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Species Richness, Distribution, and Relative Abundance of Freshwater Mussels (Bivalvia: Unionidae) of the Buffalo National River, Arkansas

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Abstract

The Buffalo River in north-central Arkansas is approximately 246 km long and flows through the Boston Mountains and Springfield and Salem Plateaus to the White River near Buffalo City. The Buffalo River is America's first National River with the National Park Service owning 11% of land in the watershed. The objectives of this project were to survey the entire perennially wet length of river, search for mussels of conservation concern, and document the freshwater mussel assemblages. During 2004 and 2005, 235 km of the river were qualitatively and quantitatively surveyed. We documented 64 mussel assemblages. Time constrained qualitatively sampled assemblages (n=41) resulted in a mean richness of 7.8 with a range of 2 to 12 species. Quantitatively sampled mussel assemblages (n=23) had a mean richness of 9.5, ranging from 4 to 16 species and a mean density of 6.9 individuals/m^2, ranging from 1.3 to 25.6 individuals/m^2. Detrended correspondence analysis revealed 4 distinct community types dominated by: 1) *Ptychobranchus occidentalis* (Conrad 1836)*, 2) Villosa iris* (Lea 1829)*,* 3) *Cyclonaias tuberculata* (Rafinesque 1820), and 4) *Actinonaias ligamentina* (Lamarck 1819) that represented approximate species gradients along the river's length. Previous surveys collectively recorded a total of 26 species for the river, however; only 23 species were identified in this survey with no federally listed threatened or endangered species found. The Buffalo National River has a moderately diverse and abundant native freshwater mussel fauna. Seventy-eight percent of the current species are considered to be of conservation concern (S1-S3). Consequently, the Buffalo National River may prove to be an important refuge for a declining mussel resource.

Introduction

Freshwater mussels of the families Unionidae and Margaritiferidae (Mollusca: Bivalvia) are found throughout the world except Antarctica. However, they reach their greatest diversity in North America with over 300 taxa recognized (Williams et al. 1993, Turgeon et al. 1998). Freshwater mussels are America's most threatened faunal group, with greater than 70% being imperiled or extinct (Bogan 1993, Williams et al. 1993, Bogan 1997, Vaughn and Taylor 1999, Lydeard et al. 2004, Strayer et al. 2004).

The reasons for such drastic declines in both richness and abundance vary, however, most explanations involve anthropogenic habitat degradation (e.g., impoundments, river channelization, exotic species introductions, bank erosion, etc.) (Williams et al. 1993, Watters 1996, Ricciardi et al. 1998, Brim Box and Mossa 1999, Vaughn and Taylor 1999, Anthony and Downing 2001, Strayer et al. 2004). Exotic species such as Asian clam (*Corbicula fluminea* (Muller 1774)) or zebra mussel (*Dreissena polymorpha* (Pallas 1771)) may negatively impact native bivalves in many ways such as: resource competition (space and seston), ingestion of sperm, glochidia, or freshly sloughed juveniles (Strayer 1999a). Reservoirs alter both the impounded area and the downstream habitat. Within the impounded area of the reservoir, shallow riffle/run habitats (with which mussels are often associated) are inundated eliminating host fish spawning habitats, increasing sedimentation, and interfering with host fish infestation strategies (Brim-Box and Mossa. 1999). Meanwhile, the dam itself has been shown to be a barrier to host fish migration (Watters 1996). Vaughn and Taylor (1999) documented a gradient of unionid extirpation below reservoirs with a gradual linear increase in richness and abundance downstream of the dam. Similar findings occurred at confluences of tributaries containing reservoir tail water, where abundances were greatly diminished compared to upstream of the confluence. River channelization creates many problems such as increased sedimentation, bank destabilization, and incision of the riverbed upstream of the channelization (Statzner et al. 1988, Newson and Newson 2000). In

agricultural areas, locations with higher topographic relief are correlated with decreasing mussel density and species richness due to increased erosion and river destabilization (Arbuckle and Downing 2002).

The Buffalo River is a free flowing river located in north-central Arkansas that is famous for recreational hiking, canoeing, and camping. The river originates within the Boston Mountains, passes through both the Springfield and Salem Plateaus, and flows approximately 241 river kilometers (rkm) through the Ozark uplift until it joins the White River near Buffalo City, Arkansas (Figure 1), approximately 45 rkm downstream of Bull Shoals Reservoir and 20 rkm upstream of the confluence of the tailwaters of the Norfork Reservoir with the White River. The Buffalo River watershed is approximately 3,427 km^2 with ownership 60% private and 40% public. The National Park Service owns a 212 km-long corridor along the main channel encompassing 11% of the watershed. Remaining public lands within the watershed are divided between the Ozark National Forest (26%) and the Arkansas Game and Fish Commission (3%) (Moix and Galloway 2004). Within this watershed, private land use is primarily agricultural, consisting mostly of logging and cattle grazing.

The freshwater mussel resources of the Buffalo River were first documented by Meek and Clark in 1910 when they searched approximately 161 rkm downstream from what is now Arkansas Highway 7 (Meek and Clark 1912). They identified 26 freshwater mussel assemblages and a total of 22 species. A water quality survey in the 1970's only listed bivalves (Babcock and MacDonald 1973). A unionacean checklist for the state of Arkansas (Gordon et al. 1979) listed 26 species occurring in the Buffalo River. In the mid 1990s, Harris (1996) checked the status of the 26 assemblages originally identified by Meek and Clark (1912). While Harris (1996) sampled 41 sites, the exact locations of the Meek and Clark (1912) assemblages were not known and hindered direct comparisons. Harris (1996) provided a list of 20 sites that may correspond to 15 of the original 26 mussel assemblages.

Harris (1996) also documented 2 species not previously recorded by Meek and Clark for the Buffalo River: *Fusconaia flava* (Rafinesque 1820) and *Ptychobranchus occidentalis* (Conrad 1836). Harris (1996) attributed these species additions to possible misidentifications and taxonomic "lumping" with other species (*Pleurobema sintoxia* (Rafinesque 1820) and *Elliptio dilatata* (Rafinesque 1820), respectively) by Meek and Clark.

Harris (1996) did not observe 3 species previously documented by Meek and Clark (1912): *Lampsilis siliquoidea* (Barnes 1823), *Potamilus purpuratus* (Lamarck 1819), and *Ligumia recta* (Lamarck 1819). Harris (1996) attributed the lack of observing *L. siliquoidea* to it being generally an uncommon species in the White River drainage. He suspected that the latter 2 species might be extirpated from the drainage due to the formation of Bull Shoals and Norfork Reservoir dams and the subsequent limitation of fish host migration into the Buffalo River due to the thermal barrier created by the tailwater release from the dams on the White River. These studies resulted in a combined tally of 26 species, but left approximately one third of the river, the portion upstream of Arkansas Highway 7, unsurveyed.

