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A NEW SPECIES OF THE GENUS *YURIRIA* JORDAN & EVERMANN, 1896 (ACTINOPTERYGII, CYPRINIDAE) FROM THE AMECA BASIN OF THE CENTRAL MEXICAN PLATEAU

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ABSTRACT

A new cyprinid species is described based on morfometric, meristic and genetic characters. The new species identified, *Yuriria amatlana* **sp. nov.**, inhabits the high Ameca Basin in the central plateau of Mexico. This Mexican minnow differs from *Yuriria alta* and *Yuriria chapalae* in terms of the following characters: (50-52) 53-54 pored lateral-line scales; 10 upper transverse-line scales, 5-6 lower transverse-line scales and 8-10 gill rakers. Body coloration is light yellowish-brown. Compared to *Yuriria alta* and *Yuriria chapalae*, the new species has a less conspicuous dark grey band running from the start of the dorsal fin to the head. Cytochrome *b* gene sequences differ from those of *Yuriria alta* and *Yuriria chapalae* in terms of 29 fixed nucleotide positions (molecular autopomorphies). Calculated genetic divergences for the cytochrome *b* gene were: `$D_{HKY}$ = 3.8 (3.2-4.4%) between *Yuriria amatlana* sp. nov. and *Y. alta*; `D_{HKY}= 5 (4.8-5.2%) between *Y. amatlana* sp. nov and *Y. chapalae*; and `D_{HKY}= 2.6 (2.1-3.3%) between *Y. chapalae* and *Y. alta*.

Key words: Mexico Central Plateau, *Yuriria amatlana* **sp. nov.**, Cyprinidae, Cypriniformes, Ameca Basin, Taxonomy, Conservation, Endangered species.

RESUMEN

Una nueva especie del género *Yuriria* Jordan & Evermann, 1896 (Actinopterygii, Cyprinidae) de la cuenca del río Ameca en la Mesa Central Mexicana

Se describe una nueva especie, *Yuriria amatlana* **sp. nov**., en base a caracteres morfométricos, merísticos y genéticos. La nueva especie proviene de la parte alta de la cuenca del río Ameca en la Meseta Central de México. Esta especie se diferencia de *Yuriria alta* y *Yuriria chapalae* por una combinación de los siguientes caracteres: (50-52) 53-54 escamas en una serie longitudinal, 10 escamas en una serie transversal por encima de la línea lateral y 5-6 escamas por debajo de la línea lateral y 8-10 branquiespinas. El color del cuerpo es amarillo-marrón claro. La nueva especie tiene una banda gris oscura menos

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marcada en el cuerpo desde el comienzo de la aleta dorsal hacia la cabeza con respecto a *Yuriria alta* y *Yuriria chapalae*. La nueva especie se diferencia de *Yuriria alta* y *Yuriria chapalae* en 29 posiciones nucleotídicas fijadas (autopomorfias moleculares) para el citocromo *b*. La divergencia genética entre *Yuriria alta* y *Yuriria amatlana* sp. nov. para el citocromo *b* fue de `$D_{HKY}$ = 3.8 (3.2-4.4%); entre *Y. amatlana* sp. nov. y *Y. chapalae* fue `D_{HKY} = 5 (4.8-5.2%) y entre *Y. chapalae* y *Y. alta* fue `D_{HKY} = 2.6 (2.1-3.3%).

Palabras clave: Mesa Central Mexicana, *Yuriria amatlana* **sp. nov.**, Cyprinidae, Cypriniformes, Cuenca del Ameca, Taxonomía, Conservación, Especie en peligro.

Introduction

Along with *Algansea* Girard, 1856 and *Notropis* Rafinesque, 1818, *Yuriria* completes the three cyprinid genera that characterize the endemic cyprinid fauna of Central Mexico. Phylogenetic relationships between the three genera are currently unresolved owing to their extensive genetic and morphologic differentiation. Several authors have assigned *Yuriria* to different clades within the Phoxinini cyprinids (see Chernoff & Miller, 1986; Mayden, 1989; Mayden, 1991; Schönhuth & Doadrio, 2003). Mayden's (1989) results show *Yuriria* in a polytomy forming part of a large clade supported by a single synapomorphy, an opening in the posterior myodome (OPM). Mayden's OPM clade contained 22 genera formed primarily by eastern North American cyprinids (including *Notropis* and *Hybopsis* Agassiz, 1854), but also included *Agosia* Girard, 1856, *Oregonichthys* Hubbs in Schultz, 1929, *Richardsonius* Girard, 1856 and *Yuriria*, genera typically considered part of the western North American freshwater fish fauna (Uyeno, 1961). Based also on osteological and external characters, Coburn and Cavender (1992) argued for the dismemberment of Mayden's OPM clade and reassigned its members to all three major clades of North American phoxinins that they recognized (a shiner clade sister to a chub clade, plus a "western" clade), and redescribed the genus *Yuriria* as a large polytomy at the base of the 'western' clade of North American cyprinids comprised of another 20 genera. In a recent study, Schönhuth and Doadrio (2003) based on molecular characters suggested a close relationship between the genus *Yuriria* and the genus *Notropis* of Central Mexico, and ascribed *Yuriria* to a sister clade of the *Notropis calientis* Jordan & Snyder, 1899 group. Adopting a conservative criterion and pending a more extensive taxonomic revision, they proposed changing the taxonomic name *Yuriria alta* (Jordan, 1880) to *Notropis altus*. In a recent taxonomic revision of the freshwater fish of Central Mexico (Miller *et al.* 2005), different characters of the dorsal, pectoral and pelvic fins (position and size) are used as a taxonomic criterion to differentiate the genus *Yuriria* from other cyprinid genera. Within the *Yuriria*, two species have been described: *Yuriria alta* and *Yuriria chapalae* (Jordan & Snyder, 1899). However, more recent revisions have interpreted *Y. chapalae* as a junior synonyn of *Y. alta* (see Gilbert, 1998).

The genus *Yuriria* is widely distributed across the Mesa Central of Mexico, occurring in the Cuitzeo, Zacapu and Chapala lakes, rivers of the Lerma-Santiago drainage basin, and the headwaters of the Ameca and Panuco river basins (Miller & Smith, 1986; Espinosa *et al*., 1993; Lyons *et al*., 1998, 2000; Mercado-Silva *et al*., 2002; Miller *et al.,* 2005). The population from the Ameca river basin, designated as *Yuriria alta*, was identified as an undescribed form of *Yuriria* by Miller and Smith (1986) and Espinosa *et al.* (1993). The purpose of the present study is to characterize genetically and morphologically the *Yuriria* populations of Central Mexico including descriptions of undescribed forms.

Materials and Methods

The specimens described herein were collected using hand and seine nets and by electrofishing. All the specimens sampled were preserved in 70% ethanol. Voucher specimens are housed at the Universidad Michoacana de San Nicolás de Hidalgo (CPUM), México. Universidad Nacional Autónoma de México (IBUNAM) and the Museo Nacional de Ciencias Naturales de Madrid (MNCN).

