

A Comparative Study of the Ichthyofauna in Selected Streams on the Salt Plains National Wildlife Refuge in Oklahoma

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This paper lists fishes and their abundances in seine collections from streams of the Salt Plains National Wildlife Refuge (SPNWR) in Oklahoma. We collected a total of 15 species and one hybrid. Dominant species included the cyprinids *Cyprinella lutrensis*, *Hybognathus placitus*, *Notropis atherinoides*, and the atherinid *Menidia beryllina*. Shannon-Wiener diversity (H') and evenness measures for sites located in upstream reaches were typically higher than those for downstream sites on the same streams. Faunal similarity between pairs of sites was typically higher for comparisons involving downstream sites than for those involving upstream sites. Loglinear analyses revealed significant heterogeneity among streams in overall abundances of fishes and distributions of individual species between upstream versus downstream localities. Although our data do not afford insight regarding temporal variation in SPNWR stream fish communities, we suggest that the substantial spatial heterogeneity revealed in this study may be of considerable importance in determining habitat suitability and nesting success for piscivorous shorebirds including the endangered least tern.

INTRODUCTION

Plains-stream fish communities are typically depauperate in terms of species richness. Variation in abiotic factors such as salinity, temperature, and seasonal changes in stream flow likely represent major factors influencing plains-stream fish community structure (1,2). Data from investigations of plains-stream fish communities together with descriptions of the conditions prevailing in specific situations furnish greater understanding of the relative roles of various abiotic factors. This is important in light of the paucity of information regarding factors bearing on plains-stream fishes (3). Moreover, these data should serve as benchmarks for investigations aimed at understanding causes of the added complexity resulting from biotic interactions in upland streams, for example. Another study (4) performed contemporaneously with our study looked specifically at physico-chemical characteristics of the streams studied herein.

Several streams are located on the Salt Plains National Wildlife Refuge (SPNWR) in Alfalfa County, Oklahoma. We are not aware of any published data comparing the fish communities existing in SPNWR streams although there are a number of museum collections (pers. comm., anonymous reviewer). As a preliminary step toward elucidating the factors controlling fish community structure in SPNWR streams we surveyed and describe fish communities in five SPNWR streams. In addition, we describe variation in species abundances among and within the streams using loglinear analyses.

METHODS

Fishes were collected by seine at nine sites on five streams in the western portion of the SPNWR on 18-19 March and 1 April 1995 (Fig. 1). To provide data for comparisons within streams, samples were taken from downstream (adjacent to Great Salt Plains Reservoir) and upstream (reaches in or near headwaters) areas in all streams except Sand Creek, a stream in which we were unable to locate an upstream site far enough removed from Salt Plains Reservoir to warrant sampling. Fishes were collected by vigorous seining for an hour in all habitats within a 200-m longitudinal stretch at each site. Seining began at the upstream end of each site and proceeded downstream. We used a 4×1.2-m seine with 0.5-cm mesh to collect fishes during downstream sweeps through runs and pools or kicksets around structure such as brushpiles, embedded

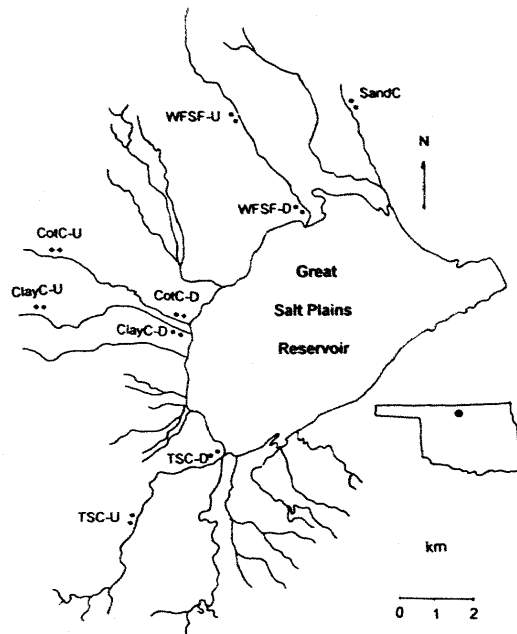


Figure 1. The Salt Plains National Wildlife Refuge showing fish collection sites.

pieces of driftwood, and rocks. Specimens were preserved in 10% formalin for subsequent species identification.

