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**A New Species of Soapfish (Teleostei: Serranidae: *Rypticus*), with
Redescription of *R. subbifrenatus* and Comments on the Use of DNA
Barcoding in Systematic Studies**

Carole C. Baldwin¹ and Lee A. Weigt²



A New Species of Soapfish (Teleostei: Serranidae: *Rypticus*), with Redescription of *R. subbifrenatus* and Comments on the Use of DNA Barcoding in Systematic Studies

Carole C. Baldwin¹ and Lee A. Weigt²

A new species of *Rypticus* is described from the Bahamas, Bermuda, Florida, and the Caribbean Sea. The species previously has been confused with the spotted soapfish, *R. subbifrenatus* Gill 1861, with which it shares a similar pattern of dark spotting on the body. The new species differs from *R. subbifrenatus* in having yellow pigment on the pectoral fin and distal portions of the soft dorsal, caudal, and anal fins in life (pale in preservative); a different configuration of dark spots on the head; usually dark spots on the belly and caudal fin; almost always four dorsal-fin spines; and modally 25 total dorsal-fin elements, 15 pectoral-fin rays, and 23 total caudal-fin rays. The lower jaw typically extends further anteriorly beyond the upper jaw in the new species than in *R. subbifrenatus*, and the caudal peduncle is usually narrower. The new *Rypticus* typically inhabits deeper waters than *R. subbifrenatus*, and is commonly found on vertical slopes and walls vs. shallow, flat areas. The new species likely would have continued to go unnoticed without examination of genetic data, as there was little reason to look further at *R. subbifrenatus* until DNA barcoding revealed two distinct genetic lineages within the species. The value of DNA barcoding data in systematic studies and the need for increased support of taxonomy are highlighted. A neotype for *Rypticus subbifrenatus* is designated.

THE soapfish genus *Rypticus* comprises nine species that inhabit tropical to warm temperate waters in the Atlantic and eastern Pacific oceans (Guimarães, 1999; Heemstra et al., 2002). In the three major systematic treatments of Atlantic members of the genus (Schultz and Reid, 1939; Courtenay, 1967; Guimarães, 1999), *R. subbifrenatus* Gill 1861 is recognized as a single valid species. The purpose of this paper is to describe a new species of *Rypticus* that previously has been confused with *R. subbifrenatus*, a discovery first suggested by DNA barcoding data and subsequently corroborated by the identification of diagnostic morphological features. DNA barcoding (Hebert et al., 2003) involves sequencing approximately 650 bp of the mitochondrial gene cytochrome *c* oxidase subunit I (COI). This paper is one of a series of publications bringing clarity to the taxonomy of western Central Atlantic shorefishes through combined genetic and morphological investigation (Baldwin et al., 2009, 2011; Tornabene et al., 2010). There continues to be controversy over the use of DNA barcoding in systematic studies. We comment on some recent literature on the topic and stress the need for increased support of taxonomy.

MATERIALS AND METHODS

Specimens used in this study were collected from numerous localities as part of an ongoing study of species diversity of western Central Atlantic shorefishes. Additional specimens were examined from museum collections. Institutional abbreviations are as listed at <http://www.asih.org/node/204>. Specimens collected as part of this study were taken with quinaldine sulfate or rotenone using snorkel gear or scuba depending on depth. Field protocol involved taking digital color photographs of fresh color patterns and subsequently a tissue sample (muscle, eye, or fin clip) for genetic analysis. Voucher specimens were preserved and later used to investigate diagnostic morphological features

of the recovered genetic lineages. Counts and measurements were made following Hubbs and Lagler (1958). Measurements were made to the nearest 0.1 mm with digital calipers. Counts of dorsal-, anal-, caudal-, and pectoral-fin rays were made from digital radiographs of specimens because thick skin covering fins makes enumerating rays in *Rypticus* difficult. The pectoral fin on one side of the body (the side resting on the x-ray machine platform) was folded forward so that left and right fins were not superimposed on one another in the radiograph. This enabled a clear view of the pectoral fin on one side; pectoral-fin counts provided in the descriptions are thus from one side only, usually the left. The fourth element in the dorsal fin is variably a spine or a ray, the determination of which is most easily made by observing the configuration of the base of the element on a radiograph, especially its articulation with the pterygiophore on which it sits. Frequently in the new species the fourth element is a spine but is segmented at the distal end, in which case it may be mistaken for a soft ray upon external examination.

Depths of specimens collected with quinaldine and rotenone are frequently given as a range of numbers (e.g., 0–15 m), making it impossible to know the exact depth of capture. Maximum depth recorded was used in comparing depth preferences of *R. subbifrenatus* and the new species.

Tissue samples for molecular work were stored in saturated salt-DMSO (dimethyl sulfoxide) buffer (Seutin et al., 1991). Genomic DNA was extracted from up to approximately 20 mg minced preserved tissue via an automated phenol:chloroform extraction on the Autogen-prep965 (Autogen, Holliston, MA) using the mouse tail tissue protocol with a final elution volume of 50 μ L. For polymerase chain reaction (PCR), 1 μ L of this undiluted genomic extract was used in a 10 μ L reaction with 0.5 U Bionline (BioLine USA, Boston, MA) Taq polymerase, 0.4 μ L 50 mM MgCl₂, 1 μ L 10X buffer, 0.5 μ L 10 mM deoxyribonucleotide triphosphate (dNTP), and 0.3 μ L 10 μ M each primer FISH-BCL (5'–TCAACYAATCAYAAAGATATYGGCAC) and FISH-BCH

¹Department of Vertebrate Zoology, National Museum of Natural History, Smithsonian Institution, P.O. Box 37012, Washington, D.C. 20013-7012; E-mail: baldwinc@si.edu. Send reprints requests to this address.

²Laboratories of Analytical Biology, National Museum of Natural History, Smithsonian Institution, Museum Support Center, 4210 Silver Hill Road, Suitland, Maryland 20746; E-mail: weigt@si.edu.