Morphological analysis

The description of the new species is based on morphological analyses of the comparative material listed in the species description (Table 1).

No specimens were collected from the type locality of *Yuriria alta* (Lake Tupátaro, Guanajuato), where the species is supposed to be locally extinct, due to complete desiccation of the lake. The population examined here was obtained from the Laja River, which forms part of the same drainage and is also

Table 1.— Localities and specimen numbers of the *Yuriria* populations used in morphometric, meristic and genetic analyses.

Tabla 1.— Localidades y número de individuos de las poblaciones de *Yuriria* usados en los análisis morfométricos, merísticos y genéticos.

Species and populations			Morphometrics	Meristics	Genetics
Species	**Locality**	**Basin**			
Y. alta	1.- La Mintzita Spring	Cuitzeo Lake	0	0	1*
	2.- Zacapu Lake	Zacapu Lake	30	30	1*
	3.- Angulo River	Zacapu Lake	0	0	1*
	4.- Laja River	Middle Lerma River	30	30	1*
	5.- Ceja Dam	Middle Lerma River	0	0	1
	6.- Duero River	Lower Lerma River	0	0	1
	7.- Juchipila River	Santiago River	0	0	1
	8.- Calvillo River	Santiago River	0	0	1
	9.- Verde River	Santiago River	0	0	1
Y. cahapalae	10.- Guaracha Dam	Chapala Lake	25	25	1
Y. amatlana	11.- Amatlan de Cañas	Ameca River	30	30	2

*Sequences obtained from Genbank.

geographically close to the type locality. Measurements were performed following Doadrio *et al.* (2002). Nineteen morphometric parameters were measured using the computer program ImageTool 3.00 and six meristic variables were counted with the help of a stereoscopic microscope. The following abbreviations were used for morphometric and meristic characters: SL, standard length; HL, head length; PrOL, preorbital length; InOW, interorbital width; PoOL, postorbital length; Hh, head height; PrP prepectoral distance; PrD, predorsal distance; PrV, preventral distance; PrA, preanal distance; DFL dorsal fin length; PFL, pectoral fin length; PvFL, pelvic fin length; AFL, anal fin length; EALP, end of the anal fin-lower extreme of caudal peduncle distance; EDUP, end of dorsal fin-upper extreme of caudal peduncle distance; BD, body depth; BLD, body least depth; DAOD, dorsal origin to anal origin fin distance. Abbreviations for the meristic characters are: D, dorsal fin rays; Pv, pelvic fin rays; A, anal fin rays; GR, gill rakers; PLS, pored lateral-line scales; UTS, upper transverse scales, LTS lower transverse scales.

To identify the variables contributing most to the differences between the four populations sampled, principal component analyses (PCA) were performed on the meristic and morphometric data collected from all the specimens examined. The PCA results for the morphometric data (not shown) indicated that all weighted characters on the first principal component (PC I) showed the same sign and were of similar magnitude, suggesting that this axis represents general size-related variation (Jolicoeur & Mosimann, 1960; Humphries *et al.,* 1981; Bookstein *et al.,* 1985). To evaluate size-free shape differences between populations, Burnaby's method was used to correct for size effects (Burnaby, 1966; Rohlf & Bookstein, 1987; Doadrio *et al*., 2002). All analyses were performed using the corrected matrix. A second PCA was conducted using a covariance matrix for morphometric characters and a correlation matrix for meristic characters. All analyses were performed using the statistics packages NTSYS v. 2.1 (Rohlf, 2000) and PAST v. 1.31. Morphometric and meristic characters were analysed independently.

Genetic analysis

Four cytochrome *b* gene sequences for *Yuriria* (AF469160-AF469163), one for *Notropis calientis* (AF469141) and one for *Notropis sallaei* (AF469 135) were obtained from GenBank. A further 8 specimens (including the new species) were collected from drainages covering the entire distribution range of the genus *Yuriria* (Table 1 and Fig. 1). The cytochrome *b* gene sequences for these 8 specimens were obtained as follows: total DNA was isolated from tissues according to standard proteinase K and phenol/chloroform extraction procedures (Sambrook *et al.,* 1989). Two overlapping fragments of the cytochrome *b* gene (1140 bp) were amplified by polymerase chain reaction (PCR). The primers used for cytochrome *b* in all samples were those described in Zardoya and Doadrio, (1998). Amplification involved an initial denaturation step

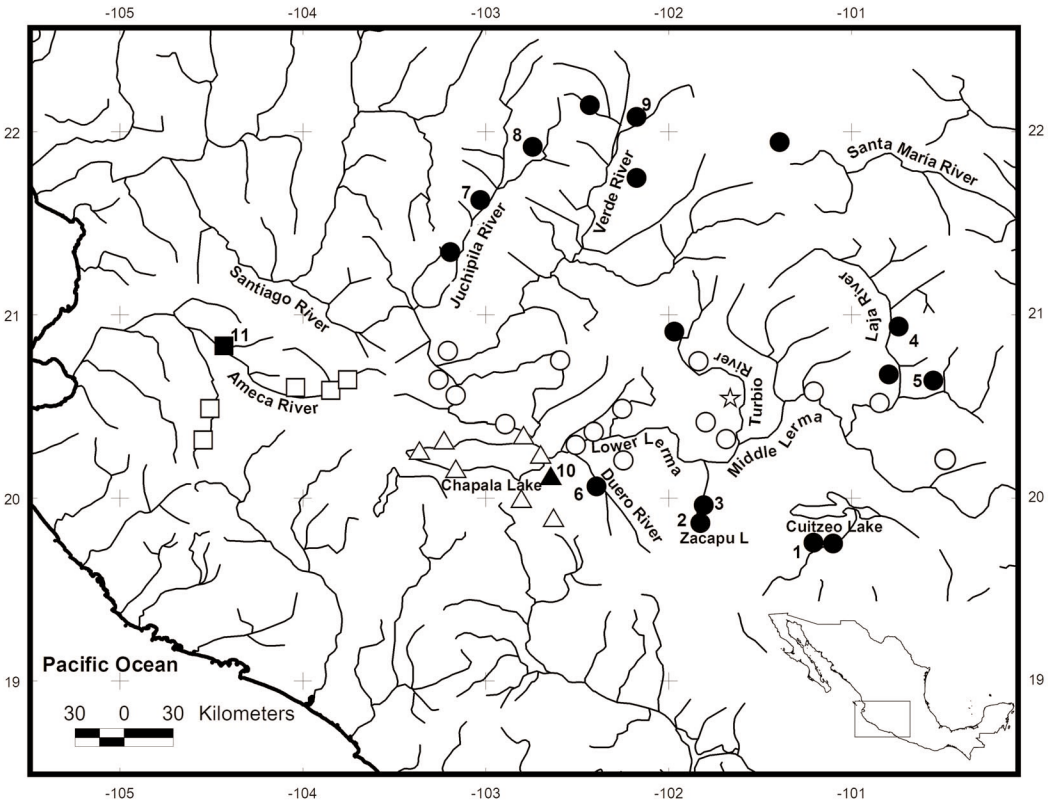

Fig. 1.— Distribution of *Yuriria alta* (circles), *Yuriria chapalae* (triangles) and *Yuriria amatlana* sp. nov. (squares). Star correspond to the Type locality of *Yuriria alta* (Lake Tupátaro). Open symbols correspond to historical occurrence points from which the species has not been collected in the last 5 years. Solid symbols represents sites from which the species has been collected in the last 5 years. Numbers correspond to the localities shown in Table 1.