Counts of individuals per species per site were used to calculate Shannon-Wiener diversity values (H'). Pairwise similarity between each of the nine communities surveyed was measured using Morisita's Index I_M (5). To gain fuller understanding of the dependence structure between species abundances and collection sites within and among streams, we analyzed data using loglinear analyses provided by the CATMOD procedure in SAS (6). Loglinear analysis is a method of categorical data analysis analogous to analysis of variance for normally distributed data (7). The results of interest from the analysis are interactions involving one or more explanatory variables (streams and sites within streams) and a response (overall number of individuals or number of individuals per species). The observed probability of each interaction was determined using a chi-squared test with $\alpha=0.05$. In most cases, there were substantial numbers of zero counts among species. Therefore, raw counts for each species were increased by 10 to provide non-zero counts required for use with the CATMOD

procedure. Moreover, two species, *Pimephales vigilax* and *Dorosoma cepedianum*, were nearly always absent and were therefore eliminated from the loglinear analysis.

RESULTS and DISCUSSION

Collection Data. The species collected and their abundances at each site are given in Table 1. We collected representatives of 15 species and one hybrid at one or more of the 9 sites; however, a typical site yielded a substantially smaller subset of species. No one species occurred in all sites, although *Menidia beryllina* appeared to be the most widespread species, occurring in all sites except COTC-U and SANDC. *M. beryllina* was dominant in a majority (67%) of samples and its abundance was an order of magnitude greater than that of the next most abundant species at sites TSC-D, CLAYC-D, and WFSF-D. Notable exceptions to this trend occurred at sites TSC-U and SANDC where several cyprinids, especially *Cyprinella lutrensis* (TSC-U and SANDC) and *Notropis stramineus* (TSC-U), were dominant. The latter site contained the most speciose assemblage with 12 of the 16 species occurring there. The number of species per site among the remaining sites ranged from 1 (COTC-D) to 11 (WFSF-D) with a mean value of 6 species per site.

Statistical Analysis. Shannon-Wiener diversity (H') and evenness values for each site are given in Table 2. Interestingly, upstream sites had higher diversity and evenness values than downstream sites in each of the four streams for which a longitudinal comparison could be made (upstream means: $H'=1.12$, evenness=0.59; downstream means: $H'=0.248$, evenness=0.12). In nearly all cases, upstream versus downstream collections for a given stream

TABLE 2. Shannon-Wiener diversity (H') and evenness measures for collections taken from sites on five western Salt Plains National Wildlife Refuge streams. Site abbreviations are those given in Figure 1.

Site	H'	Evenness
TSC-U	1.55	0.65
TSC-D	0.65	0.32
CLAYC-U	1.32	0.68
CLAYC-D	0.22	0.13
COTC-U	0.30	0.44
COTC-D	0.00	0.00
WFSF-U	1.32	0.74
WFSF-D	0.12	0.05
SANDC	0.32	0.17

TABLE 1. List of fish species with numbers captured in samples from five streams on the Salt Plains National Wildlife Refuge, Oklahoma, USA. Site abbreviations are given in Figure 1.

Species	Site								
	TSC-U	TSC-D	CLAYC-U	CLAYC-D	COTC-U	COTC-D	WFSF-U	WFSF-D	SANDC ^a
<i>Dorosoma cepedianum</i> ^b	9	0	0	0	0	0	0	0	0
<i>Cyprinus carpio</i>	10	2	9	0	2	0	0	1	0
<i>Cyprinella lutrensis</i>	509	4	0	1	0	0	1	0	802
<i>Hybognathus placitus</i>	129	38	3	30	0	0	8	7	6
<i>Notropis atherinoides</i>	156	21	0	0	0	0	29	2	12
<i>Notropis stramineus</i>	573	1	0	0	0	0	0	4	29
<i>Pimephales promelas</i>	47	11	1	1	0	0	0	1	0
<i>Pimephales vigilax</i>	0	0	0	0	0	0	0	1	0
<i>Ictalurus punctatus</i>	0	0	0	0	0	0	10	21	2
<i>Fundulus zebrinus</i>	10	0	5	11	20	0	0	1	0
<i>Gambusia affinis</i>	78	5	13	1	0	0	2	0	1
<i>Menidia beryllina</i>	1	445	45	927	0	4	40	2161	0
<i>Morone hybrid</i> (wiper)	0	0	2	0	0	0	0	1	5
<i>Lepomis cyanellus</i> ^d	2	0	0	0	0	0	0	0	0
<i>Lepomis humilis</i>	0	0	0	0	0	0	0	0	1
<i>Lepomis macrochirus</i>	3	0	0	0	0	0	0	1	0

a,b,c Not included in loglinear analyses.