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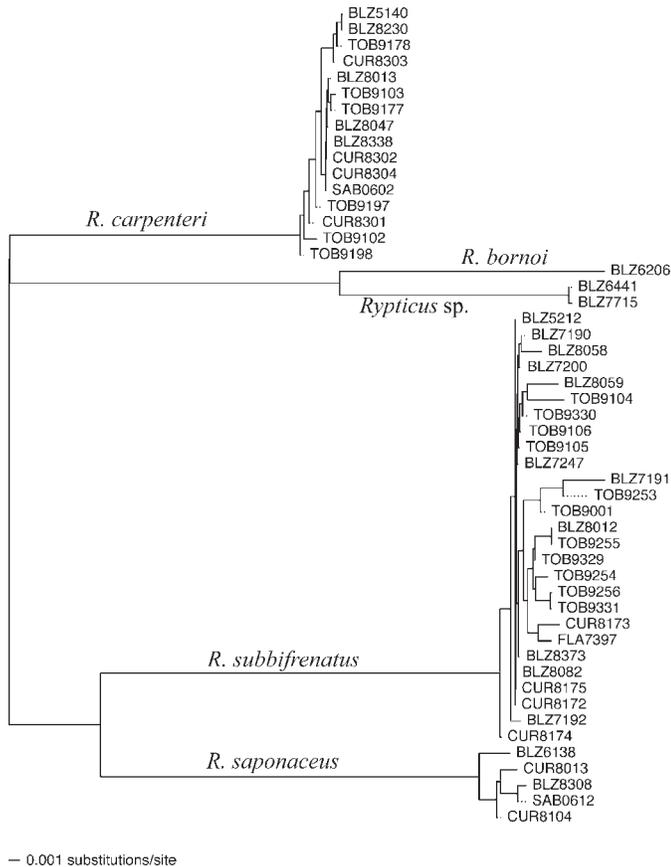


Fig. 1. Neighbor-joining tree derived from cytochrome c oxidase I sequences showing several genetically distinct lineages of western Atlantic *Rypiticus*.

(5′-TAAACTTCAGGGTGACCAAAAAATCA). The thermal cycler program for PCR was one cycle of five min at 95°C; 35 cycles of 30 s at 95°C, 30 s at 52°C, and 45 s at 72°C; one cycle of five min at 72°C; and a hold at 10°C. The PCR products were purified with Exosap-IT (USB, Cleveland, OH) using 2 μL 0.2X enzyme and incubated for 30 min at 37°C. The reaction was then inactivated for 20 min at 80°C. Sequencing reactions were performed using 1 μL of this purified PCR product in a 10 μL reaction containing 0.5 μL primer, 1.75 μL BigDye buffer, and 0.5 μL BigDye (ABI, Foster City, CA) and run in the thermal cycler for 30 cycles of 30 s at 95°C, 30 s at 50°C, four min at 60°C, and then held at 10°C. These sequencing reactions were purified using Millipore Sephadex plates (MAHVN-4550; Millipore, Billerica, MA) per manufacturer's instructions and stored dry until analyzed. Sequencing reactions were analyzed on an ABI 3730XL automated DNA sequencer, and sequence trace files were exported into Sequencher 4.7 (GeneCodes, Ann Arbor, MI). Using the Sequencher program, ends were trimmed from the raw sequences until the first and last ten bases contained fewer than five base calls with a confidence score (phred score) lower than 30. After trimming, forward and reverse sequences for each specimen were assembled. Each assembled pair was examined and edited by hand, and each sequence was checked for stop codons. Finally the consensus sequence (655 bp) from each contig was aligned and exported in a nexus format (*sensu* Swofford, 2002).

A neighbor-joining tree (Saitou and Nei, 1987) and distance matrix were generated using PAUP*4.1 (Swofford,

2002) on an analysis of Kimura two-parameter distances (Kimura, 1980). The neighbor-joining tree is intended only to show genetic distances in COI among individuals, not reflect interspecific phylogenetic relationships. The label for each entry on the tree is our DNA number, and we include that number in the Material Examined sections and figure captions. Abbreviations used in DNA numbers reflect geographical location: BAH—Bahamas, BLZ—Belize, CUR—Curacao, FLA—Florida, SAB—Saba Bank (Netherland Antilles), TCI—Turks and Caicos, TOB—Tobago. Material of *Rypiticus* not listed in the species accounts below but represented in the neighbor-joining tree is as follows: *R. saponaceus*—DNA number BLZ 6138 (no voucher); USNM 403508, DNA number BLZ 8308; USNM 403509, DNA number CUR 8013; USNM 403510, DNA number CUR 8104; USNM 388469, DNA number SAB 0612; *R. bornoi*—USNM 401244, DNA number BLZ 6206; *Rypiticus* sp.—DNA number BLZ 6441 (juvenile, no voucher); DNA number BLZ 7715 (larva, no voucher); *R. subbifrenatus*—DNA number FLA 7397 (no voucher). The COI sequences are deposited in GenBank (accession numbers JN828088–JN828138). In the "Other material examined" sections, SL is not provided for specimens that were used only for purposes of determining geographical distributions of the new species and *R. subbifrenatus*. Photo credits are given only for images taken by individuals other than the authors.

RESULTS

Five genetic lineages of *Rypiticus* are represented in our data set (Fig. 1). One lineage is *R. saponaceus*, another *R. bornoi*, and a third an unidentified lineage known only from one larval and one juvenile specimen from Belize. The remaining two lineages comprise specimens originally identified as *R. subbifrenatus*. Those lineages, which, on average, are 8.2% divergent in COI (Table 1), represent two morphologically and usually ecologically distinct species. Here we describe one of those lineages as a new species of *Rypiticus* and redescribe *R. subbifrenatus*.

Rypiticus carpenteri, new species

Slope Soapfish

Figures 2–5, Table 2

Rypiticus subbifrenatus (non Gill, 1861).—Courtenay, 1967:259, fig. 8a (black and white drawing).—Böhlke and Chaplin, 1968:291 (black and white drawing).—Smith, 1997:fig. 74 (color photograph).—Williams et al., 2010:fig. 59 (color photograph, reproduced here as Fig. 4, 54 mm SL).—Kells and Carpenter, 2011:219 (color illustration).

Holotype.—USNM 387946, 54.0 mm SL, Netherland Antilles, Saba Bank, 17°34′54″N, 63°24′24″W, 27–30 m, field number SABA-06-09, J. Williams, J. Van Tassell, and P. Hoetjes, 7 January 2006.

Paratypes.—(DNA vouchers). Belize: USNM 401039, DNA number BLZ 8047, 42.0 mm SL, off north end of Carrie Bow Cay, 16°48′09.5″N, 88°04′54.4″W, 0–3 m, field number CB08-3, C. Baldwin, L. Weigt, and Z. Foltz, 15 May 2008; USNM 401040, DNA number BLZ 8230, 31 mm SL, Belize Barrier Reef, south of South Cut, 16°45′43.2″N, 88°04′27.0″W, 12–14 m, field number CB08-21, C. Baldwin, D. Smith, L. Weigt, and Z. Foltz, 22 May 2008; USNM 401041, DNA number BLZ 8338, 46.8 mm SL, Belize Barrier

Table 1. Average (and Range) Kimura Two-parameter Distance Summary for Species of *Rypticus* Based on Cytochrome c Oxidase I (COI) Sequences of Individuals Represented in the Neighbor-Joining Tree in Figure 1. Intraspecific averages are shown in bold.

