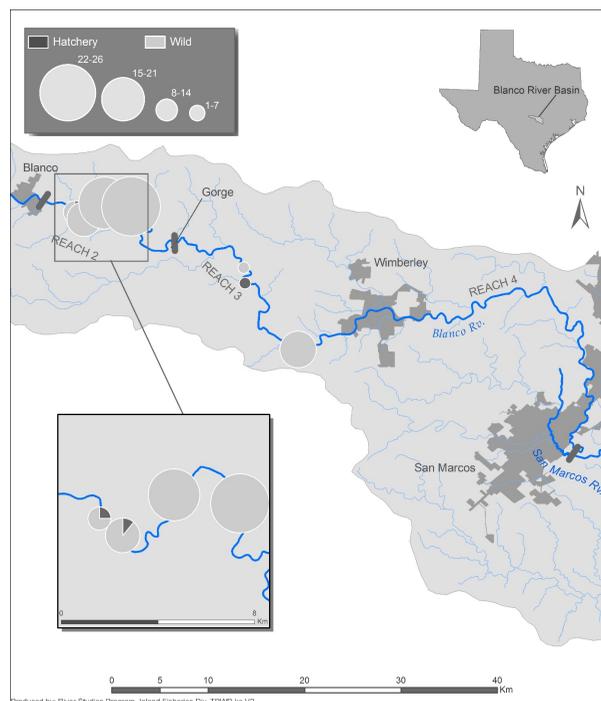
stream of the barrier given the enduring SMB and hybrids in these reaches.

While multiple sites were stocked with hatchery offspring, most GB recovered in post-stocking collections did not have primary hatchery origins. In post-stocking collections individuals resolved as GB, but not assigned to hatchery parents were significantly smaller by length (mean = 90.2 mm; range = 77–130 mm) than the GB assigned to hatchery parents (mean = 182.5 mm; range = 148–223 mm) (Mann–Whitney  $U$ -test,  $U = 429$ ,  $p < 0.0001$ ) indicating they were potentially offspring of stocked fish (secondary hatchery origins). This hypothesis was supported by the lack of GB detected in a previous genetic study in this system (Littrell et al. 2007) and our pre-stocking screening, which suggested no other source was present to produce these GB. Even assuming these unassigned GB were derivatives of an undetected refuge population, we would expect to resolve population substructure between these fish and hatchery broodfish derived from an independent source (i.e., South Llano River); however, Bayesian clustering of multi-locus genotypes (Pritchard et al. 2000; Falush et al. 2003) suggested all samples were most likely derived from a single panmictic population. This suggests that not only were the initial stocking efforts successful in reintroducing GB to a portion of the Blanco River, but they have been successfully reproducing.

Previous efforts to restore GB have required regular supplemental stockings to maintain GB influence in the face of introgression pressure from congeners (Fleming et al. 2015); however, in upper Johnson Creek, isolated from congeners by downstream barriers, GB have persisted for several years after the cessation of stocking efforts (Fleming and Smith 2019, this volume). By comparison, the gorge at the lower end of Reach 2 in the Blanco River is much larger than the barriers separating upper and lower Johnson Creek. Thus, if a sustaining GB population



**Figure 5.** Guadalupe Bass (GB) and Smallmouth Bass or hybrids (HYB) detected in fall 2015 at Blanco River, TX sampling sites in the post-stocking monitoring effort upstream and downstream from the gorge barrier. Circles are scaled by sample size.



**Figure 6.** Stocked fish (HATCHERY) and wild fish (WILD) detected among Guadalupe Bass in fall 2015 at Blanco River, TX sampling sites in the post-stocking monitoring effort upstream and downstream of the gorge barrier. Circles are scaled by sample size.

can persist in upper Johnson Creek, we are relatively confident in the persistence of GB upstream of the gorge in the Blanco River. Natural reproduction should also relieve the need for additional hatchery stockings, except if necessary to introduce novel genetic variation (Carlson et al. 2014). In addition, the presence of a sustaining population in Reach 2 may beneficially impact reaches downstream of the barrier.

