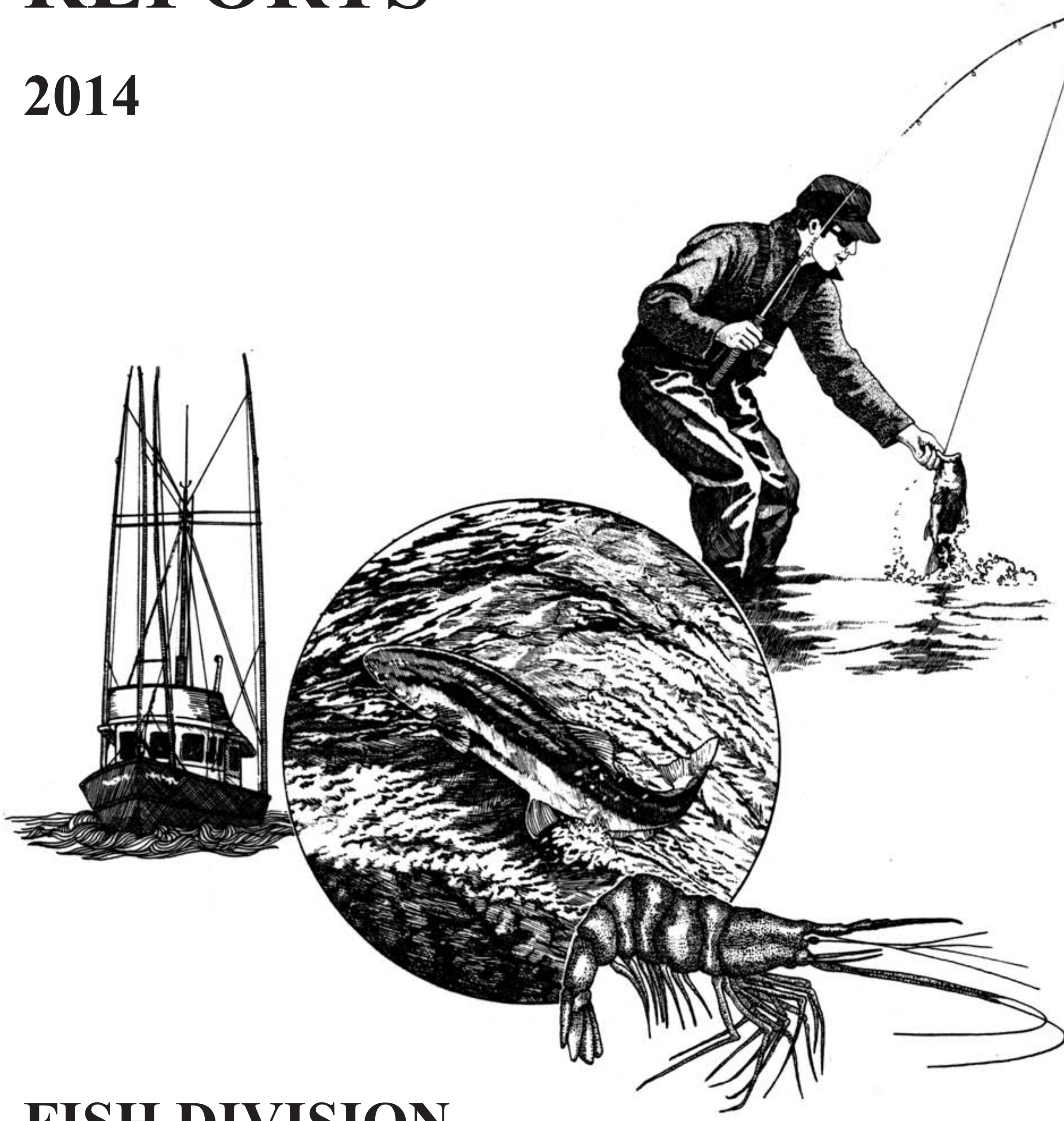
PROGRESS REPORTS

2014



FISH DIVISION

Oregon Department of Fish and Wildlife

2014 Millicoma Dace Investigations

ANNUAL PROGRESS REPORT

FISH RESEARCH PROJECT
OREGON

PROJECT TITLE: **Distribution and Abundance of Millicoma Dace in the Coos Basin, Oregon**

Photograph of Millicoma dace (credit- D. Markle) and its habitat.

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CONTENTS

Page

Abstract— The Millicoma dace (*Rhinichthys cataractae)* is a form of longnose dace endemic to the Coos River drainage in southwestern Oregon. Sparse species records in the Oregon State University Ichthyology Collection and infrequent recent encounters prompted a survey to assess the current status and distribution of these fish. We surveyed locations that had historically supported Millicoma dace using backpack electrofishing to document presence/absence, estimate dace capture and detection probabilities and abundance, and conduct a power analysis to inform future sampling design. We used an N-mixture model to estimate abundance and capture probability for Millicoma dace at each sampling location. We evaluated the effects of habitat covariates on both capture probability and abundance at each sample site. We found Millicoma dace were widespread and relatively abundant throughout their historical range. We only found Millicoma dace associated with native fishes; we did not collect any nonnative fish during our surveys. We collected Millicoma dace exclusively from swift water habitats, which were relatively uncommon in the basin, and found them typically associated with cobble or boulder substrates. Millicoma dace were most abundant in the South Fork Coos and West Fork Millicoma River subbasins. Abundance estimates ranged from 19 to 720 dace per sampling location with a total estimated abundance (sum of site estimates) of over 4,100 dace for the sites we sampled. We estimated a mean capture probability for Millicoma dace of 10% (range 3–13%). Model simulations to inform future sampling design had little power to detect declines in abundance using a 2-state design (present/absent), improved power using a 3-state occupancy design (absent/rare/abundant), and the best power using an N-mixture design.