In this paper, we discuss the results of a 2 year qualitative and quantitative survey of the native freshwater mussel resources of the Buffalo National River with implications for future long-term monitoring. During the survey process, we documented the status of the 41 Harris (1996) sites, the 2 species believed to be extirpated (*Ligumia recta* (Lamarck 1819) and *Potamilus purpuratus* (Lamarck 1819)), and federally protected endangered and threatened taxa.

Materials and Methods

Qualitative Survey

The main stem of the Buffalo River was qualitatively and quantitatively surveyed from Dixon Ford in the Ozark National Forest to the confluence with the White River near Buffalo City from June through August in 2004 and 2005 (Figure 1). Qualitative sampling was performed in areas where mussel assemblages were not historically known and consisted of time-constrained walking visual, snorkeling, or diving searches, which have been shown to maximize species richness determinations while remaining cost effective (Strayer et al. 1997, Vaughn et al. 1997, Strayer and Smith 2003). The mussel assemblages were typically searched for a total of 1 person-hour (e.g., 2 searchers for 30 minutes or 3 searchers for 20 minutes, etc.). All individuals were identified to species following Turgeon et al. (1998), and voucher specimens were curated in the Arkansas State University Museum of Zoology, Unionoida Collection. After the timed search, species, relative abundance, location of assemblage (7.5 minute USGS quadrangle maps), and GPS coordinates were recorded for each sampling reach. Site codes were assigned using river kilometer

(rkm) number (upstream from mouth) on National Geographic maps of the Buffalo National River.

Quantitative Survey

Quantitative sampling was performed in the summers of 2004 and 2005 at sites where mussel assemblages were identified from Harris' (1996) previous survey and followed a stratified random quadrat sampling design (Christian and Harris 2005). The physical extent of each mussel assemblage was visually (via snorkeling) determined, using a minimum criteria of 1 mussel/m^2 mean, and demarcated with weighted string buoys. When appropriate, assemblages were stratified based on differences in substrate composition, river morphology, or assemblage shape. In order to maximize species

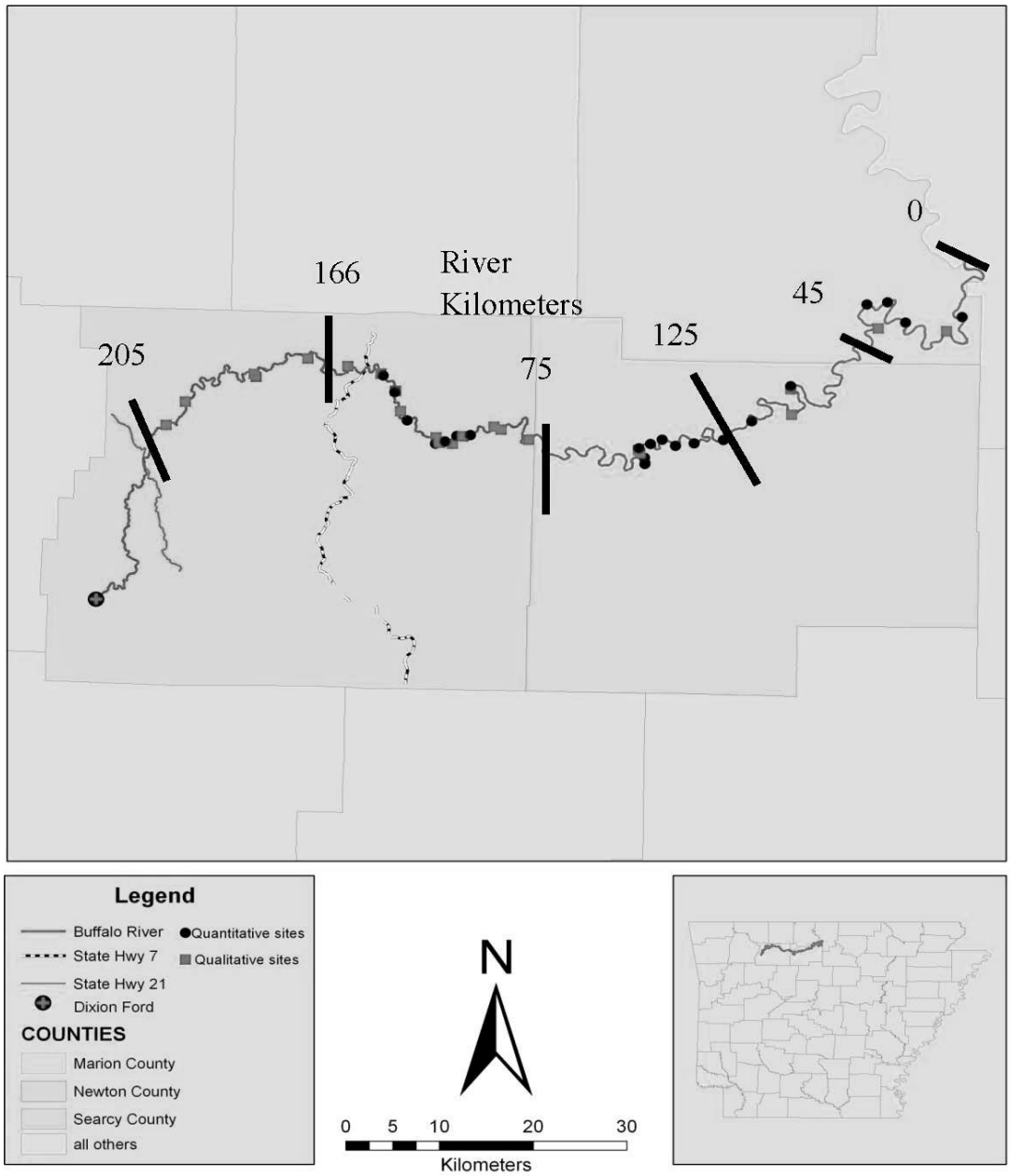

Figure 1. Buffalo National River located in north central Arkansas and flowing through Newton, Searcy and Marion Counties, Arkansas with State Highways 21 and 7 indicated. Qualitative sampling sites indicated by red squares and quantitative sampling sites indicated by black circles.

richness and abundance estimates, assemblage sampling was based on 10% of total area, with a minimum of 15 and a maximum of 25 1-m^2 quadrats (Christian and Harris 2005). Once the number of total samples was determined, samples were divided proportionally among strata based on stratum area to total area (e.g., Stratum 1 is 20% of total area, it receives 20% of the number of samples) with a minimum of 3 samples per stratum.

Quadrat sample sites were obtained from a random numbers table and applied in an X, Y coordinate style. Mussels within a 1-m^2 quadrat (constructed of 2.5 cm diameter weighted PVC pipe) were collected by excavating the substrate to a depth of 10-15 cm, and visually or tactily searching through the substrate. Mussels were placed in a mesh bag and taken to the surface where they were identified, weighed, measured (length, width, and height), and then returned to the site of collection.