<i>Rypticus</i>	<i>carpenteri</i> (n = 16)	<i>subbifrenatus</i> (n = 27)	<i>saponaceus</i> (n = 5)	<i>bornoi</i> (n = 1)	sp. (n = 2)
<i>carpenteri</i>	0.1% (0–0.3)	–	–	–	–
<i>subbifrenatus</i>	8.2% (7.5–9.5)	0.3% (0–1.5)	–	–	–
<i>saponaceus</i>	7.9% (7.2–8.3)	8.2% (7.5–9.1)	0.3% (0–0.6)	–	–
<i>bornoi</i>	9.0% (8.4–9.4)	11.0% (10.4–12.0)	10.3% (10.0–10.7)	0.0% (0.0)	–
sp.	8.7% (8.3–9.1)	10.5% (10.0–11.5)	10.3% (10.0–10.6)	4.8% (4.8)	0.0% (0.0)

Reef, south of South Cut, 16°45'79.2"N, 88°04'24.8"W, 14–29 m, field number CB08-31, C. Baldwin, D. Smith, L. Weigt, and Z. Foltz, 25 May 2008. Curacao: USNM 401042, DNA number CUR 8303, 50.5 mm SL, Blue Bay, 12°07'57.14"N, 68°59'06.03"W, 0–25 m, field number CUR08-5, C. Baldwin, D. Smith, and L. Weigt, 14 March 2008; USNM 401043, DNA number CUR 8304, 22.0 mm SL, collected with USNM

401042. Saba: USNM 401051, DNA number SAB 0602, 40.3 mm SL, Saba Bank just south of Poison Bank, 17°28'46.7"N, 63°13'39.8"W, 24–7 m, J. T. Williams, J. Van Tassell, and P. Hoetjes, 4 January 2006. Tobago: USNM 401044, DNA number TOB 9103, 50.0 mm SL, Store Bay, 11°09'20.9"N, 60°50'32.1"W, 5–10 m, field number TOB09-4, C. Baldwin, D. Smith, and L. Weigt, 16 March 2009;

**Fig. 2.** Color in preservative of (A) *Rypticus carpenteri*, new species, holotype, USNM 387946, 54.0 mm SL and (B) *Rypticus subbifrenatus*, neotype, USNM 106516, 61.0 mm SL. Note pale vs. dark pectoral and vertical fins.

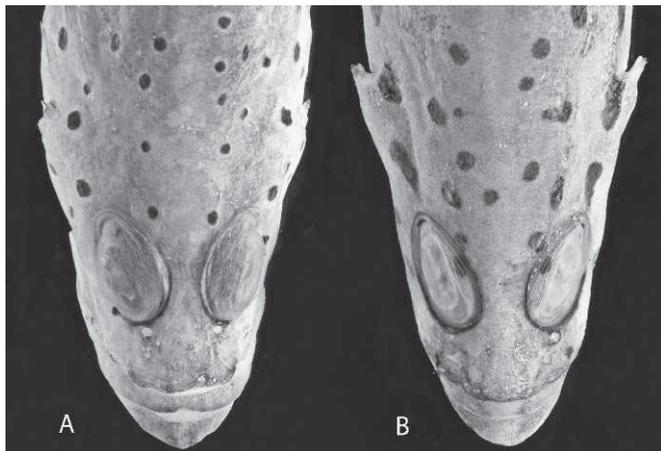


Fig. 3. Interorbital pigment in (A) *Rypticus carpenteri*, new species, UF 158246, 69.6 mm SL and (B) *Rypticus subbifrenatus*, USNM 318539, 74.0 mm SL.

USNM 401045, DNA number TOB 9177, 67.3 mm SL, Buccoo Reef, 11°11'17.0"N, 60°50'44.7"W, 15–18 m, field number TOB09-5, C. Baldwin, D. Smith, and L. Weigt, 17 March 2009; USNM 401046, DNA number TOB 9178, 81.0 mm SL, collected with USNM 401045; USNM 401047, DNA number TOB 9198, 56.2 mm SL, Buccoo Reef, 11°11'10.0"N, 60°50'45.7"W, 10–11 m, field number TOB 09-6, C. Baldwin and D. Smith, 17 March 2009. (Non DNA vouchers or DNA vouchers not represented in tree in Fig. 2). Bahamas: USNM 386966, 53 mm SL, Exuma, North Perry Buoy, Perry Institute of Marine Science, 23°46'52"N, 76°06'03"W, 24 m, field number VT 05-421, J. Van Tassel et al., 31 May 2005. Belize: USNM 379513, 56.0 mm SL, Carrie Bow Cay, 2002 (no other collection data). Dominica: USNM 389826, 3, 22.0–54.0 mm SL, Soufriere Bay at Scotts Head, 9–14 m, field number VGS 64-29, V. Springer, R. Blatcher, and R. Reckeweg, 15 November 1964. Navassa: USNM 360388, 57.0 mm SL, just S of NW point on shelf off W side of island, 24–30 m, field number NAV 99-25, J. Williams, B. Collette, L. Micheletti, and C. Thacker, 6 May 1999. Saba: USNM 387750, 3, 26.0–40.5 mm SL, Saba Bank just south of Poison Bank, 17°28'46.6998"N, 63°13'39.7986"W, 24–27 m, J. T. Williams, J. Van Tassel, and P. Hoetjes, 4 January 2006. Tobago: USNM 401052, 2, 55.0 and 63.0 mm SL, Buccoo Reef, 11°11'06"N, 60°49'22"W, 14 m, field number JTW 90-10, J. Williams, J. Howe, G. Johnson, S. Blum, M. Nizinski, and T. Munroe, 10 September 1990. Turks and Caicos: USNM 401048, DNA number TCI 9462, 75.5 mm SL, Highlands Bay, 21°29'53"N, 71°31'1"W, 0–7 m, field number TCI 09-10, C. Baldwin, L. Weigt, J. Williams, M. Fagan, B. Matulis, C. Castillo, and J. Moyer, 10 October 2009; USNM 401049, DNA number TCI 9463, 54.5 mm SL, collected with USNM 401049; USNM 401050, DNA number TCI 9703, 63.1 mm SL, the Arch, 21°28'57"N, 71°31'1"W, 10–17 m, field number TCI 09-25, J. Williams, M. Fagan, B. Matulis, and J. Catlin, 13 October 2009. U.S. Virgin Islands: UF 164326, 53.5 mm SL, St. Croix off Buck Island Reef National Monument, 17°47'34.8"N, 64°36'37.02"W, 11 m, field number BUIS 2005-149/150, Spieler et al., 12 October 2005; UF 158253, 86.4 mm SL, St. Croix off NE shore of Buck Island Reef National Monument, 17°47'29.8"N, 64°36'53.75"W, 8–10 m, field number BUIS 2001-29, W. Smith-Vaniz and L. Rocha, 3 August 2001.