INTRODUCTION

The longnose dace *Rhinichthys cataractae* is widespread in North America and in Oregon. The Millicoma dace is a form of longnose dace endemic to the Coos River drainage in southwestern Oregon and is a strategy species under the Oregon Conservation Strategy. Bisson and Reimers (1997) first described the unique characters of Millicoma dace and nearby Umpqua dace *R. evermanni* and found large morphological differences between these coastal longnose dace and those inhabiting Columbia River tributaries, likely resulting from prolonged geographical isolation. McPhail and Taylor (2009) conducted a phylogeographical maximum likelihood analysis that indicated that, together, the Umpqua and Millicoma dace form a distinctive Oregon coastal clade within the *R. cataractae* species group (originated from a common *R. cataractae* like ancestor) and the Millicoma dace likely evolved from the Umpqua dace (sister taxa). They noted substantial genetic divergence of Millicoma dace from Umpqua dace and argued that the Millicoma dace warrants specific taxonomic status (distinct species).

A recent review of fish museum records from the Oregon State University (OSU) Ichthyology Collection revealed 22 records for Millicoma dace, collected from 15 locations in the Coos drainage between 1961 and 1997 (Table 1; Figure 1). Recent conversations with Drs. Doug Markle and Brian Sidlauskas, OSU, and Mike Gray, ODFW Coos-Coquille District Biologist, indicated concern regarding the current status and distribution of these dace and prompted this study.

The objectives of this study were to: 1) survey locations that had historically supported Millicoma dace using backpack electrofishing to document presence/absence, 2) estimate dace capture and detection probabilities and abundance, and 3) conduct a power analysis to inform future sampling design, i.e. estimate the optimum allocation of sampling effort (number of locations and sampling occasions) to detect changes in status over time.

METHODS

We sampled locations within the known historical range of Millicoma dace from 8 to 18 September, 2014. The historical range was estimated from OSU Ichthyology Collection records. We included some additional sampling sites to better describe upstream distribution. At each location, we used single-pass backpack electrofishing to sample a section (length) of stream that was six times the wetted width and included at least two riffle-pool sequences. We flagged the upstream and downstream boundaries. We placed the Millicoma dace that we captured in a five gallon bucket until the entire site was sampled. After sampling was completed, we measured the Millicoma dace to the nearest 1 mm. If Millicoma dace were collected at a location, we repeated the sampling on one more occasion, 1–3 d later. If no dace were collected at a site, we repeated the sampling two more times, if time permitted. We recorded the other fish species collected and categorized their abundance as few (1–9 individuals) or many (>10 individuals), with the exception of Coho salmon *Oncorhynchus kisutch*, which were counted to satisfy National Oceanic and Atmospheric Administration 4(d) permit reporting requirements.

Table 1. Millicoma dace occurrence records from the Oregon State University Ichthyology Collection. Map codes refer to map locations on Figure 1. Map locations in many cases are approximate, due to imprecise records. All site locations are in UTM zone 10T.

Map code	Subbasin	Date	Local name	UTM_E	UTM_N
1	West Fork Millicoma River	19-Aug-1997	West Fork Millicoma River	422086	4820357
2	West Fork Millicoma River	2-Sep-1997	West Fork Millicoma River	422086	4820357
3	West Fork Millicoma River	20-Jul-1961	West Fork Millicoma River near a fish ladder; location estimated	418909	4816746
4	West Fork Millicoma River	31-Jul-1969	West Fork Millicoma River	415471	4813974
5	West Fork Millicoma River	31-Jul-1969	West Fork of Millicoma River, about 6 miles upstream	411704	4804491
6	Coos River	26-Aug-1967	Millicoma River	414651	4806235
7	East Fork Millicoma River	10-Sep-1971	Millicoma River at Allegany	416699	4808377
8	East Fork Millicoma River	1-Jul-1972	Millicoma River 2 miles above Allegany	417360	4809803
9	East Fork Millicoma River	8-Sep-1992	Millicoma River at Nesicka Co. Park, 4 mi upstream from Allegany	419486	4810364
10	East Fork Millicoma River	12-Jul-1971	Millicoma River at Nesicka Co. Park, 4 mi upstream from Allegany	419412	4810968
11	East Fork Millicoma River	12-Jul-1971	Millicoma River at wayside 4 mi above Allegany	419407	4810979
12	East Fork Millicoma River	9-Oct-1967	Millicoma River at Millicoma wayside	419410	4810976
13	East Fork Millicoma River	9-Oct-1967	Millicoma River	421057	4810999
14	Upper South Fork Coos River	27-Jan-1980	South Fork Coos River at Cox Creek confluence	424755	4801403
15	Upper South Fork Coos River	19-Apr-1980	Cox Creek at mouth	424755	4801403
16	Upper South Fork Coos River	19-Apr-1980	Mouth of Cox Creek, trib. to S Fork of Coos River	424565	4801228
17	Upper South Fork Coos River	19-Apr-1980	Cox Creek	424585	4799623
18	Upper South Fork Coos River	3-Aug-1969	South Fork Coos River	432839	4798314
19	Upper South Fork Coos River	3-Sep-1979	South Fork Coos River at Tioga Creek confluence	434334	4796250
20	Upper South Fork Coos River	3-Aug-1969	Unnamed Creek	434234	4796455
21	Upper South Fork Coos River	3-Nov-1979	Tioga Creek 2.7 mi from mouth	434754	4794020
22	Upper South Fork Coos River	3-Nov-1979	Tioga Creek	434382	4790915