Barriers have been used, with varying levels of success, as management tools for native fish protection and restoration in the southwest (Rinne and Turner 1991; Carpenter and Terrell 2005) and throughout North America (Meronek et al. 1996; Harig et al. 2000); however, the primary measure of effectiveness has been the ability to prevent interactions with populations downstream of the barrier (Carpenter and Terrell 2005). The literature is lacking with respect to the seeding effect of restored populations, upstream of a barrier, on the prevalence of nonnatives or magnitude of introgression in downstream populations; however, gene flow in lotic systems is commonly asymmetric with greater dispersal and migration in the downstream direction (Müller 1954; Hänfling and Weetman 2006; Caldera and Bolnick 2008; Raeymaekers et al. 2009). The presence of barriers amplifies this asymmetry making upstream movement more difficult, but in many cases having little effect on downstream movement (Junker et al. 2012). In addition, even low levels of gene flow, from highly divergent populations, can have substantial demographic effects across a barrier (Fitzpatrick et al. 2016). Most protective barriers are located on smaller order lotic stretches and reproduction from restored populations may easily exceed a limited carrying capacity providing an excess of progeny that may move downstream (Waters 1972). Thus, it is reasonable to assume that the restored above barrier population established in the Blanco River would annually integrate progeny into below

barrier populations. This should, to some degree, suppress the frequency of nonnatives in downstream stretches by occupying available niches and providing resource competition. This is an idea that requires careful evaluation, however the same-source stocking of downstream sites, in addition to above barrier sites, in this study does not allow for conclusions about this potential seeding effect.

Future efforts for the Blanco River include periodic genetic monitoring throughout the basin, and stockings upstream of barriers in tributary streams in Reaches 3 and 4. If SMB and hybrids are identified upstream of tributary barriers, concerted efforts could be made to remove them and create additional GB populations for seeding the mainstem without additional hatchery stockings. Drought conditions are sure to return to Texas and this may again provide optimal conditions to conduct such efforts. Future monitoring results from the 2015 and 2016 stockings in Reach 1 are also of particular interest. During years with average or above average rainfall, portions of this reach are free running and could provide suitable habitat for GB. While we and others (Bean et al. 2007) did not detect GB in this portion of the river, we wonder if it is because they were never present, or if habitat is truly not conducive to their long-term persistence. If a naturally reproducing population could be established in this reach it might be maintained during even more severe droughts than that experienced in 2011. Individuals taking refuge in the many impoundments in this reach might provide progeny for downstream seeding even if all enduring pools in Reach 2 went dry.

## Acknowledgments

Funding for this project was provided through the Federal Sport Fish Restoration Act. The authors acknowledge TPWD Inland Fisheries Division staff Kevin Mayes, Clint Robertson, Karim Aziz, John Botros,

Roy Kleinsasser (retired), Marcos De Jesus, Greg Cummings, Darin Gossett, Archib Grubh, Steve Boles, Kevin Kolodziejczyk, Gary Garrett (retired), Beth Bendik, Tom Heeger, Megan Bean; and Texas State University staff and students Stephen Curtis, Virginia Dautreuil, Kristy Kollaus, and Sarah Robertson, for assistance in SMB removal efforts; TPWD A.E. Wood State Fish Hatchery staff Carl Kittel, the late Rob Schmid, Michael Matthews, Chris Thibodeaux, and Hugh Glenewinkel for producing the GB used for stocking; TPWD River Studies Program Cartographer Karim Aziz for producing manuscript figures; and, The Meadows Center for Water and the Environment staff Thom Hardy, Kristy Kollaus, and Tom Heard for aerial imagery used to locate enduring pools. Gratitude goes to the landowners along the Blanco River who gave us access to their property during all phases of the project.