Summary statistics for quantitatively sampled mussel assemblages included mean assemblage areas, mean richness, densities (individuals m^{-2}), and sample variances and standard deviations for individual species and quadrats. We calculated species population estimates and assemblage total community numeric standing crop (CNSC) using the equation summarized below (Sampford 1962). The total number of individuals for an assemblage is:

$$\left(X = \sum_{o}^{i} y_i * g_i\right)$$

where x is the total number of mussels in an assemblage, i is the number of strata, y_i is the sample total (total individuals collected), and g_i is the raising factor ($g_i = 1/f_i$, where f_i is the fraction sampled and is defined by n_i/N_i with n_i being the number of sample units counted in the ith stratum, and N_i being the total potential number of sampling units in the ith stratum).

Ninety five percent confidence intervals (95% CI) were calculated using:

$$\left(X = \left[t * \sqrt{\sum_{o}^{i} N_i\, 2 * S^2\, y_i} * \frac{1 - f_i}{n_t}\right]\right)$$

where $S^2 y_i$ is the sample variance from counts in the n_i sampling units in the ith stratum and t is the student's t for effective degrees of freedom.

Sampling efficiency of the quantitative sampling was assessed using 2 methods. One described by Southwood (1978) is represented by:

$$(n = (s \div (Ex))\ 2$$

where n = sample size, s = standard deviation, E = standard error as a decimal and x = mean richness or density. The second, reported by Downing and Downing (1992), is represented by:

$$(n = m^{0.5} D^2)$$

where m is the mean density and D is SE/m where SE is the standard error of the samples. Both of these formulas were used to determine the number of quadrat samples needed to estimate mean species richness and mean density with 80% and 90% confidence limits.

Sampling efficiency was also assessed as our ability to sample all species within an assemblage by comparing our species richness to first and second order Jackknife estimates using PC-ORD software (McCune and Mefford 1999) where:

$$\left(Jack1 = S + rl\frac{n-1}{n}\right)$$

where S = the observed number of species, rl the number of species occurring in 1 sample unit, and n = the number of sample units and

$$\left(Jack2 = S + \frac{rl(2n-3)}{n} - \frac{r2(n-2)}{n(n-1)}\right)$$

Community Structure Analysis

Both quantitative and qualitative data were used to determine community structure. Data was standardized between the 2 datasets by converting the species by site data matrix into relative abundance (percent of assemblage) data. Classification of mussel communities along the river continuum was conducted using detrended correspondence analysis (DCA). The analysis consisted of two matrices: the primary matrix is a site by species table using percent of the assemblage; the secondary matrix was site by approximate river km. These matrices were imported into the statistical software PC-Ord (McCune and Mefford 1999). After the initial eigen values were acquired, biplots for species making up at least 5% of the total mussels collected were examined to determine site clustering.

Results

During 2004 and 2005, a total of 235 rkm was qualitatively and quantitatively surveyed with 33 qualitative and 23 quantitative sites sampled within the

main stem of the Buffalo River (Figure 1). A total of 2195 individuals and 22 species were recorded during the qualitative surveys (Table 1). Mean species richness of qualitative surveys was 7.8 with a range of 2 to 11, and the mean number of individuals sampled per site was 65.8 with a range of 5 to 305 for the 33 sites (Table 1). Catch per unit effort (CPUE) per site averaged 58.3 and ranged from 10 to 206/hr. An additional site was qualitatively sampled on the tributary Cave Creek, resulting in a total of 25 individuals and 4 species.

For the 2004 and 2005 quantitative sampling, 23 of Harris' original 41 sites were quantitatively sampled, while 3 were qualitatively sampled. The remaining 15 Harris sites were not sampled due to various reasons. Of the 23 assemblages that were quantitatively sampled, mean area was 277 m^2 with a range of 54 to 840 m^2 (Table 2)

Mean species richness was 9.2 with a range of 4 to 15. Densities ranged from 1.3 to 25.5 individuals/m^2 with a mean of 6.9. Mean community numeric standing crop estimate was 2088 individuals per assemblage with a range of 115 to 9118.

A combined total of 3180 individuals were sampled quantitatively and qualitatively in 2004 and 2005, with 6 species comprising 89% of the total (Table 3). *Ptychobranchus occidentalis* (Conrad 1836) was the dominant species comprising 29.8% of the total. *Lampsilis reeveiana* (Call 1887), *Fusconaia ozarkensis* (Call 1887), *Actinonaias ligamentina* (Lamarck 1819), *Venustaconcha pleasii* (Marsh 1891), and *Villosa iris* (Lea 1829) comprised the remainder of the 89% (17.8%, 9.9%, 9.2%, 7.2%, and 6.6%, respectively).

Community Structure

The DCA output resulted in eigen values of 0.368 for Axis 1 and 0.274 for Axis 2, thus explaining a combined 64.2% of the overall variation of the dataset (Figure 2). Analysis of the DCA species biplots revealed 4 distinct community types dominated by 1) *Villosa iris* (Axis 1: τ*=-0.05; Axis 2:* τ*=0.47)*, *2) Ptychobranchus occidentalis* (Axis 1: τ*=-0.61; Axis 2:* τ*=-0.14), 3) Actinonaias ligamentina* (Axis 1: τ*=0.48; Axis 2:* τ*=-0.26)*, and 4) *Cyclonaias tuberculata* (Axis 1: τ*=0.16; Axis 2:* τ*=-0.56)* that represent approximate species gradients along the river length (Figures 3- 4). *Lampsilis reeveiana*, the second most abundant species, was not associated with a community type as it was distributed along the entire length of the river.

Discussion

Distribution data for freshwater mussels of the Buffalo National River has been expanded by an additional 72 rkms, resulting in 7 more mussel containing sites being documented. A previously undocumented species, *Epioblasma triquetra* (Rafinesque 1820), state ranked S1, was recorded for the Buffalo River.

Abundance and Species Richness

Unionid diversity has been shown to increase with drainage area size (Watters 1992). The Buffalo River (drainage area ~3,427 km^2) exhibits a lower unionid diversity (taxa richness of 23) compared to other streams of the Ozarks. For example, the Spring River Arkansas, which has a drainage area of ~3186 km^2, has a taxa richness of 28 (U.S. Department of Agriculture 1999, Trauth et al. 2007) and the South Fork of the Spring River has a species richness of 22 (Martin 2008). Meanwhile, historical accounts of the Little Black River, Missouri, which has a smaller drainage are of ~650 km^2, report a historical taxa richness of 32 and modern richness of 21 species (Bruenderman et al. 2001).

However, in terms of abundance, the Buffalo River has a rather abundant mussel assemblages compared to other Ozark rivers; the mean CPUE of the Buffalo River is 66 individuals/hr as compared to 7 individuals/hr in the Little Black River (Bruenderman et al. 2001). The Buffalo River's CNSC estimates, ranging from 115 to 9118 individuals, were similar to those for the Spring River (Rust 1993) that ranged from 288 to 9883 individuals.

Historical Comparisons

Harris' (1996) survey reported 5 species that comprised 82% of the total; listed in descending order of abundance they were *Actinonaias ligamentina, Amblema plicata, Ptychobranchus occidentalis, Lampsilis reeveiana,* and *Cyclonaias tuberculata.* We found 6 species that comprised 80% of the total with the descending order of abundance being *Ptychobranchus occidentalis*, *Lampsilis reeveiana, Fusconaia ozarkensis, Actinonaias ligamentina*, *Venustaconcha pleasii,* and *Villosa iris*.