Other material examined.—(DNA vouchers). Belize: USNM 401294, DNA number BLZ 5140, 46.2 mm SL; USNM 401295, DNA number BLZ 8013, 37 mm SL. Curacao: USNM 401289, DNA number CUR 8301, 50.5 mm SL; USNM 401290, DNA number CUR 8302, 52.9 mm SL. Tobago: USNM 401296, DNA number TOB 9102, 57.7 mm SL; USNM 401297, DNA number TOB 9197, 65.3 mm SL. (Non DNA vouchers). Bahamas: USNM 386607, 2, 28.0 and 51.0 mm SL; USNM 386221, 2, 44.5 and 49.0 mm SL. Belize: USNM 321041, 24 mm SL. Bermuda: ANSP 148246, 2 (photos only). Colombia: UF 25296, 1; USNM 401285, 2, 66.0 and 70.0 mm SL. Curacao: USNM 401286, 3, 41.0–57.0 mm SL; USNM 401287, 6, 39.5–53.7 mm SL; USNM 401288, 2, 44.6 and 51.0 mm SL. Dominica: USNM 401283, 4, 24.0–55.0 mm SL; USNM 401284, 29.0 mm SL; USNM 389823, 3, 16.0–30.0 mm SL. Florida: UF 15991, 69.7 mm SL; UF 16132, 8; UF 117222, 1; UF 205824, 1; UF 219770, 1. Haiti: UF 116454, 2. Navassa: USNM 360397, 29.0 mm SL; USNM 359887, 2, 31.0–59.0 mm SL. Grand Cayman: UF 12816, 1. Saba: USNM 401038, 39.0 mm SL; USNM 388400, 5, 31.5–54.0 mm SL; USNM 388056, 26 mm SL; USNM 388369, 30 mm SL; USNM 401282, 31.4 mm SL. Tobago: USNM 318524, 59 mm SL. U.S. Virgin Islands (St. Croix): UF 158232, 28.0 mm SL (*Rypticus* sp. juvenile); UF 158249, 4, 48.6–56.0 mm SL; UF 158247, 1, 63.5 mm SL; UF 158246, 69.6 mm SL; UF 164394, 2, 49.7 and 65.2 mm SL; UF 164356, 56.9 mm SL; UF 164351, 2, 36.7 and 64.8 mm SL; UF 164335, 2, 37.5 and 43.2 mm SL; UF 158251, 3, 22.0–55.2 mm SL.

Diagnosis.—A species of *Rypticus* distinguished from all congeners by the following unique combination of characters: pectoral fin and distal portions of soft dorsal, caudal, and anal fins pale yellow to yellow in life, pale in preservative; head and trunk with numerous dark spots, size of spots variable but those on head posterior to horizontal through center of orbit almost always smaller than pupil; interorbital region usually with two dark spots at posterior end, spots set slightly apart from orbital rim; belly with dark spots; caudal fin and sometimes soft dorsal and anal fins usually with at least a few, sometimes tiny, dark spots; dorsal-fin spines three or four (almost always four); total dorsal-fin elements modally 25; pectoral-fin rays modally 15; total caudal-fin rays modally 23; lower jaw extending anteriorly beyond upper jaw, mean difference between distance from tip of lower jaw to orbit and tip of upper jaw to orbit 5% head length (HL); caudal peduncle relatively narrow, average depth 11% SL.

Description.—Description based on 92 specimens, 16.0–86.4 mm SL. Counts and measurements of holotype given in parentheses. Dorsal-fin spines three or four, almost always four (four); fourth spine sometimes segmented distally but classified as spine based on articulation with pterygiophore; dorsal-fin rays 20–23, modally 21 (21); total dorsal-fin elements 24–26, modally 25 (25); anal-fin elements I, 13–15, modally 14 (14); pectoral-fin rays 14–16, modally 15 (15); total caudal-fin rays 22–25, modally 23 (23); total gillrakers 8–10, modally 9 (10). Snout length 13–23% head length (HL), mean = 19 (20); eye diameter 19–28% HL, mean = 24 (23); head length 35–44% SL, mean = 38 (37); body depth at pectoral-fin base 23–31% SL, mean = 27 (26); caudal-peduncle depth 9–14% SL, mean = 11 (11). Lower jaw extending anteriorly beyond upper jaw, distance from tip of lower jaw to orbit 18–30% HL, mean = 25 (24),