## References

- Araguas, R. M., Sanz, N., R. Fernandez, F. M. Utter, C. Pla, and J. L. Garcia-Martin. 2008. Genetic refuges for a self-sustained fishery: experience in wild Brown Trout populations in the eastern Pyrenees. *Ecology of Freshwater Fish* 17:610–616.
- Araguas, R. M., N. Sanz, R. Fernandez, F. M. Utter, C. Pla, and J. L. Garcia-Martin. 2009. Role of genetic refuge in the restoration of native gene pool of Brown Trout. *Conservation Biology* 23:871–878.
- Araki, H., and M. S. Blouin. 2005. Unbiased estimation of relative reproductive success of different groups: evaluation and correction of bias caused by parentage assignment errors. *Molecular Ecology* 14:4097–4109.
- Bean, P. T., T. H. Bonner, and B. M. Littrell. 2007. Spatial and temporal patterns in the fish assemblage of the Blanco River, Texas. *Texas Journal of Science* 59:179–200.
- Bean, P. T., D. J. Lutz-Carillo, and T. H. Bonner. 2013. Rangewide survey of the introgressive status of Guadalupe Bass: implications for conservation and management. *Transactions of the American Fisheries Society* 142:681–689.
- Birdsong, T., D. Krause, J. Leitner, J. Long, S. Robinson, S. Sammons, and J. Sedell. 2010. A business plan for conservation of native black bass species in the southeastern United States: a ten year plan. National Fish and Wildlife Foundation, Washington, D.C.
- Birdsong, T., M. Bean, T. B. Grabowski, T. B. Hardy, T. Heard, D. Holdstock, K. Kollaus, S. Magnelia, K. Tolman, and L. Clark. 2015. Application and utility of a low-cost unmanned aerial system to manage and conserve aquatic resources in four Texas rivers. *Journal of the Southeastern Association of Fish and Wildlife Agencies* 2:80–85.
- Brune, G. 1975. Major and historical springs of Texas. Report 189. Texas Water Development Board, Austin, Texas. Available: [https://www.twdb.texas.gov/publications/reports/numbered\\_reports/doc/R189/R189.pdf](https://www.twdb.texas.gov/publications/reports/numbered_reports/doc/R189/R189.pdf). (September 2018).
- Caldera, E. J., and D. I. Bolnick. 2008. Effects of colonization history and landscape structure on genetic variation within and among Threespine Stickleback (*Gasterosteus aculeatus*) populations in a single watershed. *Evolutionary Ecology Research* 10:575–598.
- Carlson, S. M., C. J. Cunningham, and P. A. H. Westley. 2014. Evolutionary rescue in a changing world. *Trends in Ecology and Evolution* 29:521–530.
- Carpenter, J. and J. W. Terrell. 2005. Effectiveness of fish barriers and renovations for maintaining and enhancing populations of native southwestern fishes. Final Report to U.S. Fish and Wildlife Service, Arizona Ecological Services Office, Interagency Agreement No. 201814N756. U.S. Geological Survey, Fort Collins Science Center, Colorado.
- Caudron, A., A. Champigneulle, R. Guyomard, and C. R. Largiader. 2011. Assessment of three strategies for restoring native Brown Trout (*Salmo trutta*) populations in northern French alpine streams. *Ecology of Freshwater Fish* 20:478–491.
- Caudron, A., and A. Champigneulle. 2011. Multiple electrofishing as a mitigate tool for