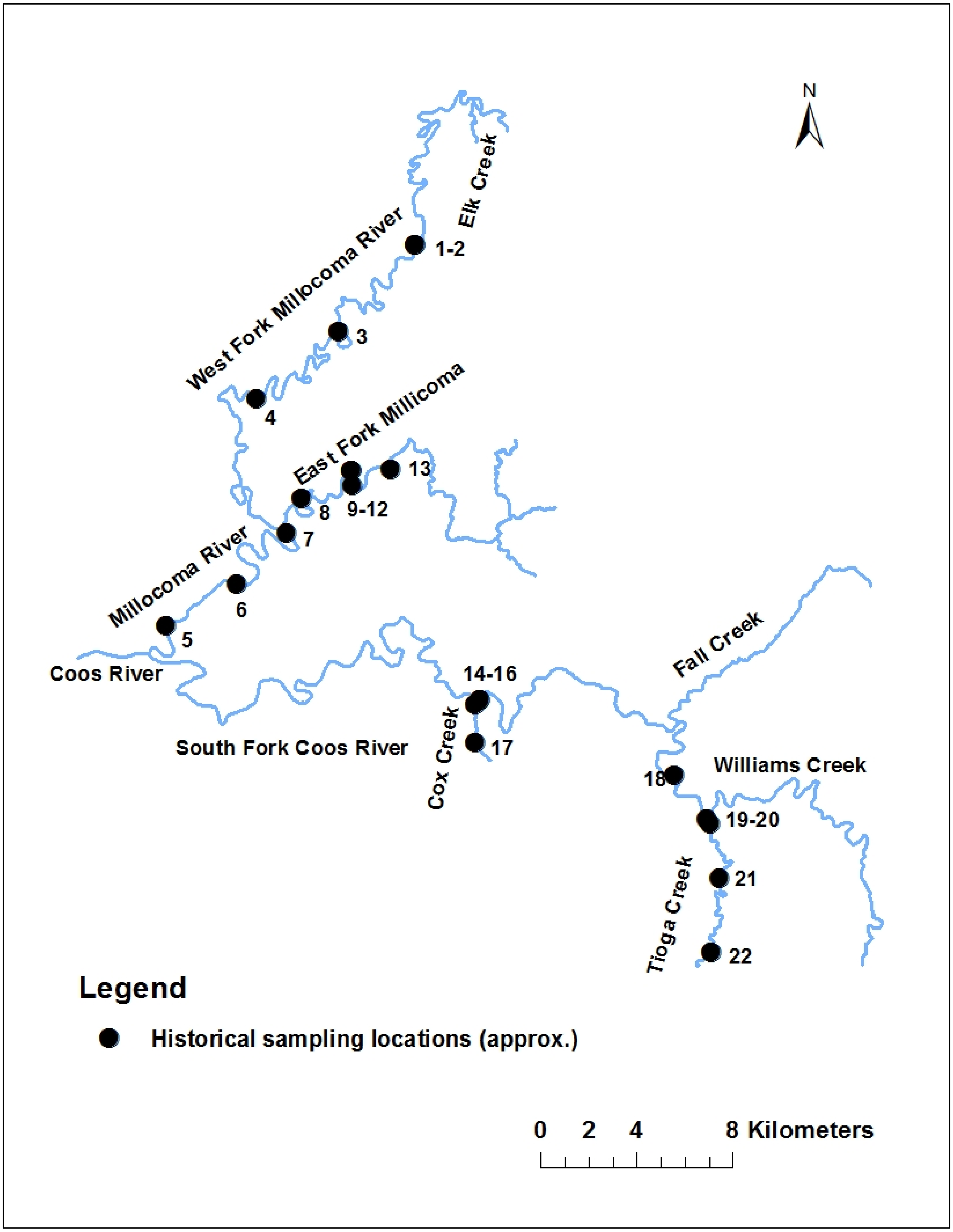


Figure 1. Historical records for Millicoma dace from the Oregon State University Ichthyology Collection. Numbers refer to sites listed in Table 1.

We collected habitat information at each location that we visited. We used a graduated measuring tape to measure stream width and site length. We determined the stream length for each sampling location by multiplying the average wetted stream width by six, thus scaling the sampling area to the size of the stream channel. At the same transect where we measured stream width (beginning of sampled section), we determined the site depth using a graduated measuring staff and calculated the average of five equally spaced measurements across the channel and recorded the dominant substrate type based on the following categories: fines- <0.063 mm, sand- 0.063-2 mm, gravel- 3-64 mm, cobble- 65-256 mm, boulder- >256 mm or bedrock. We estimated the cover provided by large wood and/or large boulders, expressed as a percentage of surface area of the site. We recorded the water temperature using a hand held thermometer. We recorded the Universal Transverse Mercator (UTM) coordinates for the start and end points at each site using a handheld Global Positioning System (GPS) and photographed each sampling location.

We used an N-mixture or binomial-mixture model, which uses data from spatially replicated populations (i.e., sampling sites) with temporally replicated counts of independent individuals (i.e., multiple sampling occasions) within a period of closure (i.e., assuming no immigration, emigration, or mortality) to estimate abundance and capture probability for Millicoma dace at each sampling location (Royle 2004; Kéry and Schaub 2012). The binomial mixture model is appealing, since it allows us to estimate abundance, corrected for imperfect capture, using simple counts without individual identification. The capture of dace present at a site was modeled assuming a binomial distribution, whereas the variation in abundance among sites was assumed to follow a negative binomial distribution.