Fig. 1.— Distribución de *Yuriria alta* (círculos), *Yuriria chapalae* (triangulos) y *Yuriria amatlana* sp. nov. (cuadrados). La estrellas corresponde a la Localidad Tipo de *Yuriria alta* (Lago Tupátaro). Símbolos vacíos corresponen a las localidades históricas donde la especie no ha sido localizada en los últimos 5 años. Símbolos llenos corresponden a localidades donde la especie ha sido colectada en los últimos 5 años. Números corresponden a las localidades señaladas en la Tabla 1.

at 94°C for 2 min, followed by 35 cycles as follows: denaturation at 94°C (1 min), annealing at 48°C (1 min), and extension at 72°C (1.45 min), with a final extension of 7 min at 72°C. PCR were prepared in 25 µl reaction containing final concentrations of 0.4 µM of each primer, 0.2 mM of each dNTP, 1.5 mM $MgCl_2$, and 1U of Taq DNA polymerase (Biotools). PCR products were checked on 1.5% agarose gels, and cloned using the pGEM-T vector (Promega) into *Escherichia coli* JM109. Positive clones were sequenced using the FS-Taq Dye Deoxy Terminator cycle-sequencing kit (Applied Biosystems). The DNA sequences of both strands were determined using M13 universal (forward and reverse) sequencing primers. All samples were sequenced on an Applied Biosystems 3700 DNA sequencer following the manufacturer's instructions. Chroma-tograms and alignments were checked by visual inspection. We used Modeltest 3.7 (Posadas & Crandall, 1998) to find the best evolutionary model that fit our data. The aligned data were analysed using the Bayesian inference method with the program Mr. Bayes 3.1.1 (Hueselsenbeck & Ronquist, 2001) by simulating a Markov chain for 1,000,000 cycles. Based on the HKY model obtained by Modeltest, genetic distances (D_{HKY}) between species were obtaining using the program Sequencer 6.1.0 (written by B. Kessing and available at http://nmg.si.edu/). Pairwise genetic distances were also obtained for each pair of populations

using HKY distances as implemented in PAUP 4.0b10 (Swofford, 2002).

Yuriria amatlana sp. nov.
(Fig. 2A, Table 2)

HOLOTYPE. (Table 2, Fig. 2A) CPUM-1631, 58.62 mm SL. Río Chiquito, Ixtlan del Río, Amatlan de Cañas, Nayarit, Mexico. Geographic coordinates: latitude 20º48´2.1´´N, longitude 104º 25´37.1´´W. Coll. R. Pérez-Rodríguez and R. Rosas-Valdez, 9 June 2005.

PARATYPES. CPUM-1610-1630, 21 individuals; IBUNAM-P 14437, 5 individuals and MNCN-259039-41, 3 individuals. Same data as for the holotype.

COMPARATIVE MATERIAL. *Yuriria amatlana* sp. nov. 22 specimens CPUM-1610-1630 and 1631, 5 specimens IBUNAM-P 14437 and 3 specimens MNCN-259039-41 (Río Chiquito de Amatlan, Ixtaln del Río, Amatlan de Cañas, Ameca River Drainage, Nayarit); *Yuriria chapalae* 20 specimens CPUM-1595-1614 and 5 specimens IBUNAM-P14493 (Guaracha Dam, near San António Guaracha, Chapala Lake Drainage, Michoacan); *Yuriria alta* 30 specimens MNCN-208.235 (Tributary of la Laja River, Balneario de Xote, near San Miguel de Allende, Guanajuato); and *Yuriria alta* 30 specimens MNCN-208.870 and MNCN-208.885 (Outflow of Zacapu Lake, near Panindicuaro, Michoacan) (Table 1).

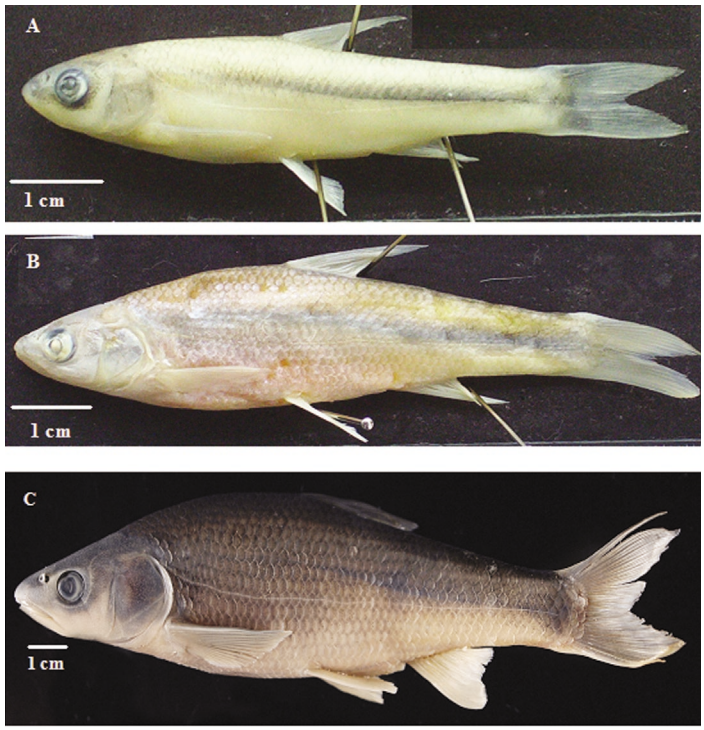

Fig. 2.— A) *Yuriria amatlana* sp. nov. Holotype CPUM-1630 from the Amatlan de Cañas population, Ameca River Basin, B) *Y. chapalae* from the Guaracha Dam population, Chapala Lake Basin, and C) *Y. alta* from the Zacapu population, Zacapu Lake Drainage.

Fig. 2.— A) *Yuriria amatlana* sp. nov. Holotype CPUM-1630 de la población de Amatlan de Cañas, cuenca del río Ameca. B) *Y. chapalae* de la presa de Guaracha, cuenca del lago Chapala, y C) *Y. alta* de la población de Zacapu, Cuenca del Lago Zacapu.