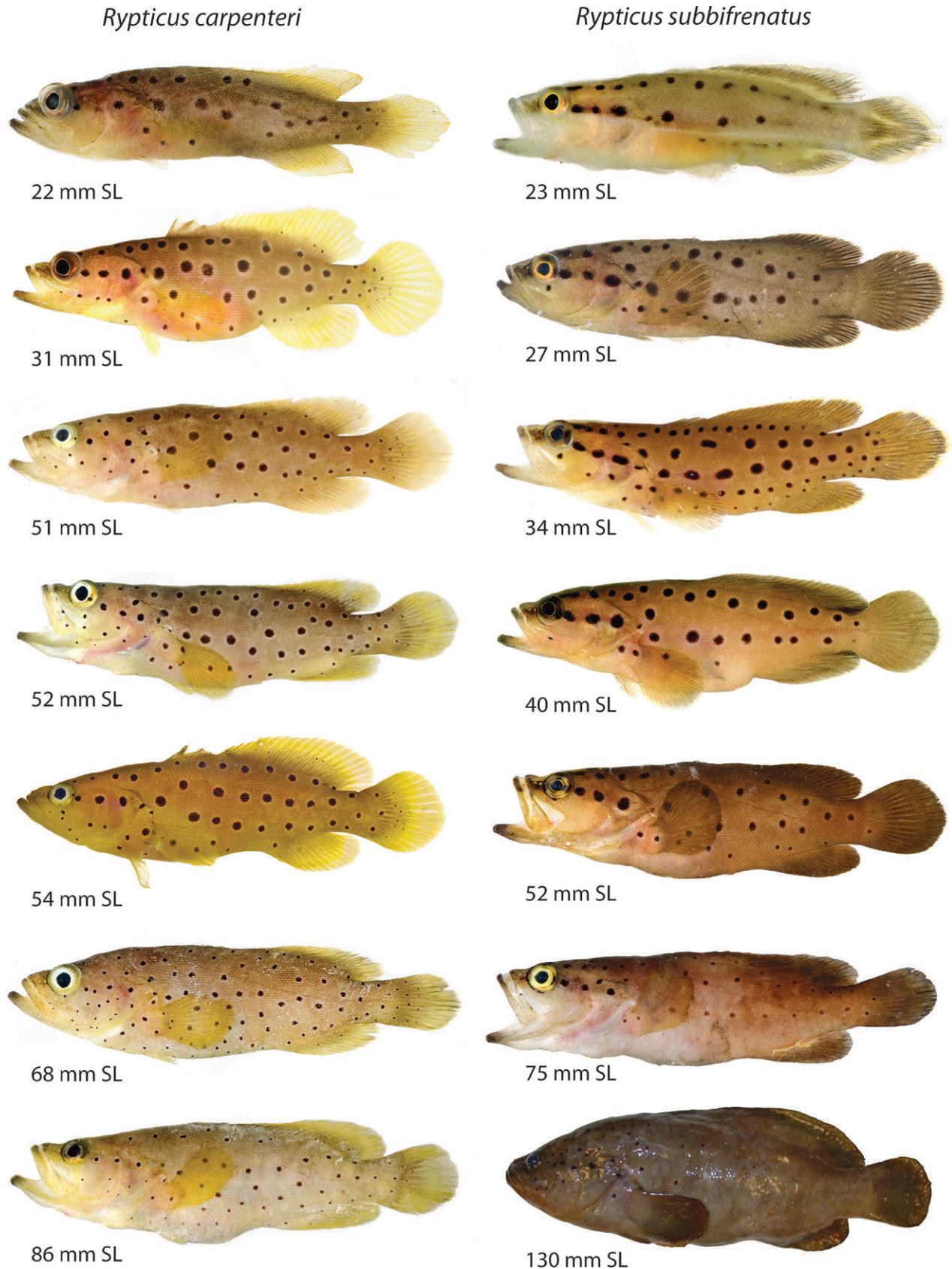


Fig. 4. Comparisons of color patterns between *Rypticus carpenteri*, new species, and *Rypticus subbifrenatus*. Left column, top to bottom: USNM 401043, DNA number CUR 8304; USNM 401040, DNA number BLZ 8230; USNM 401294, DNA number BLZ 5140 (photo by J. Mounts); USNM 401044, DNA number TOB 9103; USNM 387946, holotype (photo by J. T. Williams); USNM 401297, DNA number TOB 9197; USNM 401046, DNA number TOB 9178. Right column, top to bottom: USNM 401279, DNA number BAH 10090; USNM 401265, DNA number TOB 9256; USNM 401274, DNA number BLZ 5212 (photo by J. Mounts); USNM 401245, DNA number BLZ 7190 (photo by J. Mounts); USNM 401262, DNA number TOB 9106; USNM 401037, DNA number BLZ 8059; DNA number FLA 7397 (no voucher).

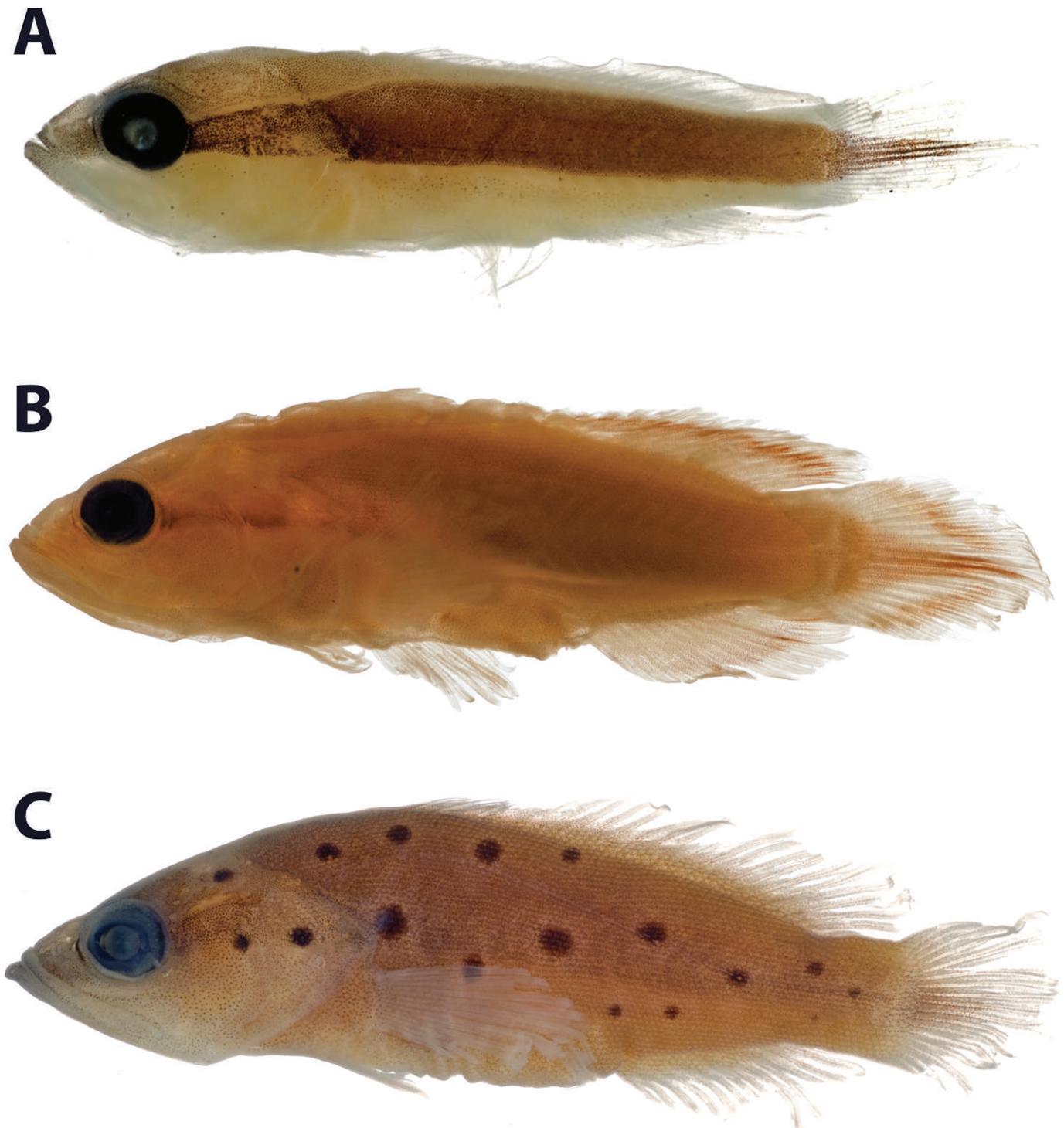


Fig. 5. (A) Juvenile *Rypticus* sp., UF 158232, 12.5 mm SL; (B) juvenile *Rypticus subbifrenatus*, UF 18047, 17.0 mm SL; and (C) juvenile *Rypticus carpenteri*, new species, USNM 389823, 16.0 mm SL.

difference between that measurement and snout length (tip of upper jaw to orbit) 2–10% HL, mean = 5 (3). Both jaws with multiple rows of small conical teeth—no enlarged canines, but teeth near premaxillary symphysis largest; thick chevron-shaped patch of teeth on vomer; elongate patch of teeth on each palatine, patch tapering posteriorly.