The N-mixture model also allowed us to evaluate evidence for the effect of covariates on both capture probability and abundance at a sample site. We included the following habitat covariates as potential predictors for the capture probability submodel: stream width, substrate type, stream temperature, percent cover, average depth, and cross-sectional area. We also evaluated the following habitat covariates as predictors for the abundance submodel: stream temperature, percent cover, average depth, sample unit length, and cross-sectional area. We evaluated the effect of these variables by systematically fitting alternative submodels with and without the predictors and selected the best model using Akaike's Information Criteria with a small sample bias adjustment (AICc; Burnham and Anderson 2002). During the model selection procedure, the same covariate (e.g., average depth) was not included simultaneously in both submodels to avoid model convergence and parameter identifiability problems. We calculated 95% confidence limits for abundance estimates using the asymptotic variance for lambda, which represents the density of occurrences within a time interval, as described by Royle (2004). All models were fit using R package UNMARKED (Fiske and Chandler 2011). Goodness-of-fit of the best supported models was evaluated using a bootstrap goodness-of-fit test as implemented in R package AICcmodavg (Mazerolle 2014).

We assume that future efforts to evaluate changes in Millicoma dace populations will have limited resources at hand to conduct surveys and will need to obtain unbiased estimates of the status of dace populations. We also believe that these future efforts will likely attempt to avoid excessive handling of fishes. To accommodate these conditions, the most useful sample designs will likely employ occupancy or N-mixture models to obtain unbiased estimates. We evaluated the effectiveness of potential sample designs using two occupancy estimators, single season and multi-state occupancy, and the N-mixture model described earlier. The single season occupancy estimator incorporated two states: dace absent and present, whereas the multi-state occupancy estimator incorporated three states: dace absent, present, and abundant with the conditional binomial maximum-likelihood estimator (MacKenzie et al. 2006). For all simulations, we assumed that future sampling will be conducted over a one month time period by a field crew that can complete a total of 80 to 100 site visits (40-50 sites and two visits per site). Simulations began with an initial number of fish at the specified number of sample sites. Fish were distributed among sites assuming a negative binomial distribution with a mean abundance of 230 and standard deviation (SD) of 190 (i.e., the mean and SD estimated during this study). Fish then were sampled during two visits assuming a binomial distribution with an average capture probability of 10% and SD of 5% (i.e., the mean and SD estimated during this study). If the simulated number of fish caught was greater than 0, the species was assumed to be detected during a visit. For the multi-state occupancy models, we further classified populations as abundant when the catch during a visit exceeded the 90th percentile of catches at all sites and visits. The mean abundance for the second simulated survey year then was reduced by a fixed amount for each simulation scenario, which ranged from 10-90% among scenarios. The variation in abundance among sites for the second simulated year was set at 83% (190/230) of the mean. The number of sites sampled and the number of visits per site were identical between the first and second simulated year. The single season and N-mixture model models were fit using UNMARKED (Fiske and Chandler 2011) and the multi-state occupancy models using RMARK (Laake 2013), implemented in the R statistical environment (R Development Core Team 2008). For all simulations, statistically significant decreases in population size from year one to two were evaluated using a likelihood ratio test. Power for each combination of number of sample sites visited and decrease in abundance from year one to two were estimated as the proportion of 100 replicate simulations where the p-value was less than or equal to the 0.10.

RESULTS

We sampled 18 locations in the Coos River drainage and collected Millicoma dace from 16 of these locations (Figure 2). We collected dace from 14 of these locations on both the first and second sampling occasions and the numbers of individuals caught were remarkably consistent across repeat sampling visits at these locations (Table 2). At the two locations where we did not collect Millicoma Dace, Cox Creek and East Fork Millicoma site 4, we were only able to sample on one occasion due to time constraints. Cox Creek had a steep cascade over bedrock near its mouth, possibly limiting Millicoma dace distribution. The East Fork Millicoma River site 4 was the most upstream location sampled in this drainage.

We collected Millicoma dace exclusively from swift water habitats, which were relatively uncommon in the basin, and found them typically associated with cobble or boulder substrates.