DIAGNOSIS. *Yuriria amatlana* sp. nov. differs from its sister species, *Y. alta* and *Y. chapalae*, according to the following set of characters: 9, rarely 10 (mean = 9.36, SD = 0.49) branched rays on the pelvic fin (*vs*. 10, rarely 8-9 or 11 in *Y. chapalae* and 8, rarely 7 in *Y. alta*); (50-52) 53-54, (mean = 52.36, SD = 1.39) pored lateral-line scales [*vs.* (48-50) 51 in *Y. chapalae* and (47-49) 50, (51) in *Y. alta*], and 10 scales in a transverse series up to the lateral line (*vs.* 9, rarely 8 in *Y. chapalae* and *Y. alta*) (Table 3). Body coloring light yellowish-brown (vs. yellow to golden coloration in *Notropis amecae* males). Dark grey band running from the start of the dorsal fin to the head less conspicuous than that observed for *Y. alta* and *Y. chapalae* (Fig. 2). Thirty-three fixed nucleotide positions, or autopomorphic characters, in the cytochrome *b* sequence with respect to its sister species *Y. alta* and *Y. chapalae* (Table 4). Genetic divergences for the cytochrome *b* gene`$D_{HKY}$= 3.8% (range 3.2% to 4.4%) between *Yuriria amatlana* and *Y. alta*;`D_{HKY}= 5 % (range 4.8% to 5.2 %) between *Y. amatlana* and *Y. chapalae*; and`D_{HKY} = 2.6% (range 2.1% to 3.3%) between *Y. chapalae* and *Y. alta*. No sexual dimorphism was detected in our analysis. This species is clearly distinguished with respect to its co-distributed related species (*Notropis amecae*) and other members of the Central Mexico *Notropis* by having (50-52) 53-54, (mean 52.36, SD = 1.39) pored lateral-line scales (*vs.* 11-34 in *N. amecae*; 1-15 in *N. calientis* and 39-64 in *N. sallei*) and a complete lateral line (incomplete in the *Notropis calientis* group and incomplete to complete in *N. sallei*).

DESCRIPTION. D= II-III (7) 8; A= II-III (7) 8; P= I-II (15) 16 (17); Pv= II (9) 10; C= (34-35) 36; GR= (8) 9 (10), PSL = (50-52) 53-54, UTS = 10, LST= 5 (6); pharyngeal teeth 4-4. All morphometric and meristic measurements are shown in Table 2. Like the other species in the genus, *Yuriria* specimens have two small barbels at the mouth commissure.

Table 2.— Statistical parameters for the morphometric and meristic characters of *Yuriria amatlana* sp nov., *Y. chapalae* and *Y. alta*. Each morphometric variable is divided by standard length. Variable codes are given in the methods section (SD = standard deviation).

Tabla 2.— Parámetros estadísticos para los caracteres morfométricos y merísticos de *Yuriria amatlana* sp. nov., *Y. chapalae* y *Y. alta*. Cada variable morfométrica es dividida por la longitud estándar. Los códigos de las variables se indican en la sección de métodos (SD = desviación estándar).

Species	***Yuriria amatlana* sp. nov**			***Yuriria chapalae***		***Yuriria alta***			
Population	**Holotype**	**Ameca River (n = 30)**		**Guaracha Dam (n = 25)**		**Zacapu lake (n = 30)**		**Lajas lake (n = 30)**	
Morphometrics		**Range**	**Mean ± SD**	**Range**	**Mean ± SD**	**Range**	**Mean ± SD**	**Range**	**Mean ± SD**
SL (in mm)	58.66	43-92	60.28 ± 10.5	104-57	86.13 ± 13.3	161-112	134.8 ± 14.7	94-47.4	64 ± 11.6
HL	14.36	.23-.26	.25 ± 0.007	.21-.26	.24 ± 0.01	.24-.28	.26 ± 0.009	.25-.30	.27 ± 0.01
PrOL	3.53	.04-.07	.05 ± 0.005	.04-.07	.06 ± 0.008	.05-.09	.07 ± 0.007	.05-.08	.07 ± 0.007
InOW	3.82	.06-.07	.06 ± 0.003	.04-.06	.05 ± 0.004	.04-.05	.04 ± 0.002	.05-.08	.07 ± 0.008
PoOL	7.04	.11-.13	.12 ± 0.006	.11-.14	.13 ± 0.006	.13-.15	.14 ± 0.005	.11-.15	.13 ± 0.008
Hh	9.95	.16-.18	.17 ± 0.005	.14-.23	.16 ± 0.01	.13-.17	.16 ± 0.007	.13-.19	.17 ± 0.01
PrP	15.10	.47-.51	.48 ± 0.008	.24-.48	.27 ± 0.04	.27-.30	.28 ± 0.006	.27-.31	.30 ± 0.01
PrD	28.84	.24-.29	.26 ± 0.01	.47-.51	.48 ± 0.01	.47-.54	.51 ± 0.01	.48-.57	.52 ± 0.01
PrV	29.19	.49-.51	.50 ± 0.006	.47-.52	.49 ± 0.01	.50-.55	.52 ± 0.01	.49-.56	.53 ± 0.01
PrA	39.61	.66-.72	.69 ± 0.01	.65-.73	.71 ± 0.01	.69-.77	.72 ± 0.01	.69-.77	.72 ± 0.01
DFL	14.04	.22-.26	.23 ± 0.008	.17-.23	.20 ± 0.01	.16-.22	.19 ± 0.01	.17-.22	.19 ± 0.01
PFL	12.55	.17-.21	.19 ± 0.01	.22-.27	.24 ± 0.01	.18-.24	.21 ± 0.01	.21-.27	.23 ± 0.01
PvFL	9.54	.13-.16	.15 ± 0.006	.14-.18	.17 ± 0.008	.13-.16	.15 ± 0.07	.09-.20	.15 ± 0.01
AFL	9.08	.14-.19	.16 ± 0.009	.15-.19	.17 ± 0.01	.07-.16	.14 ± 0.01	.13-.21	.16 ± 0.01
EALP	20.12	.31-.34	.33 ± 0.009	.30-.36	.33 ± 0.01	.26-.33	.30 ± 0.01	.26-.34	.29 ± 0.01
ADUP	31.43	.51-.54	.53 ± 0.01	.48-.57	.52 ± 0.01	.20-.57	.51 ± 0.08	.47-.55	.51 ± 0.01
BD	13.23	.20-.23	.22 ± 0.007	.22-.29	.25 ± 0.01	.26-.31	.29 ± 0.01	.24-.27	.25 ± 0.009
BLD	6.52	.10-.11	.11 ± 0.004	.10-.14	.12 ± 0.08	.10-.12	.11 ± 0.004	.10-.12	.11 ± 0.005
DAOD	17.19	.27-.31	.29 ± 0.01	.29-.35	.31 ± 0.01	.27-.35	.32 ± 0.01	.28-.32	.30 ± 0.009
Meristics									
D	7	7-8	7.03 ± 0.18	7-8	7.04 ± 0.20	6-7	6.96 ± 0.18	6-7	6.96 ± 0.18
Pv	9	9-10	9.36 ± 0.49	8-11	9.68 ± 0.86	7-8	7.96 ± 0.18	7-8	7.96 ± 0.18
A	7	7-8	7.06 ± 0.25	7-8	7.64 ± 0.48	6-8	6.96 ± 0.32	6-7	6.93 ± 0.25
PLS	53	50-54	52.36 ± 1.39	48-51	50.20 ± 0.95	47-51	50.10 ± 1.06	47-51	48.73 ± 1.29
UTS	10	10	10	8-9	8.68 ± 0.41	8-9	8.94 ± 0.21	8-9	8.94 ± 0.24
LTS	5	5-6	5.23 ± 0.33	5-6	5.23 ± 0.43	5	5	5-6	5.08 ± 0.14
GR	9	8-10	8.86 ± 0.57	7-9	8.28 ± 0.59	7-8	7.08 ± 0.28	7-9	7.6 ± 0.66