Coloration.—In life, background color pale tan to light olive, some specimens with darker olive coloration and few with some reddish brown mixed in. Pectoral fin and outer

portions of soft dorsal, caudal, and anal fins pale yellow to yellow. Yellow pigment also present in some specimens on jaws, ventral portion of eye, and cheek. In preservative, head and trunk usually tan, sometimes darker (brown) and sometimes very light in small specimens. Pigment posterior to eye variable—usually three or four (occasionally two or five) dark, round spots in a row, all usually smaller than pupil; some specimens with scattered small spots posterior to eye in no apparent pattern. Two dark spots present at posterior end of interorbital region, spots set slightly apart

Table 2. Frequency Distributions of Counts for *Rypticus carpenteri*, New Species, and *R. subbifrenatus*.

	Dorsal spines		Dorsal soft rays						
	III	IV	20	21	22	23	24	25	
<i>R. carpenteri</i>	2	77	12	55	7	1	–	–	
<i>R. subbifrenatus</i>	62	59	–	13	53	43	6	1	
	Total dorsal elements					Anal soft rays			
	24	25	26	27	28	11	13	14	15
<i>R. carpenteri</i>	13	51	12	–	–	–	10	63	3
<i>R. subbifrenatus</i>	–	33	67	16	1	1	20	90	6
	Pectoral rays				Total caudal rays				
	13	14	15	16	22	23	24	25	26
<i>R. carpenteri</i>	–	15	61	1	5	58	9	3	–
<i>R. subbifrenatus</i>	2	1	39	71	1	1	16	91	7
	Total gill rakers								
	6	7	8	9	10	11			
<i>R. carpenteri</i>	–	–	2	63	15	–			
<i>R. subbifrenatus</i>	3	6	29	66	10	2			

from orbital rim (Fig. 3A). Trunk with numerous dark spots—some nearly as large as pupil in some specimens, all very small in others, spots decreasing in relative size with increasing standard length (Fig. 4). Belly usually with multiple, very small spots; spots small even in specimens with larger trunk spots. Caudal fin typically with numerous small to tiny spots, but some specimens with only one or two spots on basal portion of caudal fin. A few small spots usually present on soft dorsal fin, and sometimes a few spots present on anal fin. Outer portions of soft dorsal, caudal, and anal fins pale in preservative.

Smallest genetically identified specimen of *R. carpenteri* (22.0 mm SL, Fig. 4) with characteristic yellow pectoral and vertical fins (pale in preservative), small spots behind middle of eye, a couple of small dark spots on belly, and some fairly large dark spots on trunk. A 31 mm SL specimen (Fig. 4) with bright yellow pectoral and vertical fins and numerous large dark trunk spots. Additional but smaller spots present on belly, caudal peduncle, and caudal fin. Several small specimens (24–28 mm SL) not analyzed genetically with classic *R. carpenteri* pigment patterns. One 16.0 mm SL specimen (Fig. 5C) with remnants of juvenile midlateral stripe; this specimen identified as *R. carpenteri* based on absence of features present in genetically identified small specimens of *R. subbifrenatus*—i.e., elongate dark blotches or stripes of pigment behind eye and alternating dark/pale areas on vertical fins (see young *R. subbifrenatus* in Fig. 4, 23 mm SL, and Fig. 5B; also “*Rypticus subbifrenatus*” description below). A 12.5 mm SL specimen (Fig. 5A) possibly a juvenile *R. carpenteri* based on absence of alternating dark/pale areas on vertical fins, but size at which the distinctive pattern of pigment on vertical fins develops in *R. subbifrenatus* unknown. In a color image of the 12.5 mm specimen, dark body stripe outlined in white, and vertical and pectoral fins yellow (except where dark body stripe extends onto caudal fin).

Largest specimen in genetic lineage of *R. carpenteri* 86.0 mm SL (Fig. 4). In addition to yellow pigment on jaws, lower portion of eye, and anterior portion of the cheek, this specimen with bright yellow pectoral fin and pale yellow second dorsal, caudal, and anal fins (all yellow areas pale in preservative). Dark body spots relatively small and scattered over entire trunk, including posterior portion of body and belly as in smaller adults. Largest specimen of *R. carpenteri* not analyzed genetically 86.4 mm SL (UF 158253). This specimen also with small dark body spots scattered over the entire trunk, and distal portions of pectoral and vertical fins pale in preservative.

Distribution.—Bahamas, Belize, Bermuda, Colombia, Curacao, Dominica, Florida, Grand Cayman, Haiti, Navassa, Saba, Tobago, Turks and Caicos, and U.S. Virgin Islands–St. Croix (Fig. 6).

Habitat.—*Rypticus carpenteri* inhabits clear tropical waters to depths of 40 m, but is found most commonly between 6 and 30 m (Fig. 7). Mean maximum depth of specimens examined herein is 17 m, and only six specimens were collected at depths <5 m. *Rypticus carpenteri* lives among coral or rocks on steep slopes, vertical walls, or in other areas with large vertical relief, although a few specimens have been taken among coral heads in shallow flat areas.

Etymology.—Named in honor of Michael Carpenter, station manager for the Smithsonian’s research station at Carrie Bow Cay, Belize, for more than 30 years. Mike’s dedication to maintaining this remote station benefited a multitude of marine scientists (and marine science). We thank him for his good-natured support in the field, and the first author is grateful for his enduring friendship. The common name, Slope Soapfish, is in reference to the occurrence of the species on steep slopes and other areas of vertical relief.