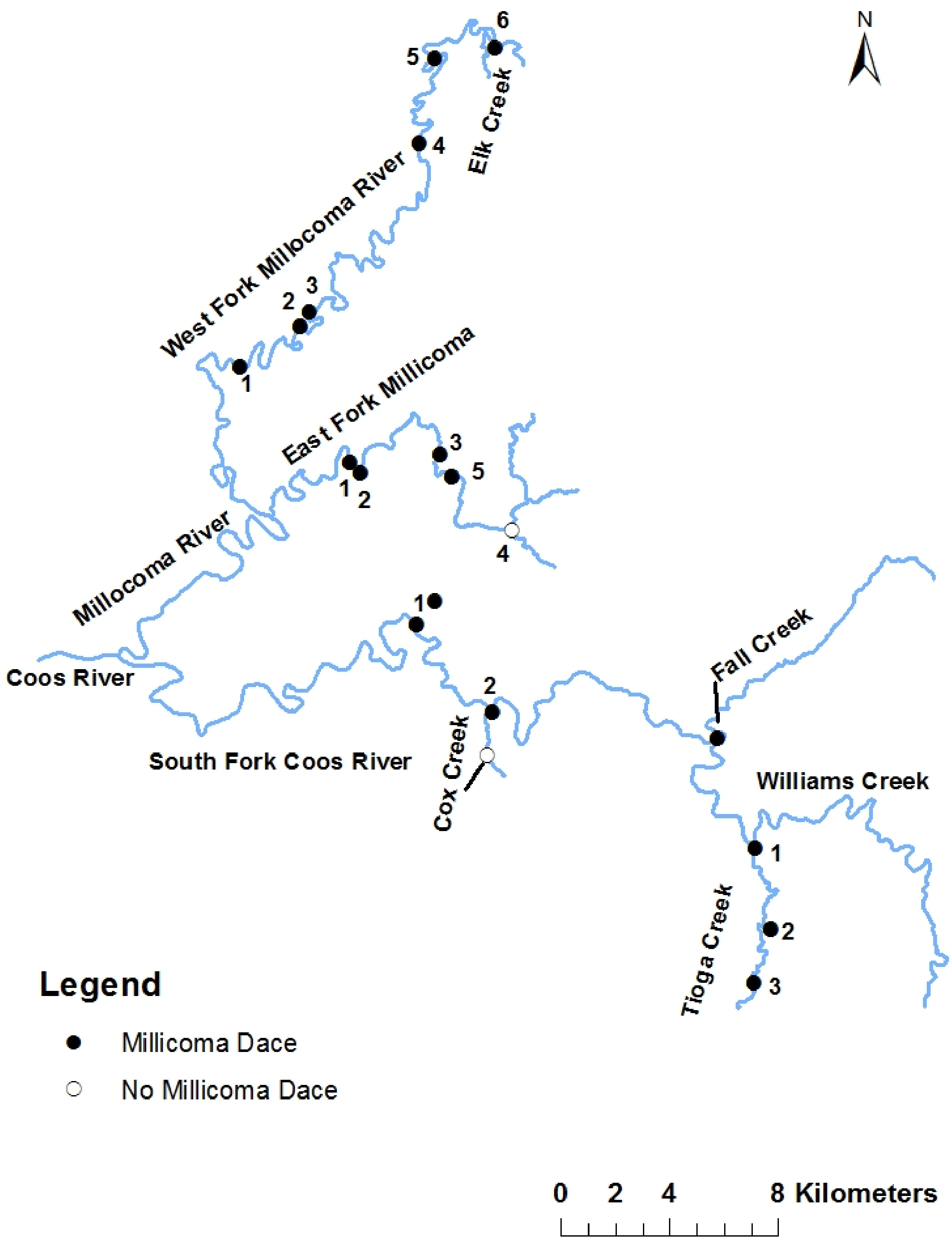


Figure 2. Sampling locations for Millicoma dace in the Coos River drainage, September 2014. Site numbers refer to those listed in Table 2.

When the Coos basin was previously logged, the timber was transported downstream using splash dams. When these dams were removed to float the logs downstream, the stream bed was severely scoured, thus resulting in low habitat complexity and a stream substrate that was dominated by bedrock. This damage has been slow to heal. The majority of the stream channels in the study area also had low channel gradient and were dominated by pools and glides.

We collected 11 non-target fish species during our sampling, including speckled dace *Rhinichthys osculus*, coastrange sculpin *Cottus aleuticus*, riffle sculpin *C. gulosus*, rainbow trout *Oncorhynchus mykiss,* cutthroat trout *O. clarkii*, Coho salmon *O. kisutch*, threespine stickleback *Gasterosteus aculeatus*, redside shiner *Richardsonius balteatus*, Tyee sucker *Catostomus tsiltcoosensis*, Pacific lamprey *Lampetra tridentata*, and Western brook lamprey *Lampetra richardsonii (Table 2)*.

Table 2. Fish and habitat details for 2014 Millicoma dace sampling locations. Fish codes: MD- Millicoma dace, SPD- speckled dace, CRS- coastrange sculpin, RS- riffle sculpin, TR- rainbow or cutthroat trout, CO- Coho salmon, SKB- threespine sticklebacks, RSS- redside shiner, TSU- Tyee sucker, PLAM- Pacific lamprey, and BLAM- brook lamprey.