The body is moderately deep, laterally compressed and elongated. Its maximum height is 4.09-4.81 (mean = 4.4) times the standard length and minimum body height 8.15-9.84 (mean = 8.9) times the standard length. Ventral and dorsal profile moderately arched in the anterior half of the body. The mouth is protractile, terminal and oblique. Snout slightly rounded, preorbital distance 14.83-18.30 (mean = 16.9) times the standard length. Head longer than high and moderately pointed, cephalic length 3.6-4.2 (mean = 3.9) times the standard length and cephalic height 5.44-6.35 (mean = 5.8) times the standard length. The scales are large and not tightly imbricated. Lateral line completed and strongly curved in the pectoral fin region. The dorsal and anal fins are short, dorsal fin is 3.78-4.8 (mean = 4.2) times the standard length and anal fin is 5.22-6.87 (mean = 5.9) times the standard length. The pelvic fin arises at or slightly behind the origin of the dorsal fin, predorsal distance is 1.9-2.11 (mean = 2.0) times the standard length and preventral distance 1.8-2.09 (mean = 1.9) times the standard length. Caudal fin deeply forked. The caudal peduncle is long, anal peduncle distance 2.86-3.34 (mean = 3.0) times the standard length and dorsal peduncle distance 1.81-1.98 (mean = 1.8) times the standard length.

Table 3.— Summary of the diagnostic characters of the populations of *Yuriria* spp. In brackets number of individuals analyzed.

Tabla 3.— Resumen de los caracteres diagnósticos de las poblaciones de *Yuriria* spp. Entre paréntesis el número de individuos analizados.

Characters	***Yuriria amatlana* sp. nov.**	***Yuriria chapalae***	***Yuriria alta***
Number of pored scales in a lateral series	50(4)-51(5)-52(5)-53(8)-54(8)	48(1)-49(6)-50(5)-51(13)	47(7)-48(9)-49(12)-50(20)-51(12)
Number of scales in transverse series	16(5)-17(13)-18(12)	13(1)-14(11)-15(13)	14(4)-15(55)-16(1)
Pelvic fin branched rays	9(19)-10(11)	8(3)-9(5)-10(14)-11(3)	7(2)-8(58)
Anal fin branched rays	7(28)-8(2)	7(9)-8(16)	6(3)-8(1)-7(56)
Gill rakers	8(8)-9(20)-10(2)	7(5)-8(8)-9(12)	7(25)-6(34)-9(1)
Body colour	Light yellow-cream	Reddish-yellow	Dark brown

PIGMENTATION PATTERN. The body color of preserved specimens is light yellowish-brown. Individuals show a dark lateral stripe, more conspicuous and broad in the postdorsal region of the body, and less apparent and more diffuse in the predorsal region. *Yuriria amatlana* sp. nov. has a dark patch in the caudal peduncle at the end of the lateral stripe in the hypural region. The base of the dorsal fin shows fine pigment stripes and most of the specimens analysed have dark spots in the dorsal region. Snout and upper part of the head pigmented. All fins clear and unpigmented.

ETYMOLOGY. The name "*amatlana*" was taken from the name of the region of the type locality, Amatlan de Cañas.

DISTRIBUTION AND HABITAT. The type locality of *Y. amatlana* sp. nov. is the Río Chiquito, near Ixtlan del Río in the Ameca river drainage, approximately 6 km south of the town of Amatlan de Cañas, in the state of Nayarit. The taxon is only known in the Ameca basin. The presence of *Yuriria* in the Ameca basin has been reported in the Teuchitlan River, Atenguillo river, Ameca river near the town of Ameca and in Ahuacatlan, all in the state of Jalisco, western Central Mexico (Miller & Smith, 1986; Espinosa *et al.,* 1993; Miller *et al.,* 2005; University of Michigan Museum of Zoology and CPUM fish-database) (Fig. 1). At its type locality, the river is 10 m wide on average and depth is 1 m average. The substrate is principally sand and gravel, with a considerable number of boulders on the river bed. Riparian vegetation is a gallery forest composed mainly of *Taxodium* sp., with roots penetrating the river bank. When the river was sampled in the rainy season, the water was a turbid brown colour with high amounts of suspended material. Water temperature was 22ºC. Water flow is rapid with some meanders showing moderate flow. Aquatic vegetation was poor at the time of sampling, possibly because of swelling of the river. Fish were captured in the fast flow areas of the river. Associated native fish fauna were *Xenotoca melanosoma* Fitzsimons, 1972, *Goodea atripinnis* Jordan, 1880, *Ilyodon furcidens* (Jordan & Gilbert, 1882), *Ictalurus* sp., *Agonostomus monticola* (Bancroft, 1834) and *Scartomyzon austrinus* (Bean, 1880), along with the introduced *Cyprinus carpio* Güldenstädt, 1772 and *Oreochromis* sp.

CONSERVATION STATUS. The species is known from only a few sites within the Ameca River system, and now can be found only in the headwaters of the Ameca river. Although the sampling effort made in its distribution area has been intense, in the last three years no specimens of *Yuriria amatlana* sp. nov. have been collected at five of the six historical sites which were previously reported, representing more than 85% of extinction in previously known populations (Fig. 2). The sites where the species has recently disappeared have been mostly affected by the introduction of exotic species, water pollution and the use of water for agricultural or recreational purposes. According to the criteria and categories of the International Union for the Conservation of Nature and Natural Resources (IUCN, 2001 - http://app.iucn.org/webfiles/doc/SSC/RedList/RedListGuidelines.pdf), this species should be considered critically endangered (A 2a,c,e).

Comparative data and Discussion

The results of our meristic and morphometric analysis of specimens of *Y. amatlana* sp nov. (*n* =

Table 4.— Molecular diagnostic characters for the cytochrome *b* gene in the genus *Yuriria*. Ts= transition and Tv= transversion within the same base position.

Tabla 4.— Caracteres moleculares diagnósticos para el gen citocromo *b* en el género *Yuriria*. Ts= transición y Tv= transversión dentro de las mismas posiciones.