This apparent assemblage structure shift may have several explanations. First, Harris' (1996) sampling design was qualitative in nature, while the present study is a combination of qualitative and quantitative sampling design. Much work has taken place to determine differences, effectiveness, and similarities of

Table 1. River kilometer site code, species sampled, species richness, and total number of individuals for the 2004 and 2005 Buffalo River qualitative mussel survey sites

Site	Taxon											
	Actinonaias ligamentina	*Alasmidonta marginata*	*Amblema plicata*	*Cyclonaias tuberculata*	*Cyprogenia aberti*	*Elliptio dilatata*	*Fusconaia flava*	*Fusconaia ozarkensis*	*Lampsilis cardium*	*Lampsilis reeveiana*	*Lampsilis siliquoidea*	*Lasmigona costata*
204.3										1		1
182.6			1					125		11	1	2
182.5								24		11		
199.9								1		3		
178.1	1							4	1	25		
174.1	4	1	26					10	3		5	5
166.1								8		10		
162.3	1									6		3
162.2	1		1					2		8		
160.1										3		
159.6	1					2		2		14		
158.9	2					1				5		
156.7				6		15		1		6		
146.4					1	1		1		16		1
146.4	3		2						1	5		1
146.4	1		2					2	1	4		
145.9	20		13	1					1	5		2
145.5				1	1	20		3		22		
144.0	3			6		3	1			17		1
142.3	6			9		17		3		32		
138.2	9			4		9		1	1	8		
136.9	7			2		44		7		24		
137.9				1		8		1		20		
129.1	7		1	4					2	6		3
103.8	2			2		7		6		16		
102.8	1		1	17			4	4	1	20		1
91.6	8		1	3				3	1	10		
79.5	2							2	2	31		1
71.8	18		1	2		1		8		23		3
67.3	5		2	1				11		4		1
66.9	71		2	38		2		21		26		23
66.8	20		4	2		1	1			8		13
17.5	9			13		6		10	1	41		
CAVE CR								1				
TOTAL	202	1	57	112	2	137	6	261	15	441	6	61

Table 1 continued.

Site	Taxon *Pleurobema sintoxia*	*Potamilus purpuratus*	*Ptychobranchus occidentalis*	*Quadrula cylindrica*	*Strophitus undulatus*	*Toxolasma lividus*	*Tritogonia verrucosa*	*Venustaconcha pleasii*	*Villosa iris*	*Villosa lienosa*	Taxa	Total
204.3									7	4	4	13
182.6	4		158							3	8	305
182.5			7			1			2	2	6	47
199.9			5						9	17	5	35
178.1			1					5	9	1	8	47
174.1	8					3					9	65
166.1									2	1	4	21
162.3			5					4			5	19
162.2			3	3					2		7	20
160.1			2								2	5
159.6			15			1		2	5		8	42
158.9			1					4	4		6	17
156.7			25					4	5		7	62
146.4			79					10	2		8	111
146.4									1	1	7	14
146.4			3						3	2	8	18
145.9			1					1			8	44
145.5			123					7	1		8	178
144.0			7		8			1	2		10	49
142.3	3		29		1	1		15	6		11	122
138.2			3					1			8	36
136.9			37		2			1	2		9	126
137.9			22					15			6	67
129.1			12								7	35
103.8			4				3	2	5		9	47
102.8			7				1	4			11	61
91.6	2	6	8				1		2		11	47
79.5								4	9		7	59
71.8			1					6	1		10	64
67.3			2								7	26
66.9			10				1	1	11		11	206
66.8			1	1					2		10	53
17.5	1		17						11		9	109
CAVE CR			20					3	1		4	25
TOTAL	18	6	608	4	11	6	6	90	104	31	22	2195

Table 2. The 2004 and 2005 river kilometer code, assemblage area, species richness, average density (# / m^2), and community numeric standing crop estimates (CNSC) ± 95% confidence intervals (CI) for the 2004 and 2005 quantitative mussel survey sites data for the Buffalo River.

Taxon	162.0	161.1	160.1	159.6	158.9	156.7	154.8	154.5	152.1	105.2	104.3	102.8	100.7
A. ligamentina	1	2			9	2	4		3	3	2	8	3
A. marginata									1				
A. plicata		1				4	2		2			1	16
C. tuberculata				3	2	1	14	9	2			4	10
C. aberti									1				
E. dilatata	2		1	9	11	1	24	43	29			2	30
F. flava													7
F. ozarkensis		4		2	5	4	10	1	4		3	7	8
L. cardium	1						3			1			
L. reeveiana	5	13	12	7	24	17	32	6	15	10	16	22	10
L. siliquoidea													
L. costata					3	1	1					3	
P. sintoxia	2	1	1		2		9	1		1			
P. purpuratus													
P. occidentalis	12	8	57	38	17	21	96	59	365	25		3	9
Q. cylindrica	6												
S. undulatus							24		2				
T. lividus					1	1							
T. verrucosa		1											
V. pleasii	8	39	16	1	34	7	35	4	6	1	7	6	2
V. iris	7	27		1	39	35	1	1	4	2	4	35	
V. lienosa	2												
area ($m^{2)}$	78	160	120	60	192	180	420	300	210	84	54	540	796
Taxa richness	10	9	5	7	11	11	13	8	12	7	5	10	9
Total	46	96	87	61	147	94	255	124	434	43	32	91	95
mean density	3.1	6.4	7.3	10.2	7.8	5.9	10.6	5	17.4	3.9	2.1	3.6	5.6
CNSC (± 95% CI)	239 ±82	1024 ±334	870 ±376	610 ±149	1506 ±299	940 ±282	4284 ±1221	1488 ±606	3654 ±1404	322 ±180	115 ±121	1966 ±724	4546 ±1243

Table 2 continued.

Taxon	98.6	96.9	93.7	86.7	82.9	66.9	42.6	34.6	28.3	10.9
A. ligamentina	1	36		10	5	11	7	88	7	2
A. marginata	8	2						7	1	
A. plicata				3			9	2	1	
C. tuberculata	6	41		4		10	3	32	28	2
C. aberti		1								
E. dilatata	9	10		2					7	
F. flava										
F. ozarkensis	45	52		12	10	10	1	58	12	4
L. cardium	1	1			1			5	1	
L. reeveiana	11	40	20	22	7	19	4	41	27	39
L. siliquoidea										
L. costata		8	1	5		14		32	4	8
P. sintoxia	2	4		1				17	1	
P. purpuratus				1						
P. occidentalis	5	71		3	1	1		82	29	34
Q. cylindrica										
S. undulatus										
T. lividus				3	3			1		
T. verrucosa				1				1		
V. pleasii	29	20	5	4		1		2		
V. iris	9	2	7	17		10			23	5
V. lienosa				1	8					
area (m^2)	81	840	150	668	165	165	175	349	338	257
Taxa richness	11	13	4	15	7	8	5	13	12	7
Total	126	288	33	89	35	76	24	368	141	94
mean density	8.4	11.5	2.2	3.6	2.1	4.5	1.3	25.5	5.5	4.4
CNSC	680	9677	330	2405	340	738	233	9118	1836	1095
(± 95% CI)	±458	±6787	±103	±998	±105	±314	±103	±2986	±511	±1201

Table 3. Total number of individual samples and the percent of total for each species based on combined qualitative and quantitative survey data in 2004 and 2005.