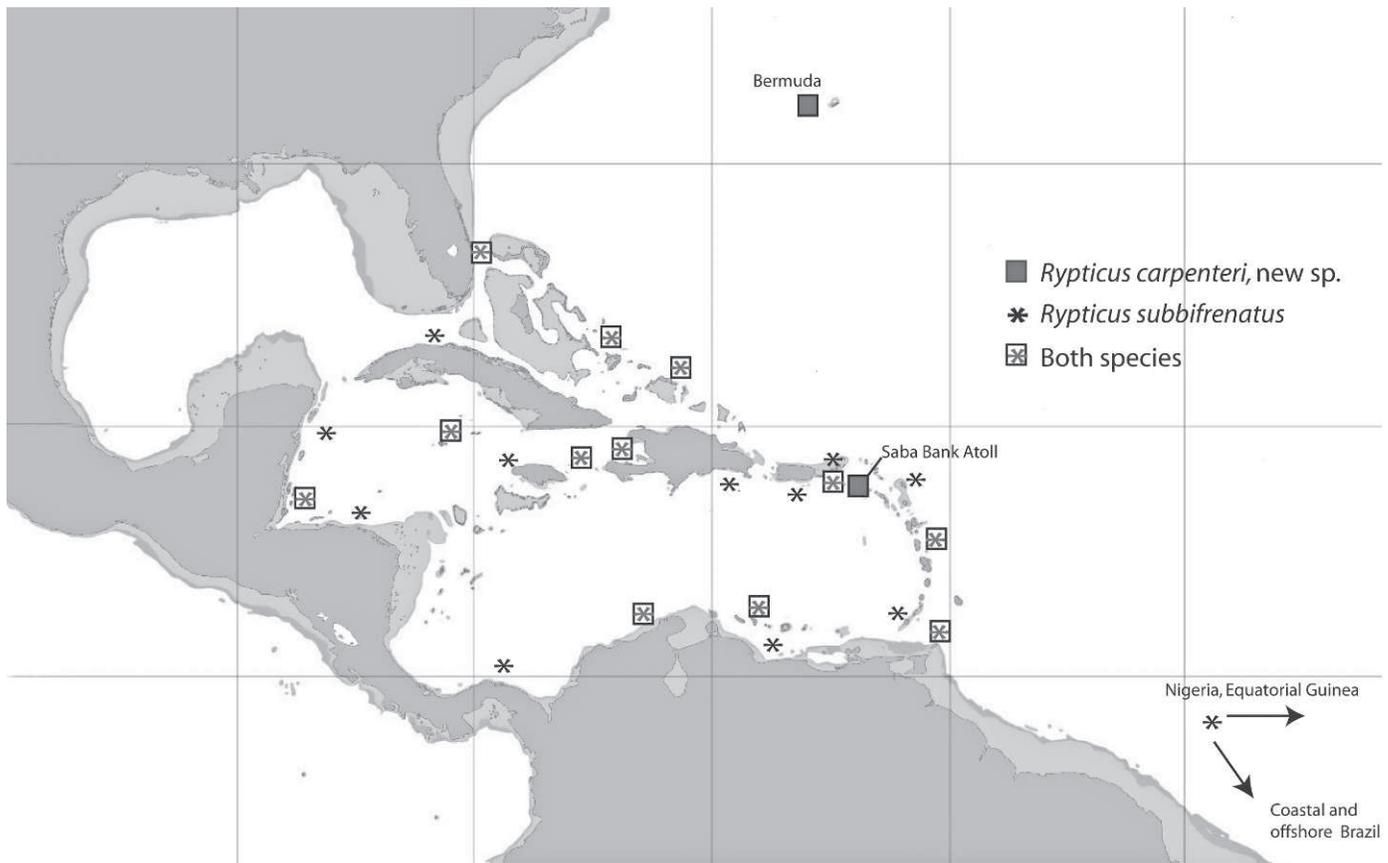


Fig. 6. Distributions of *Rypticus carpenteri*, new species, and *Rypticus subbifrenatus*.

***Rypticus subbifrenatus* Gill, 1861**

Spotted Soapfish
Figures 2–5, Table 2

Rhypticus subbifrenatus Gill 1861:53 (type locality St. Thomas, U.S. Virgin Islands).

Rhypticus nigromaculatus Steindachner 1867:42 (description; Barbados).

Rypticus subbifrenatus Gill 1861.—Humann and DeLoach, 2002:189 (unnumbered color photo).

Designation of a neotype.—Courtenay (1967) indicated that there is no known type material of *R. subbifrenatus* Gill, and our attempts to locate type material were unproductive. To clarify the taxonomic status of *R. subbifrenatus* in light of the discovery of the similar *R. carpenteri*, we designate USNM 106516 as a neotype of *R. subbifrenatus* Gill. A diagnosis and redescription of *R. subbifrenatus* are provided below.

Neotype.—USNM 106516, 61.0 mm SL, U.S. Virgin Islands, St. Thomas, Smith Beach, field number Smithsonian–

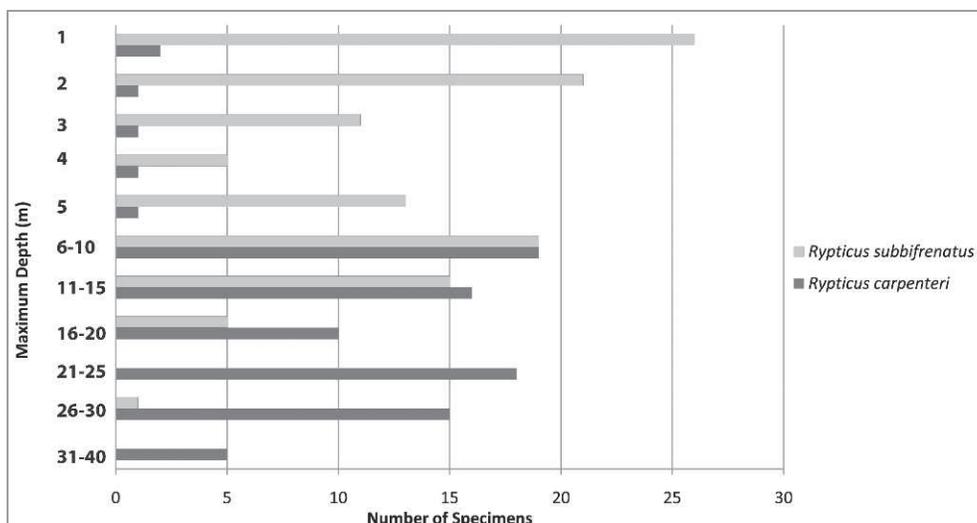


Fig. 7. Comparison of depths of capture of *Rypticus carpenteri*, new species, and *Rypticus subbifrenatus*.

Hartford Expedition station 68, W. Schmitt, 25 April 1937.