BP position / Species	36	45	108	115	141	174	282	294	348	351	354	366	375	408	423	444	459	462	498	537	561	579	580	591	609	654
Y. alta	G	C	G	C	C	C	C	T	G	A	C	G	A	T	A	T	G	T	A	C	C	C	G	A	A	T
Y. chapalae	A	C	A	C	T	T	C	T	G	G	C	A	A	T	G	C	G	C	T	C	T	C	A	A	A	T
Y. amatlana	G	**T**	G	**T**	C	C	**T**	**C**	**A**	A	**T**	A	**T**	**C**	A	T	**C**	T	A	**T**	C	**T**	G	**G**	**G**	**C**
Substitution type	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Tv	Ts	Ts	Ts	Tv	Ts	Tv	Ts	Ts	Ts	Ts	Ts	Ts	Ts

BP position / Species	699	703	705	714	732	777	801	810	813	816	849	867	906	918	919	930	966	972	984	1003	1017	1050	1077	1131
Y. alta	C	A	G	G	A	A	T	C	G	A	C	A	A	T	C	T	A	G	A	C	G	T	T	G
Y. chapalae	C	G	G	G	A	G	T	T	A	G	C	A	A	T	C	A	A	G	G	C	A	T	T	A
Y. amatlana	**T**	A	**A**	**A**	**G**	A	**C**	C	A	A	**T**	**G**	**G**	**C**	**T**	A	**G**	**A**	A	**T**	A	**C**	**C**	G
Substitution type	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Tv	Ts	Ts	Ts	Ts	Ts	Ts	Ts	Ts

30), *Y. chapalae* (n = 25) and *Y. alta* (n = 60), are provided in Table 2 and Figure 3.

MORPHOMETRICS

As discussed above, specimens of the genus *Yuriria* from the Ameca river basin show many diagnostic meristic and genetic differences with respect to their two sister species *Y. alta* and *Y. chapalae*, and therefore warrant designation as a new species, *Yuriria amatlana* sp. nov.

In an exploratory PCA including morphometric measurements, PCI explained 93.29% of the variation and eigenvectors showed closed values with the same symbol, suggesting the influence of standard length on the results (Bookstein *et al.,* 1985; Doadrio *et al.,* 2002). A second PCA conducted with a Burnaby corrected matrix, revealed 51% of variance in PCI and a cumulative 63.84 % in PCII. The characters found to contribute most to variation were interorbital width, head height and the distance from the snout to the base of the ventral fin and pectoral fin in PCI, and body depth in PCII (Table 5). The variation pattern was more influenced by PCI (Fig. 3A) and the most differentiated population was that from the La Laja River. No well-defined groups emerged, and no evident morphological diagnostic characters appeared among the three species (*Y. alta*, *Y. chapalae* and *Y. amatlana*) (Fig. 3A). Despite morphology having been largely used as the basis for species descriptions, many species show a high degree of phenotypic plasticity depending on habitat conditions, and the influence of allometry in morphometric measurements has been widely recognized (Hood & Heins, 2000; Trapani *et al.,* 2005). We conclude that morphologic measurements alone are not appropriate diagnostic characters for the identification of *Yuriria* species. Thus, other sources of information such as the biogeographic, meristic, pigmentation patterns and molecular data are used here for species recognition. In our PCA analyses based on meristic characters, PCI explained 41.62% of variance and PCI + PCII explained a cummulative 63.17% of the variance. Moreover, high eigenvector values were associated with the characters branched rays on pelvic fin, number of pored scales in the lateral series and gill rakers in PCI, separating the two populations of *Y. alta* with respect to *Y. chapalae* and *Y. amatlana*, and anal fin rays and scales in a transverse series in PCII, separating *Y. chapalae* from *Y. amatlana* (Table 6). For the meristic characters, the analysis indicated a variation pattern with the formation of three well-defined groups, with practically no overlap among ellipses (Fig. 3B).