Taxon	Number Collected	Percent
Actinonaias ligamentina	292	9.2
Alasmidonta marginata	12	0.4
Amblema plicata	62	1.9
Cyclonaias tuberculata	77	2.4
Cyprogenia aberti	2	0.1
Elliptio dilatata	187	5.9
Fusconaia flava	12	0.4
Fusconaia ozarkensis	315	9.9
Lampsilis cardium	23	0.7
Lampsilis reeveiana	567	17.8
Lampsilis siliquoidea	6	0.2
Lasmigona costata	120	3.8
Pleurobema sintoxia	47	1.5
Potamilus purpuratus	7	0.2
Ptychobranchus occidentalis	949	29.8
Quadrula cylindrica	7	0.2
Strophitus undulatus	26	0.8
Toxolasma lividus	6	0.2
Tritogonia verrucosa	10	0.3
Venustaconcha pleasii	230	7.2
Villosa iris	211	6.6
Villosa lienosa	12	0.4
Total	3180	99.9

sampling methodologies (Downing and Downing 1992, Miller and Payne 1993, Hornbach and Deneka 1996, Strayer et al. 1997, Vaughn et al. 1997, Obermeyer 1998, Strayer 1999b, Metcalfe-Smith et al. 2000, Strayer and Smith 2003, Smith 2006). These differences in design, as well as the additional 72 rkm surveyed on the upper river may account for the apparent shift in overall river composition. This is especially true of *Ptychobranchus occidentalis* as 1 assemblage, (RK 182.6) located in the additional 72 rkm previously unsurveyed, had the second highest densities for the entire river and was overwhelmingly dominated by *P. occidentalis.* The present survey also more intensely sampled riffle/run habitats compared to previous studies which may explain the increase of *Venustaconcha pleasii* as they are typical of headwaters and use many darter species common in the Buffalo River as their fish host (Barnhart and Roberts 1997, Riusech and Barnhart 2000, Petersen and Justus 2005).

A second plausible explanation may be shifts in host fish abundance and distributions. The apparent increase in *Lampsilis reeveiana* and *Villosa iris* may be attributable to the combination that they are host generalists utilizing members of the sunfish family (Barnhart and Roberts 1997), which are abundant in the Buffalo River (Peterson and Justus 2005). Conversely, *Fusconaia ozarkensis* is reported to parasitize minnows including *Luxilis cardinalis, L. zonatus*, and *Phoxinus eyrthrogaster* (Barnhart and Roberts 1997), and Peterson and Justus (2005) do not list any of these as occurring in the Buffalo River. However, Meek and Clark (1912) reported small fishes "…the more common being *Notropis zonatus*". This may have actually been *Luxilus pilsbryi* as *Luxilus* was later elevated from genus *Notropis* (Robison and Buchanan 1988, Petersen and Justus 2005). *Luxilus pilsbryi* is an endemic to the Interior Highlands, as is *Fusconaia ozarkensis,* and thus may indicate a symbiotic phylogeographic relationship.

Finally, apparent hydrologic instability (e.g., eroding banks, obvious channel movement from 1996 to present, etc.) may have different effects on the life history stages of various species of both host fishes and unionids. Due to long, relatively sedentary life spans, freshwater mussels require areas of the channel capable of withstanding substantial scouring flood events (Strayer 1993b, Di Maio and Corkum 1997, Brim Box and Dorazio 2002, Peck 2005). Fish may be able to handle the shifting sediments over time better than the relatively sedentary unionids.

For the purpose of this study, specific site comparisons were restricted to the more recent Harris (1996) survey due to the lack of exact locality data for Meek and Clark survey stations (Harris 1996). Although the Harris (1996) survey was largely a qualitative survey, "semi-quantitative" sampling was conducted at 6 sites and consisted of 2 or 3 m^2 quadrat samples per site.

At the Harris' BR11, Site RK 156.7 of current study, we found a species richness of 8, compared with the 7 species found by Harris resulting in total site diversity of 9 species. Four of 9 species were observed on both sampling dates, with 3 being observed only in the 1996 survey and 4 only being observed in the current survey. The 3 species observed previously at BR11, but not observed in this survey, included: *Actinonaias ligamentina, Alasmidonta viridis,* and *Cyprogenia aberti*. *Alasmidonta viridis* is a rare species in the Buffalo River, Harris (1996) observed 2 individuals from separate sites. Therefore, *A. viridis*' absence from this site in the current study is not