Date	Location	Subbasin	Water Temperature	Pass	Shock time (min)	Length	Width	Dominant substrate	Average depth	Cover (%)	MD	SD	CRS	RS	TR	CO	SKB	RSS	TSU	PLAM	BLAM
09/08/14	Tioga Creek 1	SF Coos	17.5	1	45	55.2	9.2	cobble	0.09	25	16	many		many	few		few	many			
09/10/14	Tioga Creek 1	SF Coos	17.0	2	52	55.2	9.2	cobble	0.09	25	18	many		many	few			many			
09/09/14	Tioga Creek 2	SF Coos	15.5	1	35	48.0	8.0	cobble	0.16	20	1	many		many		2					
09/09/14	Tioga Creek 2	SF Coos	16.0	2	33	48.0	8.0	cobble	0.16	20	4	many		many							
09/08/04	Tioga Creek 3	SF Coos	16.0	1	45	54.0	9.0	gravel	0.08	10	4	many	few	many							few
09/09/14	Tioga Creek 3	SF Coos	15.0	2	44	54.0	9.0	gravel	0.08	10	6	many	few	many		2					few
09/09/14	Fall Creek	SF Coos	15.0	1	45	48.6	8.1	boulder	0.15	20	13	many	few	many		2		few			
09/09/14	Fall Creek	SF Coos	15.5	2	45	48.6	8.1	boulder	0.15	20	14	many		many	few	1		few			
09/09/14	SF Coos River 1	SF Coos	22.0	1	40	64.0	28.0	bedrock	0.21	10	20	many		many	few			many			
09/09/14	SF Coos River 1	SF Coos	22.0	2	45	64.0	28.0	bedrock	0.21	10	16	many		many	few			many			
09/09/14	SF Coos River 2	SF Coos	20.5	1	40	66.0	11.0	gravel	0.11	5	33	many			few	1		many			
09/10/14	SF Coos River 2	SF Coos	20.5	2	43	66.0	11.0	gravel	0.11	5	27	many			few		few	many			
09/10/14	Cox Creek	SF Coos	15.5	1	30	36.6	6.1	bedrock	0.10	5	0				few						
09/11/14	EF Millicoma River 1	Millicoma River	15.5	1	50	72.0	12.0	bedrock	0.22	20	19	many	few	many	few						
09/11/14	EF Millicoma River 1	Millicoma River	14.5	2	50	72.0	12.0	bedrock	0.22	20	19	many	many	many	few						
09/11/14	EF Millicoma River 2	Millicoma River	16.0	1	45	84.0	14.1	bedrock	0.18	20	20	many		many	few						
09/15/14	EF Millicoma River 2	Millicoma River	14.0	2	43	84.0	14.1	bedrock	0.18	20	14	many		many	few				few		few
09/15/14	EF Millicoma River 3	Millicoma River	16.0	1	21	63.8	7.2	bedrock	0.18	20	4		many		many						
09/17/14	EF Millicoma River 3	Millicoma River	16.0	2	27	63.8	7.2	bedrock	0.18	20	3	many	many		many						
09/15/14	EF Millicoma River 4	Millicoma River	13.0	1	20	50.0	10.0	bedrock	0.11	10	0			many	many						
09/15/14	EF Millicoma River 5	Millicoma River	15.0	1	43	54.2	7.5	bedrock	0.12	20	0	many			many						
09/17/14	EF Millicoma River 5	Millicoma River	14.0	2	50	54.2	7.5	bedrock	0.12	20	2	many		many	many						
09/17/14	EF Millicoma River 5	Millicoma River	14.0	3	46	54.2	7.5	bedrock	0.12	20	8	many		many	many						
09/16/14	WF Millicoma River 1	Millicoma River	14.0	1	27	81.4	16.0	bedrock	0.08	20	13	many	few	many	few						
09/18/14	WF Millicoma River 1	Millicoma River	15.0	2	29	81.4	16.0	bedrock	0.08	20	22	many	few	many	few						
09/11/14	WF Millicoma River 2	Millicoma River	16.0	1	30	64.6	7.0	bedrock	0.32	20	12	many		few	few	2					
09/17/14	WF Millicoma River 2	Millicoma River	15.5	2	26	64.6	7.0	bedrock	0.32	20	13	many	few	many	many						
09/11/14	WF Millicoma River 3	Millicoma River	16.5	1	43	83.0	12.0	bedrock	0.16	10	36	many		few	few	1					
09/17/14	WF Millicoma River 3	Millicoma River	16.5	2	58	83.0	12.0	bedrock	0.16	10	43	many	many	many	many	3					
09/16/14	WF Millicoma River 4	Millicoma River	14.0	1	37	75.0	12.5	bedrock	0.10	20	10	many		many	many						
09/18/14	WF Millicoma River 4	Millicoma River	16.0	2	28	75.0	12.5	bedrock	0.10	20	21	many		many	many						
09/16/14	WF Millicoma River 5	Millicoma River	14.5	1	25	60.0	10.0	bedrock	0.09	20	9	many		few	many						
09/18/14	WF Millicoma River 5	Millicoma River	13.0	2	23	60.0	10.0	bedrock	0.09	20	4	many		few	many						few
09/16/14	WF Millicoma River 6	Millicoma River	14.0	1	44	72.0	5.5	bedrock	0.13	20	0	many		many	many	1				few	
09/18/14	WF Millicoma River 6	Millicoma River	13.0	2	44	72.0	5.5	bedrock	0.13	20	0	many	many	many	many						
09/18/14	WF Millicoma River 6	Millicoma River	13.0	3	44	72.0	5.5	bedrock	0.13	20	3	many	many	many	many						

The top two N-mixture models both included cross-sectional area as a covariate in the abundance submodel plus dispersion, i.e., additional variation not described by the negative binomial distribution. The bootstrap goodness of fit test indicated that both models met the statistical distributional assumptions of the N-mixture model with the chi square test p value > 0.2 for both models. The best model fixed the capture probabilities (same for all locations) and the second best model calculated site-specific estimates of capture probability, including mean cross-sectional area as a covariate. The site abundance estimates were essentially identical for both models and ranged from 19 to 720 dace per sampling location with a total estimated abundance (sum of site estimates) of over 4,100 dace at the sites we sampled (Table 3). Despite the better fit for the model using fixed capture probabilities (because AIC values penalize the inclusion the additional parameter in the second best model), we chose the second best fit model because we feel that the assumption of equal capture probabilities across locations is unrealistic and was not consistent with previous studies of dace capture probabilities (Price and Peterson 2010).

The mean estimated capture probability for Millicoma dace from the second best fit model was 10% (range 3–13%). Dace were most abundant in the South Fork Coos and West Fork Millicoma River subbasins (Table 3). Parameter estimates for the models are shown in Table 4.

Table 3. Estimated Millicoma dace capture probabilities, abundance, and detection probabilities from the top two N-mixture models.