- removing nonnative Atlantic Brown Trout (*Salmo trutta* L.) threatening a native Mediterranean Brown Trout population. *European Journal of Wildlife Research* 57:575–583.
- Crawford, S., G. Whelan, D. M. Infante, K. Blackhart, W. M. Daniel, P. L. Fuller, T. Birdsong, D. J. Wieferich, R. McClees-Funinan, S. M. Stedman, K. Herreman, and P. Ruhl. 2016. Through a fish's eye: the status of fish habitats in the United States 2015. National Fish Habitat Partnership. Available: <http://assessment.fishhabitat.org/>. (October 2018).
- Curtis, S. G., J. S. Perkin, P. T. Bean, M. L. Sullivan and T. H. Bonner. 2015. Guadalupe Bass (*Micropterus treculli*) (Vaillant and Bocourt, 1874). Pages 55–66 in M. D. Tringali, J. M. Long, T. M. Birdsong, and M. J. Allen, editors. Black bass diversity: multidisciplinary science for conservation. American Fisheries Society, Symposium 82, Bethesda, Maryland.
- Edwards, R. J. 1978. The effect of hypolimnion reservoir releases on fish distribution and species diversity. *Transactions of the American Fisheries Society* 107:71–77.
- Edwards, R.J. 1980. The ecology and geographic variation of the Guadalupe Bass, *Micropterus treculii*. Doctoral dissertation. University of Texas, Austin, Texas.
- Falush, D., M. Stephens, and J. K. Pritchard. 2003. Inference of population structure using multilocus genotype data: linked loci and correlated allele frequencies. *Genetics* 164:1567–1587.
- Fitzpatrick, S. W., J. C. Gerberich, L. M. Angeloni, L. L. Bailey, E. D. Broder, J. Torres-Dowdall, C. A. Handelsman, A. López-Sepulcre, D. N. Reznick, C. K. Ghalambor, and W. C. Funk. 2016. Gene flow from an adaptively divergent source causes rescue through genetic and demographic factors in two wild populations of Trinidadian guppies. *Evolutionary Applications* 9:879–891.
- Fleming, B. P., G. P. Garrett, and N. G. Smith. 2015. Reducing hybridization and introgression in wild populations of Guadalupe Bass through supplemental stocking. Pages 537–548 in M. D. Tringali, J. M. Long, T. M. Birdsong, and M. J. Allen, editors. Black bass diversity: multidisciplinary science for conservation. American Fisheries Society, Symposium 82, Bethesda, Maryland.
- Fleming, B. P. and N. G. Smith. 2019. Spatial distribution and hybridization in Guadalupe Bass five years after remedial stocking. Pages xxx-xxx in M. Siepker and J. Quinn, editors. Managing centrarchid fisheries in rivers and streams. American Fisheries Society, Symposium 87, Bethesda, Maryland.
- Garrett, G. P. 1991. Guidelines for the management of Guadalupe Bass. PWD-RP-N3200–367-11/91. Texas Parks and Wildlife Department, Austin, Texas.
- Garrett, G. P., T. W. Birdsong, M. G. Bean, and R. McGillicuddy. 2015. Guadalupe Bass restoration initiative. Pages 379–385 in M. D. Tringali, J. M. Long, T. W. Birdsong, and M. J. Allen, editors. Black bass diversity: multidisciplinary science for conservation. American Fisheries Society, Symposium 82, Bethesda, Maryland.
- Hänfling, B., and D. Weetman. 2006. Concordant genetic estimators of migration reveal anthropogenically enhanced source-sink population structure in the River Sculpin, *Cottus gobio*. *Genetics* 173:1487–1501.
- Harig, A. L., K. D. Fausch, and M. K. Young. 2000. Factors influencing success of greenback Cutthroat Trout translocations. *North American Journal of Fisheries Management* 20:994–1004.
- Hubbs, C., R.J. Edwards, and G. P. Garrett. 2008. An annotated checklist of the freshwater fishes of Texas, with keys to identification of species. Texas Academy of Science. Available: [https://repositories.lib.utexas.edu/bitstream/handle/2152/6290/Hubbs\\_et\\_al\\_2008\\_checklist.pdf?sequence=2&isAllowed=y](https://repositories.lib.utexas.edu/bitstream/handle/2152/6290/Hubbs_et_al_2008_checklist.pdf?sequence=2&isAllowed=y). (September 2018).
- Hurst, H., G. Bass, and C. Hubbs. 1975. The biology of the Guadalupe, Suwanee, and Redeye basses. Pages 47–53 in R. Stroud and H. Clepper, editors. Black bass biology and management. Sport Fishing Institute, Washington, D.C.
- Junker, J., A. Peter, C. E. Wagner, S. Mwaiko, B. Germann, O. Seehausen, and I. Keller. 2012. River fragmentation increases localized population genetic structure and