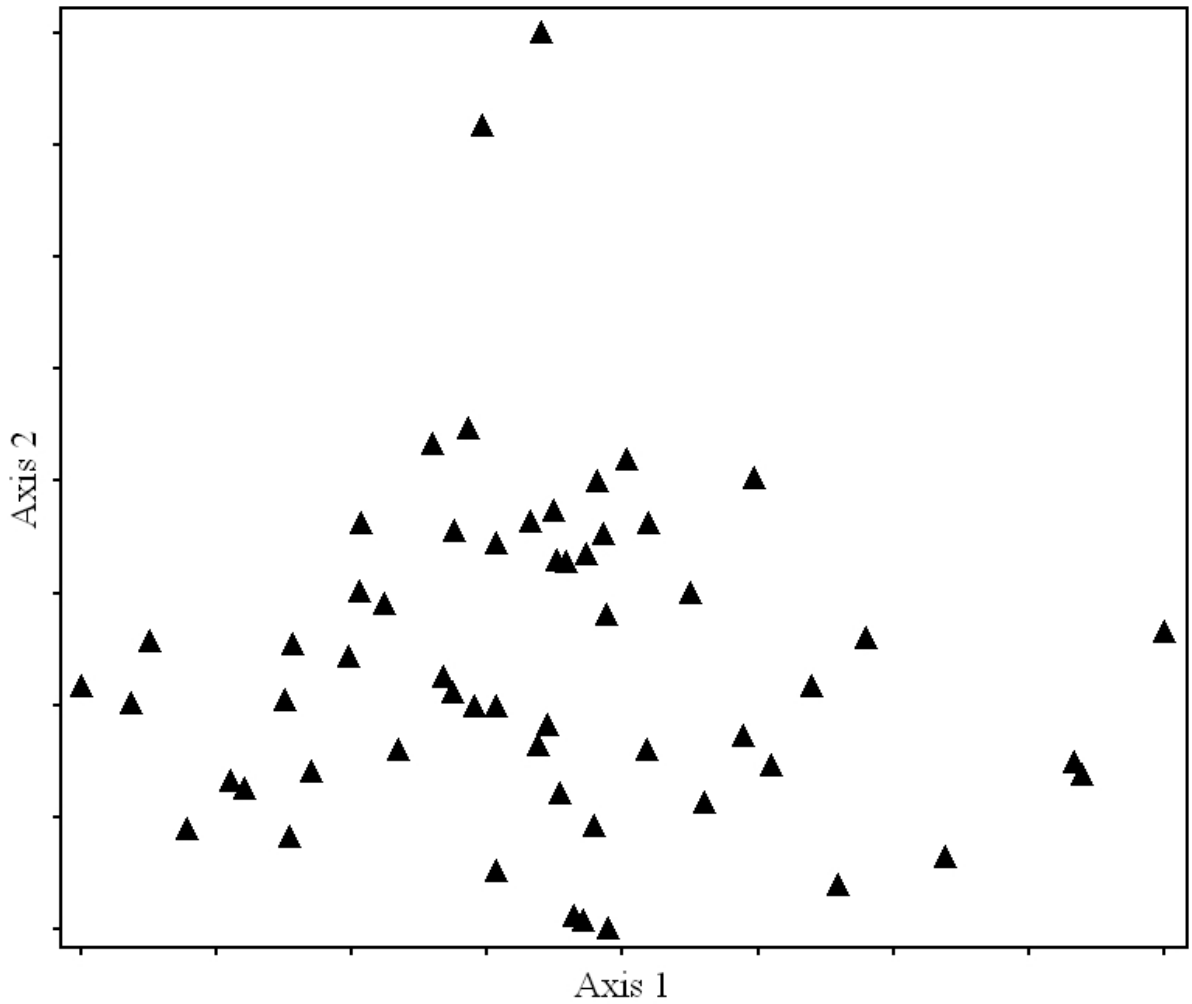

Figure 2. Detrended Correspondence Analysis axes 1 (Eigen value = 0.368) and 2 (Eigen value = 0.274) graph of the 2004 and 2005 Buffalo River qualitative and quantitative freshwater mussel relative abundance survey data. Triangles represent sites.

surprising. *Cyprogenia aberti* is a rare species in the Buffalo River and is rather diminutive in size; both attributes make it difficult to sample using random sampling (Strayer et al. 1997, Strayer and Smith 2003).

However, the absence of *Actinonaias ligamentina* during the present sampling of RK 156.7 is somewhat surprising because it is widespread within the Buffalo National River and because Harris (1996) recorded 8 individuals. The 2 species (*Venustaconcha pleasii* and *Villosa iris*) present during the present sampling, but not in the previous sampling may be a result of the more intensive sampling effort of this survey. The current mean density (5 individuals/m^2) is significantly lower than that of the previous study (28 individuals/m^2); however, this is likely an artifact of differences in the sampling design of the 2 studies, consisting of Harris' maximum density sampling versus our stratified random sampling.

At Harris site BR16, our RK 104.3, we observed a species richness of 5 compared to 7 species documented by Harris. Species composition is quite different, with only 1 (*F. ozarkensis*) of Harris' 7 species being in common with this current sampling. Our average density, 2.1 individuals/m^2, was considerably lower density than the 11.5 individuals/m^2 reported by Harris. The differences in composition and densities are presumably for the same reasons discussed above.

At Harris BR19, our Site RK 100.7, we found a species richness of 9 compared to 8 previously documented species resulting in a total richness of 12. Five of 12 species were observed for both sampling dates, with 3 species only being observed in the 1996 survey and 4 species only being observed in the current

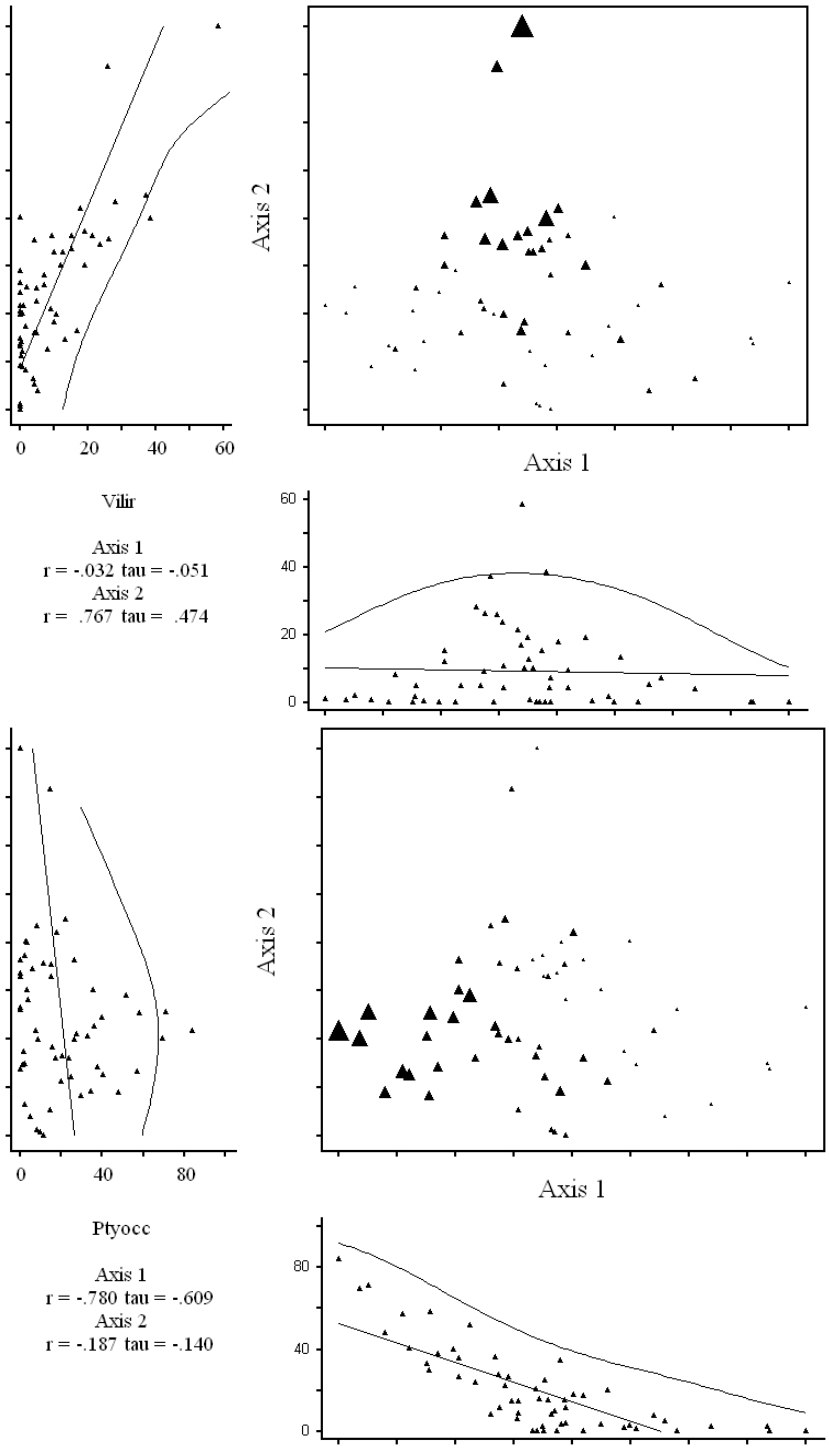

Figure 3. Detrended Correspondence Analysis axes 1 and 2 biplot of *Villosa iris* (top) and *Ptychobranchus occidentalis* (bottom) Buffalo River distribution based on 2004 and 2005 qualitative and quantitative relative abundance data. Size of triangle represents relative weighting and influence of species on a site.