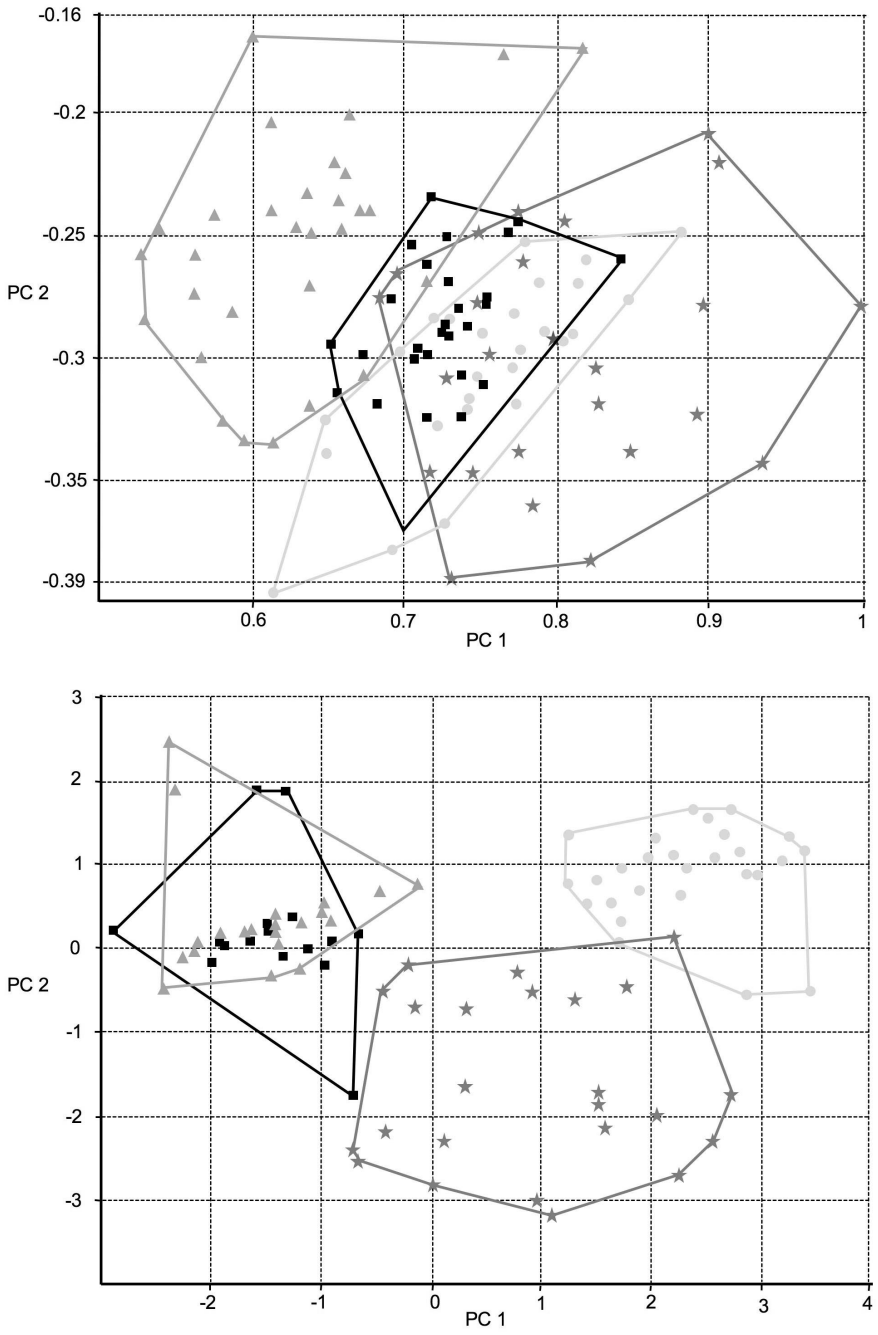

Fig. 3.— A) Plots of the first two principal components for 19 Burnaby-corrected morphometric variables. B) Plots of the first two principal components for 7 meristic variables. Triangles correspond to *Y. alta* from the Laja River population (Middle Lerma Basin); squares to *Y. alta* from the Zacapu populations (Zacapu Lake Basin); stars to the *Y. chapalae* population from Guaracha Dam (Chapala Lake Basin); and circles to *Y. amatlana* sp. nov. from the Amatlan de Cañas population (Ameca River Basin).

Fig. 3.— A) Gráficos de los primeros dos componentes principales para 19 variables morfométricas Burnaby-corregidas. B) Gráficos de los dos primeros componentes principales para 7 variables merísticas. Triángulos corresponden a *Y. alta* de la población del río Laja (Cuenca media del Lerma); cuadrados a *Y. alta* de la población de Zacapu (Cuenca del Lago Zacapu); estrellas a *Y. chapalae* de la población de la presa de Guaracha (Cuenca del Lago de Chapala); y círculos a *Y. amatlana* sp. nov. de la población de Amatlan de Cañas (Cuenca del río Ameca).

Table 5.— Eigenvectors and eigenvalues for the first four principal components obtained for 19 morphometric variables. Variable codes are given in the methods section.

Tabla 5.— Eigenvectores y eigenvalores para los cuatro primeros componentes principales obtenidos para 19 variables morométricas. Los códigos de las variables se explican en la sección de métodos.

Variable/eigenvectors	PCI	PCII	PCIII	PCIV
SL	0.040	0.003	0.041	0.001
HL	0.016	-0.020	0.035	0.000
PrOL	-0.111	0.026	0.078	-0.003
InOW	0.156	-0.143	-0.011	-0.004
PoOL	0.053	0.007	0.053	0.004
Hh	0.153	-0.012	-0.056	0.010
PrP	0.062	0.080	-0.020	0.008
PrD	0.088	0.000	0.035	0.002
PrV	0.147	-0.020	-0.001	0.003
PrA	0.124	-0.009	0.026	0.003
DFL	-0.036	-0.049	-0.017	0.001
PFL	-0.227	-0.149	-0.097	0.003
PvFL	-0.022	-0.058	0.007	0.000
AFL	-0.052	-0.082	0.086	0.007
EALP	-0.117	0.022	0.091	0.000
ADUP	0.023	0.018	-0.020	-0.050
BD	-0.027	0.107	-0.076	0.004
BLD	-0.135	0.081	-0.010	0.006
DAOD	0.015	0.036	-0.077	0.005
Eigenvalues	0.0082	0.0020	0.0015	0.0009
Percentage	51.00	12.84	9.62	5.81
Cumulative %	51	63.84	73.46	79.27

Table 6.— Eigenvectors and eigenvalues for the first three principal components obtained for 6 meristic variables. Variable codes are given in the methods section.

Tabla 6.— Eigenvectores y eigenvalores para los tres primeros componentes principales obtenidos para 6 variables merísticas. Los códigos de las variables se explican en la sección de métodos.

Variable/eigenvectors	PCI	PCII	PCIII
PSL	0.4934	0.0854	-0.3719
D	0.1346	0.0627	0.8836
Pv	0.5239	-0.35	0.080
A	0.1794	-0.8015	-0.0512
UTS	0.4472	0.448	-0.1604
LTS	0.1046	0.0427	0.3836
GR	0.4815	0.1612	0.2149
Eigenvalues	2.40	1.24	0.82
Percentage	41.62	21.55	14.25
Cumulative %	41.62	63.17	74.21

GENETICS

We found 53 variable characters, of which 45 were parsimony informative. Third codon positions were the most informative characters (29 informative characters), followed by first codon positions (15 characters). Saturation of transition and transversion changes was checked by plotting the absolute number of changes of each codon position against patristic distances. There was no ingroup evidence of saturation at any of the three positions (data not shown). The HKY model was selected as the model best fitting the data set. Rate matrix parameters were: -lnL= 2087.9932; K= 4; BIC= 4204.1450. Base frequencies were: freqA= 0.2704; freqC= 0.2776; freqG= 0.1653; freqT= 0.2868. Among-site rate variation was equal. For the Bayesian phylogenetic analysis, 5% of the generations obtained were burnt and discarded. The consensus tree revealed three main clades in the genus *Yuriria*, with high Bayesian posterior probabilities (BPP) obtained: one formed by *Y. alta* populations (BPP 96), another by the only population of *Y. chapalae* (100 BPP) and a last clade by the new taxon *Y. amatlana* (100 BPP) (see Fig. 4). Genetic distances were: $`D_{HKY}$ = 3.8% (range 3.2% to 4.4%) between *Y. alta* and *Y. amatlana*; $`D_{HKY}$ = 5% (range 4.8% to 5.2%) between *Y. amatlana* and *Y. chapalae*; and $`D_{HKY}$ = 2.6% (range 2.1% to 3.3%) between *Y. chapalae* and *Y. alta*. Pairwise genetic distances between the populations analysed are shown in table 7.

Meristic and molecular data are congruent in recognizing three well differentiated groups corresponding to the two described species (*Y. alta* and *Y. chapalae*) and the new taxon (*Y. amatlana*). Based on these characters, we confirmed our meristic data indicating the existence of a new *Yuriria* genus taxon in the Ameca river basin. Assuming a molecular clock of 1 million years per 1% pairwise differences, which is the generally accepted rate for the cytochrome *b* gene in other cyprinids, including *Notropis* species from Central Mexico (Dowling *et al*., 2002; Shönhunth, 2002; Doadrio & Carmona, 2004), the *Yuriria* species from the Ameca river diverged from the other species of *Yuriria* in contiguous basins during the Pliocene, approximately 3.8 Mya. These results are consistent with findings for other pairs of sister species inhabiting the