d *Lepomis* species abundances were pooled in loglinear analyses.

were similar in terms of numbers of species; however, disproportionate representation of *Menidia beryllina* in downstream samples apparently resulted in relatively low evenness and, therefore, low diversity for these sites.

Pairwise values of Morisita's Index of Similarity (I_M) are given in Table 3. Similarities among upstream sites averaged much less than those among downstream sites (mean I_M among upstream sites=0.21, SD=0.32; mean I_M among downstream sites 0.86, SD=0.33). The mean I_M between upstream-downstream pairs of sites (mean=0.33, SD=0.39) was intermediate between the foregoing values for downstream-downstream and upstream-upstream means. Loglinear analyses were performed at two levels. Initially, we performed an analysis in order to elucidate quantitatively the differences among streams and reaches within streams (upstream versus downstream reaches) as well as interactions between stream and reach in terms of the number of individuals for the entire species pool. The results of this first level of analysis were uniformly significant stream and reach main effects and interactions between these factors. This indicates major differences among streams ($X^2=185.2$, $P<0.001$) and reaches within streams ($X^2=22.3$, $P<0.001$) in total number of individuals in the species pool. Moreover, the difference in total number of individuals for the species pool between reaches within streams varies considerably both in magnitude and direction among streams ($X^2=136.8$, $P<0.001$). Thus, some streams had high total numbers in upstream reaches relative to downstream reaches whereas in other streams the numbers in upstream and downstream reaches are reversed.

The second level of analysis utilized loglinear analyses of data for each species in order to determine the nature of the abundance pattern with respect to streams and reaches within streams (Table 4). The

TABLE 3. Values of Morisita's Similarity Index based on counts per species for pairs of sites surveyed on SPNWR streams. Column and row abbreviations correspond to those in Figure 1.

	TSC-U	TSC-D	CLAYC-U	CLAYC-D	COTC-U	COTC-D	WFSF-U	WFSF-D	SANDC
TSC-U		0.030	0.043	0.006	0.012	0.001	0.155	0.003	0.569
TSC-D			0.901	0.991	0.000	0.197	0.672	0.985	0.010
CLAYC-U				0.868	0.086	0.171	0.767	0.848	0.001
CLAYC-D					0.012	0.998	0.696	0.999	0.001
COTC-U						0.000	0.000	0.001	0.000
COTC-D							0.676	1.000	0.000
WFSF-U								0.685	0.027
WFSF-D									0.000
SANDC									

TABLE 4. Loglinear analysis results by species. Effects tested included stream (S) and reach (R) main effects and their interaction (designated as S×R).

Species	Source	Chi-square	Prob.
<i>Cyprinus carpio</i>	S	1.53	NS
	R	2.01	NS
	S×R	2.30	NS
<i>Cyprinella lutrensis</i>	S	104.20	<0.001
	R	28.68	<0.001
	S×R	77.42	<0.001
<i>Hybognathus placitus</i>	S	103.93	<0.001
	R	1.21	NS
	S×R	43.78	<0.001
<i>Notropis atherinoides</i>	S	93.49	<0.001
	R	18.41	<0.001
	S×R	13.66	<0.001
<i>Notropis stramineus</i>	S	85.95	<0.001
	R	28.46	<0.001
	S×R	93.50	<0.001
<i>Pimephales promelas</i>	S	27.86	<0.001
	R	0.17	NS
	S×R	15.19	<0.001
<i>Ictalurus placitus</i>	S	18.27	<0.001
	R	0.40	NS
	S×R	1.05	NS
<i>Fundulus zebrinus</i>	S	3.64	NS
	R	0.15	NS
	S×R	4.17	NS
<i>Gambusia affinis</i>	S	26.63	<0.001
	R	18.27	<0.001
	S×R	11.28	<0.01
<i>Menidia beryllina</i>	S	84.36	<0.001
	R	803.22	<0.001
	S×R	23.87	<0.001
<i>Morone hybrid (wiper)</i>	S	0.03	NS
	R	0.02	NS
	S×R	0.03	NS
<i>Lepomis</i> spp.	S	0.62	NS
	R	0.29	NS
	S×R	0.62	NS