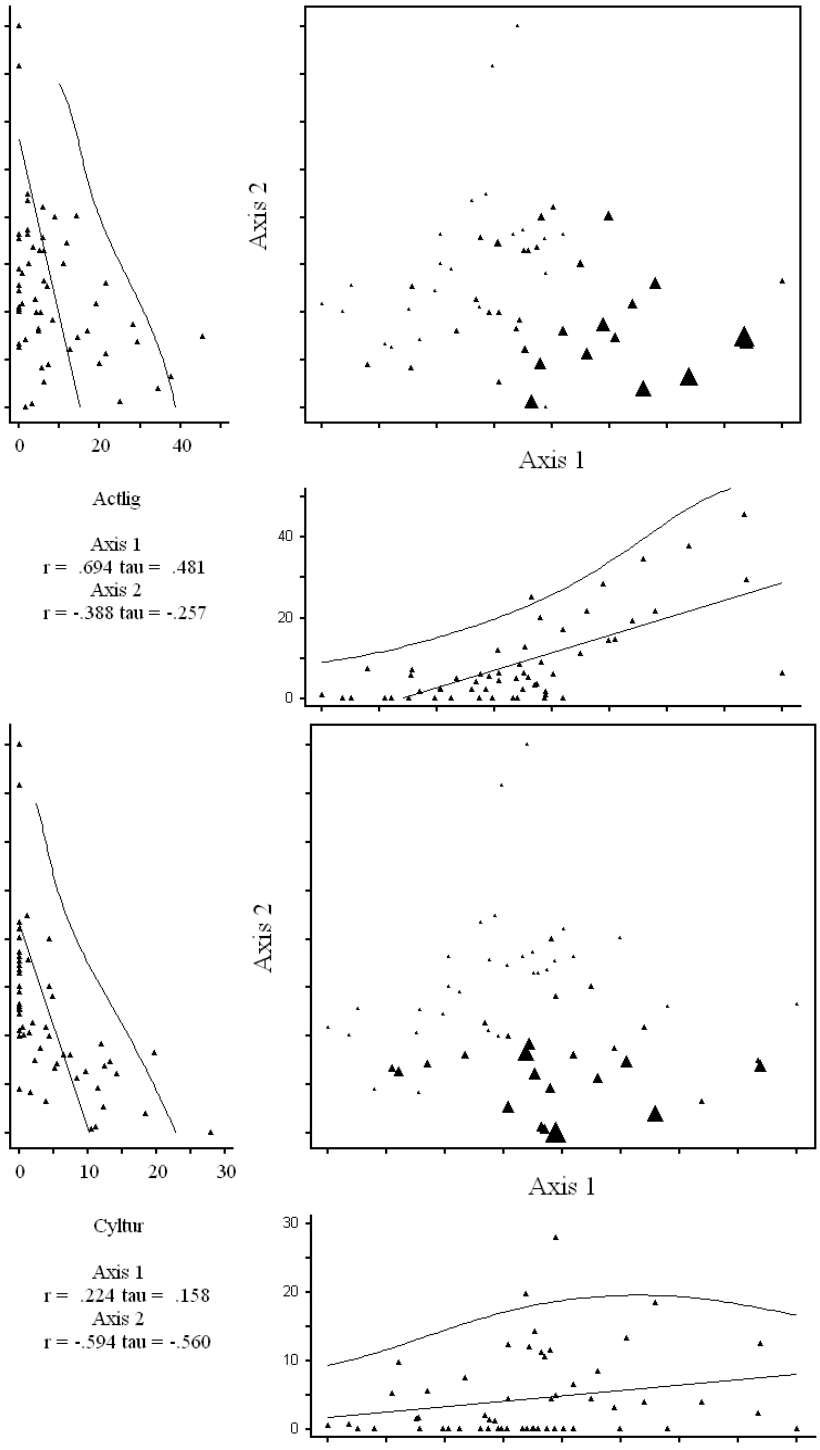

Figure 4. Detrended Correspondence Analysis axes 1 and 2 biplot of *Actinonaias ligamentina* (top) and *Cyclonaias tuberculata* (bottom) Buffalo River distribution based on 2004 and 2005 qualitative and Quantitative relative abundance data. Size of triangle represents relative weighting and influence of species on a site.

survey. The 3 species observed previously, but not currently reported include *Lasmigona costata*, *Quadrula cylindrica* and *Pleurobema sintoxia* and were represented by 1, 2, and 2 individuals, respectively. As with the previous sites, there was a considerably lower average density for the current study compared to Harris' study, 5.6 versus 11.0 individuals/m^2, respectively.

At Site RK 96.9, Harris BR21, we observed 13 species compared 9 species documented Harris. All 9 species previously reported were present in the current study, as well as 4 new species; *Cyprogenia aberti*, *Elliptio dilatata*, *Venustaconcha pleasii* and *Villosa iris*. Unlike the previously discussed sites, our average densities were similar to the Harris's densities, 11.5 individuals/m^2 versus 10 individuals/m^2, respectively. Furthermore, this site was among the highest calculated confidence levels for density estimates at 85% (Southwood 1978).

At Site RK 82.9, Harris BR27, we observed 7 species compared to 5 reported by Harris for a total richness of 10. Two of 10 species were observed for both sampling dates, with 3 species only being observed for the 1996 survey and 5 species only being observed in the current survey. Two species previously observed, but not observed in our study, include *Lasmigona costata* and *Cyclonaias tuberculata*. Harris (1996) observed 3 *C. tuberculata* individuals and 1 *L. costata*. *Amblema plicata* was not recorded in our sampling of this site, but was noted as being present in a low mussel density area (<1/m^2) below the sampled site. Average densities were considerably lower for our sampling compared to Harris, 2.1 versus 8 individuals/m^2, respectively.

At the Harris BR39, our RK 34.6 we observed a species richness of 16 compared to the 10 species of the previous study. The only species of the original 10 not observed in 2005 was *C. aberti*. However, this species was observed when the bed was sampled in 2006 as 1 of the 12 monitoring sites. The current average density of the site was more than double that of the previous survey; 25.5 individuals/m^2 versus 11.7 individuals/m^2, respectively. The increase in density and species richness at this site is not surprising given the sampling differences discussed above and the fact that numerous quadrat samples that had no or few animals present at the surface yielded densities of up to 35 individuals/m^2 and many animals were as deep as 15 cm.