- enhances asymmetry of dispersal in Bullhead (*Cottus gobio*). *Conservation Genetics* 13:545–556.
- Kalinowski, S. T., M. L. Taper, and T. C. Marshall. 2007. Revising how the computer program CERVUS accommodates genotyping error increases success in paternity assignment. *Molecular Ecology* 16:1099–1106.
- Koizumi, I., Y. Kanazawa, C. Yamazaki, Y. Tanaka, and K. Takaya. 2017. Extreme winter aggregation of invasive Rainbow Trout in small tributaries: implications for effective control. *Ichthyological Research* 64:197–203.
- Littrell, B. M., D. J. Lutz-Carrillo, T.H. Bonner, and L. T. Fries. 2007. Status of an introgressed Guadalupe Bass population in a central Texas stream. *North American Journal of Fisheries Management* 27:785–791.
- Lutz-Carrillo, D. J., C. Hagan, L. A. Dueck, and T. C. Glenn. 2008. Isolation and characterization of microsatellite loci for Florida Largemouth Bass, *Micropterus salmoides floridanus*, and other micropterygids *Molecular Ecology Resources* 8:178–184.
- Lutz-Carrillo, D. J., C. Thibodeaux, M. Elliott, N. A. Rathjen, C. Kittel, L. T. Fries, and G. P. Garrett. 2015. Inferred reproductive behavior of captive Guadalupe Bass. Pages 549–583 in M. D. Tringali, J. M. Long, T. M. Birdsong, and M. J. Allen, editors. *Black bass diversity: multidisciplinary science for conservation*. American Fisheries Society, Symposium 82, Bethesda, Maryland.
- Marshall, T. C., J. Slate, L. E. B. Kruuk, and J. M. Pemberton. 1998. Statistical confidence for likelihood-based paternity inference in natural populations. *Molecular Ecology* 7:639–655.
- Meronek, T., P. Bouchard, E. Buckner, T. Burri, K. Demmerly, D. Hatleli, R. Klumb, S. Schmidt, and D. Coble. 1996. A review of fish control projects. *North American Journal of Fisheries Management* 16:63–74.
- Morizot, D. C., S. W. Calhoun, L. L. Clepper, M. E. Schmidt, J. H. Williamson, and G. J. Carmichael. 1991. Multi-species hybridization among native and introduced centrarchid basses in central Texas. *Transactions of the American Fisheries Society* 120:283–289.
- Müller, K. 1954. Investigations on the organic drift in North Swedish streams. *Reports of the Institute of Freshwater Research Drottningholm* 34:133–148.
- National Drought Mitigation Center, United States Department of Agriculture, and National Oceanic and Atmospheric Administration. 2016. United States Drought Monitor. National Drought Mitigation Center, Lincoln, Nebraska. Available: <http://droughtmonitor.unl.edu/>. (September 2018).
- Novinger, D. C., and F. J. Rahel. 2003. Isolation management with artificial barriers as a conservation strategy for Cutthroat Trout in headwater streams. *Conservation Biology* 17:772–781.
- Perkin, J. S., Z. R. Shattuck, P. T. Bean, and T. H. Bonner. 2010. Movement and microhabitat associations of Guadalupe Bass in two Texas rivers. *North American Journal of Fisheries Management* 30:33–46.
- Pritchard, J. K., M. Stephens, and P. Donnelly. 2000. Inference of population structure using multilocus genotype data. *Genetics* 155:945–959.
- Raeymaekers, J. A. M., D. Raeymaekers, I. Koizumi, S. Geldof, F.A.M. Volckaert. 2009. Guidelines for restoring connectivity around water mills: a population genetic approach to the management of riverine fish. *Journal of Applied Ecology* 46:562–571.
- Rinne, N. and P. R. Turner. 1991. Reclamation and alteration as management techniques, and a review of methodology in stream renovation. Pages 219–246 in W. L. Minckley and J. E. Deacon, editors. *Battle against extinction: native fish management in the American west*. University of Arizona Press, Tucson, Arizona.
- Seyoum, S., B. L. Barthel, M. D. Tringali, M. C. Davis, S. L. Schmitt, P. S. Bellotti, and W. F. Porak. 2013. Isolation and characterization of eighteen microsatellite loci for the Largemouth Bass, *Micropterus salmoides*, and cross amplification in congeneric species. *Conservation Genetics Resources* 5:697–701.
- Shepard, B. B., L. M. Nelson, M. L. Taper, and A. V. Zale. 2014. Factors influencing successful eradication of nonnative Brook Trout