results of the analyses by species suggest that a subset of species account for most of the variation in total numbers of individuals among and within streams. Five species consistently showed significant effects due to streams, reaches, and stream × reach interaction. This may indicate some degree of randomness in the distribution patterns for these species; however, for some species the generality of this conclusion is questionable. For example, *Notropis stramineus* occurred in high numbers in only one upstream location with only one and four specimens collected from the remaining sites. The sample of four *N. stramineus* came from a downstream collection from the West Fork of the Salt Fork of the Arkansas River while the upstream collection from the same stream contained no individuals. Thus, this minor reversal in abundance between reaches in two streams accounted for the significant stream × reach interaction effect for this species.

One or more non-significant interactions were detected for five species, the hybrid, and *Lepomis* in the analysis by species. Species with uniformly non-significant interactions were those that tended to be rare in all collections. Exceptions were *Hybognathus placitus*, *Pimephales promelas*, and *Ictalurus punctatus*. The significant stream × reach interactions for *H. placitus* and *P. promelas* both appear to reflect large among-stream differences in abundance in addition to comparatively minor reversals among streams in abundance differences between reaches. The lack of a reach effect for these species is likely a consequence of their concomitant high abundances at a single upstream reach, TSC-U. The significant stream effect for *Ictalurus punctatus* is clearly a consequence of its occurrence in a single stream (sites WFSF-U and WFSF-D).

The pattern of higher diversity in upstream sites versus downstream sites was unexpected. It is well known that diversity of temperate stream fish communities tends to be highest in higher-order streams rather than lower-order, headwater streams (8). Although the sites surveyed were of the same order, our data suggest that the foregoing generalization may not be extended to include plains-stream fish communities; however, an attempt at explaining the pattern observed in this study would be unduly speculative without further data. Likewise, it is uncertain as to the causality behind the relatively high faunal similarities between upstream pairs of sites. Proximately, however, it is clear that the pattern is related to the comparatively depauperate downstream faunas, dominated largely by *M. beryllina*.

The fishes of the SPNWR streams sampled in this study appear to comprise two distinct assemblages with respect to abundance. The first group consists of moderate to high-abundance forms including *M. beryllina* and the cyprinids *C. lutrensis*, *H. placitus*, *N. atherinoides*, *N. stramineus*. *M. beryllina* was clearly the dominant species overall. The remaining species comprise a group consisting of low-abundance forms, several of which are likely to occur only as transients in the habitats we sampled. We

observed milt flowing from males of *Morone* hybrid and *C. carpio*, possibly indicating that these individuals had migrated into upstream habitats to spawn. It is unlikely that either of the forms occur as members of permanent populations in streams flowing directly through the salt plains since these streams are likely subject to severe desiccation during the summer. Indeed, a number of small creeks on the SPNWR are intermittent (Fig. 1), suggesting major seasonal variation in flows.

The species of the moderate- to high-abundance assemblage were randomly distributed among and within streams. This suggests that there is only weak partitioning of habitats, possibly as a consequence of generalized habits in these fishes. Another possible explanation for the widespread, random occurrence of these species is a lack of predation by fishes. However, least terns and several other shorebirds which prey on fishes nest in areas adjacent to those we sampled (9). Few birds were observed during sampling although it is likely that least terns were beginning to enter nesting grounds (M. Koenen, pers. comm.). Increased frequency of shorebirds in the area may possibly have a negative effect on the abundance of several species. *M. beryllina*, a topwater schooling species (10), is likely an important prey species for terns. In general, fish are an important food item for least terns (11); however, we were unable to find data to support the preference of one prey species over another. This suggests a need for a more detailed analysis of least tern food habits. These data together with those regarding distribution and abundance patterns of SPNWR fishes may have implications for the management of least terns. Indeed, it has been suggested that the absence of terns in otherwise apparently optimal habitats is related to the suitability of fisheries in adjacent streams (11).

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