Community Structure

The presence of 4 community types, loosely related to stream position, is consistent with previous studies showing that species are typically added (as opposed to being replaced) on a longitudinal basis (Strayer 1983). There is some overlap within stream position and community type. This fact poses some intriguing questions for requirements of native freshwater mussels (e.g., microhabitat variables, macrohabitat variables, exotic species influences, water quality, etc).

Sampling Assessment

This sampling design (developed for large deltaic blackwater rivers) seems to yield similar efficiency in mid-sized upland stream/rivers. Southwood (1978) sampling confidence levels for density are similar among this study and Cache River as well as the Spring River (Christian and Harris 2005, Trauth et al. 2007). Southwood (1978) sampling confidence levels for species richness were also similar between the large deltaic river and the current study (Christian and Harris, 2005). In order to maximize information and minimize cost this sampling design (sampling 10% of bed, with a minimum of 15 and a maximum of 25 1 m^2 samples) is appropriate for future monitoring. This may be supplemented with timed qualitative searches if data is needed for a particular rare species (e.g., *Epioblasma triquetra*).

Summary and Conclusions

The assemblage types (i.e. *Ptychobranchus occidentalis*, *Villosa iris*, *Cyclonaias tuberculata*, and *Actinonaias ligamentina*) can be linked to fish host distribution data to develop management strategies for this declining resource in addition to the geomorphological data currently being collected. While documentation of habitat requirements for unionids has proven difficult (Strayer 1983, Strayer 1993a, 1993b, Di Maio and Corkum 1995, Downing et al. 2000, Brim Box and Dorazio 2002) hosts are essential to the distribution of mussels. This can be combined with size distribution data from long term monitoring to determine recruitment and relative stability of the community types.

The effects of sampling on mussels are uncertain (Strayer and Smith 2003). These effects could include biological stresses or in the case of this sampling design microhabitat disturbance due to the nature of the excavation. However, this is a part of an ongoing long term monitoring study. Future studies could

include sampling of fish communities to assess suitable host fish relationships at the sites and additional geomorphic monitoring (e.g., after moderate to large flood events). Due to the longevity of freshwater mussels and the unknown effects of sampling mussels an appropriate time frame would be a 5 - 10 year sampling interval.

Future mollusk sampling should include a protocol for the exotic species *Corbicula* in conjunction with the freshwater mussel protocol. Sampling *Corbicula* populations may help determine if their populations are increasing, declining, or remaining stable and could be used to determine if they are influencing freshwater mussel populations. *Corbicula* may negatively impact native bivalves in many ways such as: resource competition (space and seston), ingestion of sperm, glochidia, or freshly sloughed juveniles (Strayer 1999a).

Seventy eight percent of the 23 species currently present in the Buffalo River are of conservation concern (state heritage rankings S1- S3) including 5 (excluding *Actinonaias ligamentina*) of the 6 most abundant species (Table 4). These 5 S1 – S3 species currently have relatively abundant and stable populations in the Buffalo National River. As North American freshwater mollusk decline, areas of large public ownership will become increasingly important as both a refuge for existing populations and potential seed sources for future restoration activities. Thus, the Buffalo National River represents a potential refuge area for mussel diversity and abundance in the Ozark Highlands.

Many federal and state hatcheries have turned to working with freshwater mussels and housing fish during parasitic glochidial life stage and rearing of juveniles. However, given the uncertainty of food resource requirements of both adults and juveniles, in situ rearing allows for greater success and larger individual at the time of release (Andrew J. Peck, unpublished data). Thus, the Buffalo River could also provide an area for the rearing of juvenile mussels as long as sufficient precautions are implemented to assure the genetic integrity of each ecological management unit.

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Table 4. Freshwater mussels of the Buffalo River including scientific name, common name, state heritage rank, global rank, and presence or absence in Meek and Clark (1912), Gordon et al. (1979), Harris (1996), and the present study.

Scientific Name	Common Name	State Rank	Global Rank	Meek and Clark (1912)	Gordon et al. (1979)	Harris (1996)	Present Study
Actinonaias ligamentina (Lamarck 1819)	Mucket	S5	G5	+	+	+	+
Alasmidonta marginata (Say 1818)	Elktoe	S3	G4	+	+	+	+
Alasmidonta viridis (Rafinesque 1820)	Slippershell mussel	S1	G4/G5	+	+	+	
Amblema plicata (Say 1817)	Threeridge	S5	G5	+	+	+	+
Cyclonaias tuberculata (Rafinesque 1820)	Purple wartyback	S3	G5	+	+	+	+
Cyprogenia aberti (Conrad 1850)	Western fanshell	S2	G2	+	+	+	+
Elliptio dilatata (Rafinesque 1820)	Spike	S4	G5	+	+	+	+
*Epioblasma triquetra** (Rafinesque 1820)	Snuffbox	S1	G3				+
Fusconaia flava (Rafinesque 1820)	Wabash pigtoe	S4	G5		+	+	+
Fusconaia ozarkensis (Call 1887)	Ozark pigtoe	S3	G3	+	+	+	+
Lampsilis cardium (Rafinesque 1820)	Plain pocketbook	S4	G5	+	+	+	+
Lampsilis reeveiana (Call 1887)	Arkansas brokenray	S3	G3	+	+	+	+
Lampsilis siliquoidea (Barnes 1823)	Fatmucket	S3	G5	+	+		+
Lasmigona costata (Rafinesque 1820)	Fluted shell	S3	G5	+	+	+	+
Ligumia recta (Lamarck 1819)	Black sandshell	S2	G5	+	+		
Ligumia subrostrata (Say 1831)	Pond mussel	S4	G4/G5		+		
Pleurobema sintoxia (Rafinesque 1820)	Round pigtoe	S3	G4	+	+	+	+
Potamilus purpuratus (Lamarck 1819)	Bleufer	S4	G5	+	+		+
Ptychobranchus occidentalis (Conrad 1836)	Ouachita kidneyshell	S3	G3/G4		+	+	+
Quadrula cylindrica (Say 1817)	Rabbitsfoot	S2	G3	+	+	+	+
Quadrula pustulosa (Lea, 1831)	Pimpleback	S5	G5		+		
Strophitus undulatus (Say 1817)	Creeper	S3	G5	+	+	+	+
Toxolasma lividus (Rafinesque 1831)	Purple lilliput	S2	G2	+	+	+	+
Toxolasma parvus (Barnes 1823)	Liliput	S4	G5		+		+
Tritogonia verrucosa (Rafinesque 1820)	Pistolgrip	S4	G4/G5	+	+	+	+
*Utterbackia imbecillis*** (Say 1829)	Paper pondshell	S3/S4	G5				+
Venustaconcha pleasii (Marsh 1891)	Bleedingtooth mussel	S3	G3/G4	+	+	+	+
Villosa iris (Lea, 1829)	Rainbow	S2/S3	G5	+	+	+	+
Villosa lienosa (Conrad 1834)	Little spectacle case	S3	G5	+	+	+	+

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