- from four small Rock Mountain streams using electrofishing. *North American Journal of Fisheries Management* 34:988–997.
- Slade, R. M., Jr., J. T. Bentley, and D. Michaud. 2002. Results of streamflow gain-loss studies in Texas, with emphasis on gains from and losses to major and minor aquifers. United States Geological Survey open-file report 02–068. Available: <https://pubs.usgs.gov/of/2002/ofr02-068/>. (September 2018).
- Texas Game and Fish Commission. 1957. Basic survey and inventory of fish species present, as well their distribution in the Blanco River, its tributaries and watershed lying within Blanco, Kendall and Hays counties, Texas. Project No. F9R3, Job B-10.
- Texas Parks and Wildlife Department. 2012. Texas Conservation Action Plan 2012–2016: Overview. Wendy Connally, editor. Texas Parks and Wildlife Department, Austin, Texas. Available: <http://tpwd.texas.gov/landwater/land/tcap/handbooks.phtml>. (September 2018).
- Texas State Historical Association. 2016. Description of the Narrows (Hays County). Available: <https://tshaonline.org/handbook/online/articles/rnn18>. (September 2018).
- The Nature Conservancy. 2016. Blanco River project. Available: <http://www.nature.org/ourinitiatives/regions/northamerica/united-states/texas/placesweprotect/blanco-river-project.xml>. (September 2018).
- Thomas, Z. A., T. L. Arsuffi, and S. J. Magnelia. 2015. Fishing warmwater streams with limited public access: angling behavior, economic impact, and the role of Guadalupe Bass in a twenty-four county region of Texas. Pages 123–137 *in* M. D. Tringali, J. M. Long, T. M. Birdsong, and M. J. Allen, editors. Black bass diversity: multidisciplinary science for conservation. American Fisheries Society, Symposium 82, Bethesda, Maryland.
- United States Geological Survey. 2016. U.S. Geological Survey response to flooding in Texas, May–June 2015. Available: <https://pubs.usgs.gov/fs/2016/3027/fs20163027.pdf>. (September 2018).
- Waters, T. F. 1972. The drift of stream insects. *Annual Reviews of Entomology* 17:253–272.
- Wierman D. A., Broun A. S., and B. B. Hunt. 2010. Hydrogeologic atlas of the hill country Trinity Aquifer, Blanco, Hays, and Travis counties, central Texas: prepared by the Hays-Trinity, Barton Springs/Edwards Aquifer, and Blanco Pedernales Groundwater Conservation Districts. Available: <https://repositories.lib.utexas.edu/handle/2152/8977>. (September 2018).
- Winters, K. E. 2013. A historical perspective on precipitation, drought severity, and streamflow in Texas during 1951–56 and 2011: U.S. Geological Survey scientific investigations report 2013–5113. Available: <http://pubs.usgs.gov/sir/2013/5113/>. (September 2018).