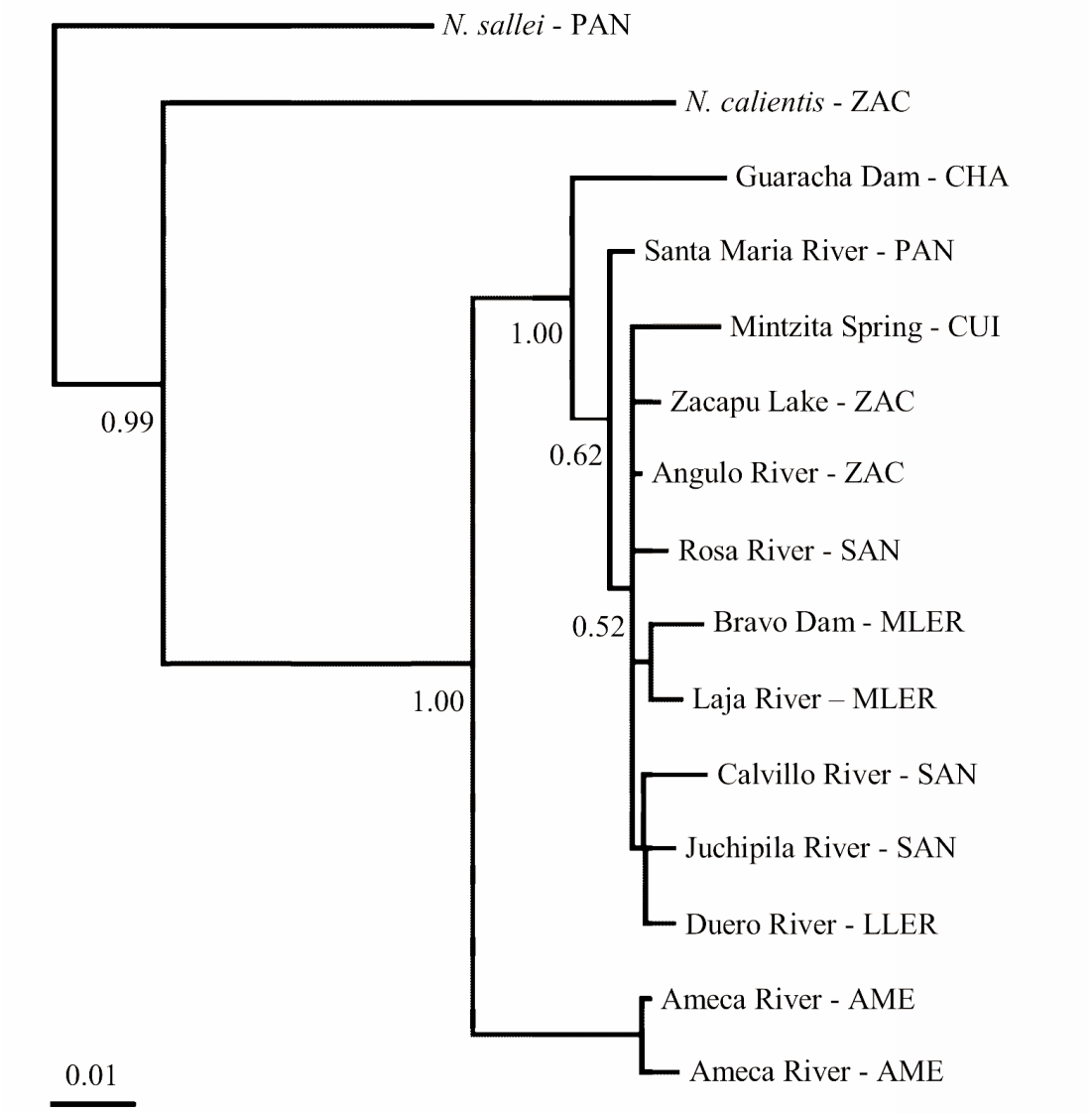

Fig. 4.— Phylogenetic tree for 12 specimens of the genus *Yuriria* recovered from cytochrome *b* sequences (1140 bp) according to a Bayesian analysis based on HKY model. Numbers below the branches indicate Bayesian posterior probabilities.

Fig. 4.— Árbol filogenético para 12 individuos del género *Yuriria* con secuencias del citocromo *b* (1140 bp) de acuerdo al análisis bayesiano con el HKY modelo. Número debajo de las ramas indican valores de probabilidades posteriores.

Ameca river basin and other drainages of Central Mexico (e.g., cladogenesis of *Allotoca goslinae* Smith & Miller, 1987 and *Ameca splendens* Miller & Fitzsimons, 1971, with an estimated divergence time of 3.7 Mya, *sensu* Doadrio & Domínguez-Domínguez, 2004). These data confirm an ancestral connection between the Ameca and contiguous basins and could suggest the cladogenetic event was induced by the same vicariant event promoted by tectonic activity during that period (see Domínguez-Domínguez *et al.,* 2006). Given the disappearance of many of its historical occurrence points, its degraded habitat and the extinction of other species in the basin, we recommend that *Yuriria amatlana* be added to the current list of endangered species.

Table 7.— Percentage of divergences (above the diagonal) and pairwise genetic distances (below the diagonal) among *Yuriria amatlana, Y. chapalae* and *Y. alta* populations obtained using the HKY model.

Tabla 7.— Porcentaje de divergencia (encima de la diagonal) y distancias genéticas pareadas (debajo de la diagonal) entre poblaciones de *Yuriria amatlana*, *Y. chapalae* y *Y. alta* usando el modelo HKY.

Species	Populations	Mintzita	Bravo	Laja	Zacapu	Angulo	Rosa	Calvillo	Juchipila	Duero	Guaracha	**Ameca**
Yuriria alta	Mintzita		1.5	1.42	1.32	1.06	1.42	1.86	1.5	1.5	3.34	**4.19**
	Bravo	0.015		0.79	0.88	0.79	1.06	1.49	1.06	1	2.87	**4.29**
	Laja	0.0142	0.0079		0.61	0.52	0.7	1.21	0.79	0.79	2.6	**4**
	Zacapu	0.0132	0.0088	0.0061		0.26	0.7	1.02	0.7	0.7	2.51	**3.72**
	Angulo	0.0106	0.0079	0.0052	0.0026		0.44	0.74	0.44	0.44	2.23	**3.44**
	Rosa	0.0142	0.0106	0.007	0.007	0.0044		1.12	0.7	0.7	2.42	**3.92**
	Calvillo	0.0186	0.0149	0.0121	0.0102	0.0074	0.0112		0.93	0.83	2.94	**4.24**
	Juchipila	0.015	0.0106	0.0079	0.007	0.0044	0.007	0.0093		0.52	2.51	**3.91**
	Duero	0.015	0.01	0.0079	0.007	0.0044	0.007	0.0083	0.0052		2.51	**3.95**
Y. chapalae	Guaracha	0.0334	0.0287	0.026	0.0251	0.0223	0.0242	0.0294	0.0251	0.0251		**5.06**
Y. amatlana	**Ameca**	**0.0419**	**0.0429**	**.0400**	**0.0372**	**0.0344**	**0.0392**	**0.0424**	**0.0391**	**0.0395**	**0.0506**	

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