	Best fitting model				Second best fitting model				
Location	Estimated capture probability	Estimated abundance	Lower confidence limit	Upper confidence limit	Estimated capture probability	Estimated abundance	Lower confidence limit	Upper confidence limit	Detection probabilities
Cox Creek	0.062	20	1	64	0.127	19	1	60	92%
EF Millicoma River 1	0.062	350	252	464	0.074	363	262	482	100%
EF Millicoma River 2	0.062	320	226	431	0.076	332	234	447	100%
EF Millicoma River 3	0.062	71	32	126	0.106	69	31	122	100%
EF Millicoma River 4	0.062	21	1	70	0.112	21	1	67	92%
EF Millicoma River 5	0.062	68	36	110	0.118	64	34	105	100%
Fall Creek	0.062	240	162	333	0.109	232	157	322	100%
SF Coos River 1	0.062	345	246	460	0.030	423	301	566	100%
SF Coos River 2	0.062	540	417	679	0.109	522	404	657	100%
Tioga Creek 1	0.062	304	214	409	0.120	288	204	388	100%
Tioga Creek 2	0.062	54	21	102	0.107	52	21	99	100%
Tioga Creek 3	0.062	97	50	160	0.124	92	48	151	100%
WF Millicoma River 1	0.062	331	235	444	0.107	322	229	432	100%
WF Millicoma River 2	0.062	225	149	316	0.083	228	151	320	100%
WF Millicoma River 3	0.062	718	576	864	0.090	720	578	865	100%
WF Millicoma River 4	0.062	290	202	395	0.108	282	196	383	100%
WF Millicoma River 5	0.062	125	70	195	0.118	119	67	186	100%
WF Millicoma River 6	0.062	26	8	54	0.124	25	8	51	96%
Total		4143				4174			

Table 4. N-Mixture model parameter estimates and standard errors.

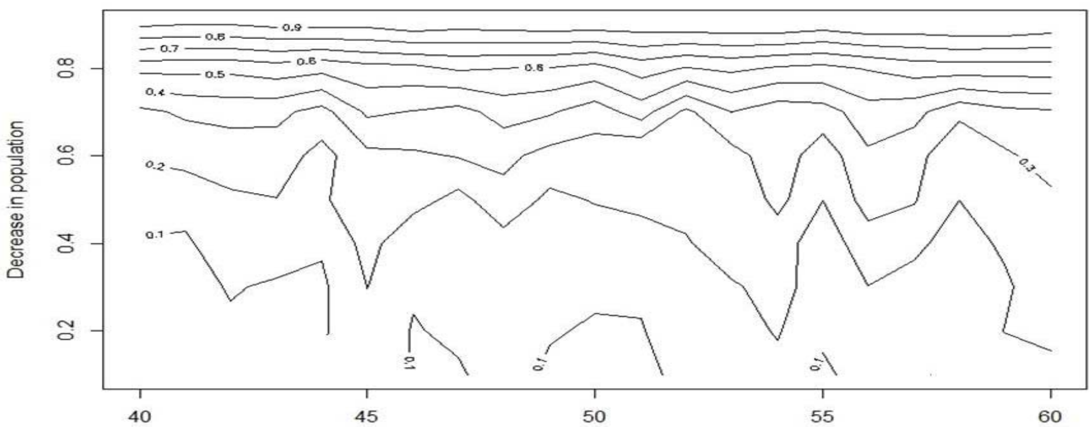
Best fitting model			Second best fitting model		
Abundance submodel	Estimate	SE	*Abundance submodel*	Estimate	SE
Intercept	3.442	1.107	Intercept	2.753	0.991
Sample unit area	0.002	0.001	Sample unit area	0.003	0.001
Dispersion	0.312	0.365	Dispersion	0.104	0.390
Capture probability submodel			*Capture probability submodel*		
Estimate			Intercept	-1.744	1.079
Intercept	-2.720	1.080	Mean cross sectional area	-0.296	0.201

We ran model simulations to inform future sampling design and allocation of effort. We had little power (<80%) to detect declines in abundance less than 80% using a 2-state design (present/absent) (Figure 3A). Power to detect a change in abundance improved using a 3-state occupancy design (absent/rare/abundant), where we have approximately 80% power to detect a 40% decline in abundance (Figure 3B), and was best using an N-mixture design, where we have approximately 80% power to detect a 30% decline in abundance (Figure 3C).

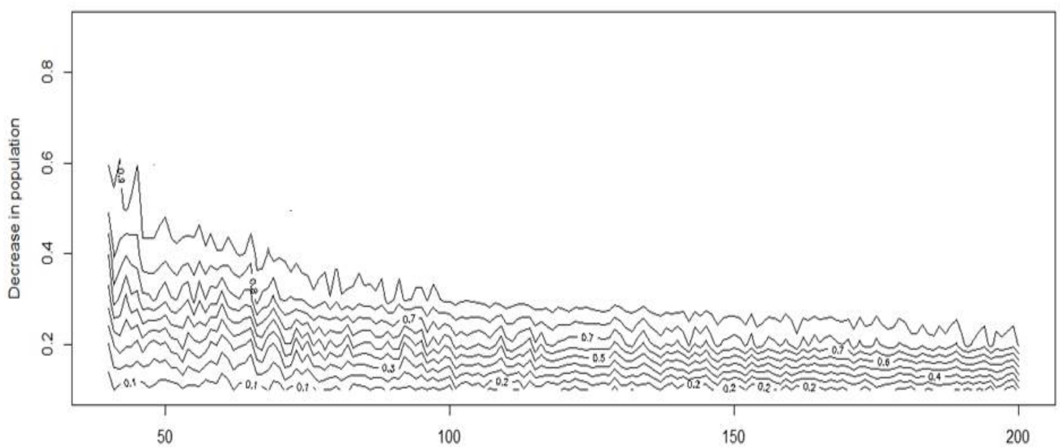
DISCUSSION

We found Millicoma dace were widespread and relatively abundant throughout their historical range. We also documented a broader species distribution than historical records suggested. We only found Millicoma dace associated with native fishes; we did not collect any nonnative fish during our surveys. Despite being widespread and relatively abundant, Millicoma dace appeared to have very specific habitat requirements (based on our field observations), preferring swift water habitats, which were relatively rare within their apparent range in the Coos drainage. We only collected Millicoma dace from riffles and rapids, primarily associated with (hiding under) cobble or boulder substrates. This secretive behavior, coupled with the relative rarity of swift water habitats, is likely responsible for the prior perceived rarity of this species. Due to the history of splash dam logging in the basin, complex stream habitats with large wood and coarse substrate are currently uncommon. Thus we believe that Millicoma dace, which are strongly cover oriented, were probably more abundant historically.

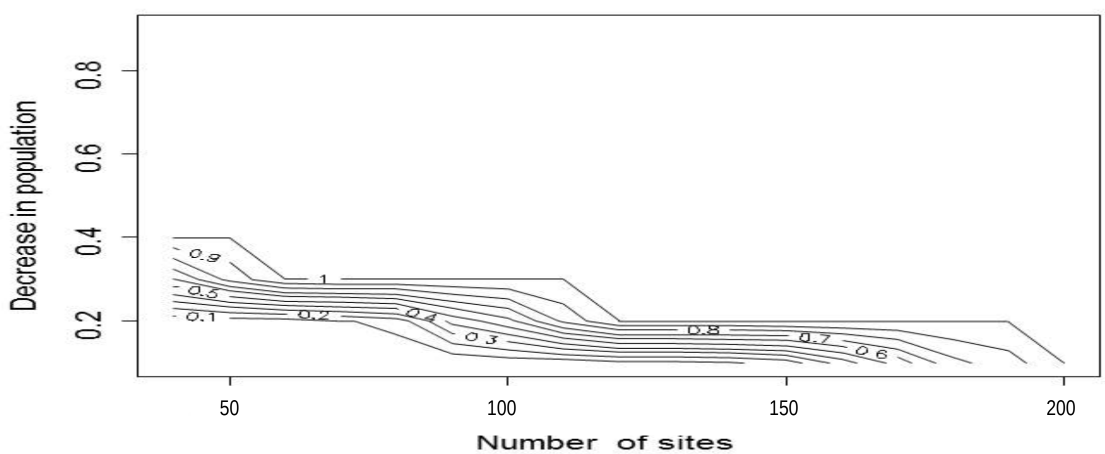
We used N-mixture models to estimate dace abundance at the sampling locations. This type of model has most commonly been used with bird counts (Kéry 2008; Kéry and Royle 2010), but never, to our knowledge, has it been used with small stream fish count data. The appeal of these models is the ability to estimate abundance and capture probability from sparse count data. These models assume: 1) each sample site is closed between visits, i.e., no immigration, emigration, birth or death; 2) capture probability is constant for all individuals present during a visit to a sample site; 3) the capture of individuals at a sample site is independent of others at that site; 4) the distribution animals among sample sites is adequately described by the chosen parametric distribution, i.e., negative binomial; and 5) there are no



A.



B.



C.

Figure 3. Plots displaying the power to detect changes in Millicoma dace abundance. A. Two-state model with two site visits. B. Three-state model with two site visits. C. N-mixture model with two site visits. Note, we assume future sampling will be limited to 40-50 sites.

false positives such as double counts or species misidentification. We believe that we met these assumptions. We conducted our surveys over a very short time period, thus meeting the assumption of closure. We collected and measured each dace, thus eliminating the possibility of double counting individuals during a sampling visit. The goodness-of-fit tests indicated that we met the distributional assumptions. Initially, we designed the current study with the idea that we would describe current dace distribution and their relative site abundance. However, because we can apply N-mixture models to our replicated count data, we gained the added benefit of obtaining site abundance estimates.

We found the detection probability for Millicoma dace using single-pass backpack electrofishing was very high (>90%) and recommend using this sampling gear for future surveys. Results from power analysis simulations indicate that an N-mixture design provides the highest power to detect changes in abundance and we recommend its usage for future abundance estimation. Because of the very high detection probabilities (dace were collected at most of the sites and on multiple occasions), restricting our monitoring to known historical locations with an occupancy estimator is probably not very useful. A better choice for future surveys would be to use a randomized design (GRTS, stratified) to select sites for the initial time period and to resample these sites during subsequent time periods (MacKenzie et al. 2006).

In summary, we found that Millicoma dace were more common, abundant, and widespread in the Coos River basin than previously thought. Despite being widespread, they apparently have very specific habitat requirements (swift water habitats with coarse substrate) and are thus patchily distributed due to the relative rarity of these habitats in the basin. We suggest periodic surveys (every 5-10 years) to assess the future status and trends of this species. These surveys would benefit by incorporating available habitat surveys and targeting sites within stream segments that have higher average gradient. We also suggest opportunistic surveys to better describe the upper distribution, distribution in smaller tributaries, and distribution in tidewater reaches. In addition, if restoration projects are implemented in the basin, we suggest addition of large wood and/or coarse substrates to increase the amount of suitable swift water habitat to benefit this and other native fish species. Lastly, we recommend the collection and analysis of morphometric and genetic data from voucher specimens that we collected during this study to determine the uniqueness of this form of longnose dace.

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