Other material examined.—(DNA vouchers). Belize: USNM 401274, DNA number BLZ 5212, 34.0 mm SL; USNM 401245, DNA number BLZ 7190, 38.0 mm SL; USNM 401246, DNA number BLZ 7191, 35.5 mm SL; USNM 401247, DNA number BLZ 7192, 31.0 mm SL; USNM 401248, DNA number BLZ 7200, 24.0 mm SL; USNM 401281, DNA number BLZ 7247, 37.4 mm SL; USNM 401275, DNA number BLZ 8012, 72.0 mm SL; USNM 401276, DNA number BLZ 8058, 73.0 mm SL; USNM 401037, DNA number BLZ 8059, 52.3 mm SL; USNM 491277, DNA number BLZ 8082, 55.0 mm SL; USNM 401278, DNA number BLZ 8373, 38.6 mm SL. Curacao: USNM 401270, DNA number CUR 8172, 46.2 mm SL; USNM 401271, DNA number CUR 8173, 58.1 mm SL; USNM 401272, DNA number CUR 8174, 62.6 mm SL; USNM 401273, DNA number CUR 8175, 57.0 mm SL. Tobago: USNM 401258, DNA number TOB 9001, 42.7 mm SL; USNM 401260, DNA number TOB 9104, 58.3 mm SL; USNM 401261, DNA number TOB 9105, 56.4 mm SL; USNM 401262, DNA number TOB 9106, 72.0 mm SL; USNM 401263, DNA number TOB 9253, 70.1 mm SL; USNM 401266, DNA number TOB 9254, 41.2 mm SL; USNM 401264, DNA number TOB 9255, 35.0 mm SL; USNM 401265, DNA number TOB 9256, 27.0 mm SL; USNM 401267, DNA number TOB 9329, 110 mm SL; USNM 401268, DNA number TOB 9330, 105 mm SL; USNM 401269, DNA number TOB 9331, 29.0 mm SL. (Non DNA vouchers or DNA vouchers not represented in Fig. 1). Antigua: UF 11377, 2; UF 11455, 1; UF 12736, 2. Bahamas: UF 206030, 2; USNM 401279, DNA number BAH 10090, 23 mm SL. Belize: USNM 401280, BLZ 10210, 17.0 mm SL; USNM 327568, 109 mm SL; USNM 276233, 2, 38.4 and 93.2 mm SL; USNM 276231, 59.0 mm SL; USNM 401037, 48.2 mm SL. Brazil: GCRL 9461, 2, 26.0 and 32.0 mm SL; GCRL 9579, 52.0 mm SL; GCRL 10834, 54.0 mm SL; GCRL 10849, 52.0 mm SL; GCRL 9390, 2, 33.0 and 39.0 mm SL; CIUFES 0872, 50.0 mm SL; CIUFES 0204, 40.0 mm SL. Colombia: UF 19078, 2; UF 24331, 4; UF 117742, 3; USNM 330397, 17, 32.8–78.0 mm SL; USNM 330385, 7, 54.0–115 mm SL; USNM 330386, 27.0 mm SL; USNM 330425, 2, 107 and 121 mm SL; USNM 330398, 2, 29.0 and 42.0 mm SL. Cuba: USNM 82432, 35.0 mm SL. Dominica: USNM 357294, 48.0 mm SL; USNM 389828, 2, 48.0 and 56.0 mm SL; 289829, 37.0 mm SL; USNM 389824, 23.0 mm SL; USNM 330392, 3, 31.2–100 mm SL; USNM 389823, 5, 43.0–85.0 mm SL; USNM 389825, 45.0 mm SL; USNM 330399, 96.6 mm SL; USNM 330415, 80.0 mm SL; USNM 330393, 5, 16.5–75.0 mm SL; USNM 330396, 6, 68.6–96.5 mm SL; USNM 389827, 28, 37.9–112 mm SL; USNM 330381, 7, 50.5–82.3 mm SL; USNM 357295, 11, 18–80.8 mm SL. Dominican Republic: USNM 314418, 55.0 mm SL. Equatorial Guinea: UF 223268, 12. Fernando Poo: ANSP 109203, 1 (photo only). Grand Cayman: UF 10686, 1; UF 17832, 3; UF 18047, 1. Grenadines: UF 139563. Haiti: UF 206710, 2. Honduras: UF 117737, 1. Jamaica: UF 228345, 2. Mexico: UF 209360, 4. Navassa: USNM 359107, 67.0 mm SL; USNM 359555, 2, 55.3 and 84.0 mm SL; USNM 359555, 95.0 mm SL; USNM 359664, 37.0 mm SL. Nigeria: USNM 201597, 53.0 mm SL; USNM 330395, 110 mm SL. Panama: CAS 13486, 31678, 31713 (photos only); UF 117734, 2; UF 117739, 8; UF 150367, 4. Puerto Rico: USNM 390568, 49.0 mm SL; USNM

390550, 2, 56.0 and 57.0 mm SL; USNM 390551, 2, 32.0 and 43.0 mm SL. Tobago: USNM 318527, 3, 28.0–73.0 mm SL; USNM 318523, 73.0 mm SL; USNM 318539, 2, 74.0 and 79.0 mm SL; USNM 318535, 2, 50 and 122 mm SL; USNM 318532, 27.0 mm SL; USNM 401259, 40.0 mm SL; USNM 318533, 5, 61.4–95.8 mm SL; USNM 318529, 93.0 mm SL; USNM 318523, 75.0 mm SL; USNM 318527, 87.0 mm SL; USNM 318543, 115 mm SL; USNM 318539, 2, 90.0 and 107 mm SL; USNM 318546, 88.0 mm SL; USNM 318530, 64.0 mm SL. Turks and Caicos: USNM 401249, TCI 9017, 47.1 mm SL; USNM 401250, TCI 9260, 82.1 mm SL; USNM 401251, TCI 9386, 77.7 mm SL; USNM 401252, TCI 9387, 57.5 mm SL; USNM 401253, TCI 9388, 51.2 mm SL; USNM 401255, TCI 9605, 81.3 mm SL; USNM 401256, TCI 9606, 45.6 mm SL; USNM 401257, TCI 9702, 71.2 mm SL. U.S. Virgin Islands (St. Thomas): USNM 8812, 4, 39.0–47.0 mm SL; (St. Croix): UF 158248, 62.6 mm SL; UF 158250, 67.6 mm SL; UF 158252, 58.9 mm SL. Venezuela: USNM 179259, 2, 39.0 and 40.0 mm SL; USNM 194094, 38.0 mm SL.

Diagnosis.—A species of *Rypticus* distinguished from all congeners by the following unique combination of characters: pectoral fin and distal portions of soft dorsal, caudal, and anal fins tan to brown in life and in preservative; head and trunk with numerous dark spots; spots on head posterior to horizontal through center of orbit usually prominent, round or oblong, and one or more usually equal in size to or larger than diameter of pupil; posterior portion of interorbital region usually with two pairs of spots (sometimes joined as a stripe), spots directly on or abutting orbital rim; belly usually without spots; caudal fin usually without spots; dorsal-fin spines three or four (nearly bimodal); total dorsal-fin elements modally 26; pectoral-fin rays modally 16; total caudal-fin rays modally 25; lower jaw extending anteriorly beyond upper jaw, mean difference between distance from tip of lower jaw to orbit and tip of upper jaw to orbit 4% HL; caudal peduncle relatively wide, average depth 13% SL.

Description.—Description based on 197 specimens, 18.0–130 mm SL. Counts and measurements of neotype given in parentheses. Dorsal-fin spines three or four, almost bimodal (three); dorsal-fin rays 21–25, almost bimodal at 22–23 (23); total dorsal-fin elements 25–28, modally 26 (26); anal-fin elements I,11 (one specimen) or I,13–15, modally 14 (13); pectoral-fin rays 13–16, modally 16 (16); total caudal-fin rays 22–26, modally 25 (25); total gillrakers 6–11, modally 9 (9). Snout length 15–23% HL, mean = 19 (19); eye diameter 19–25% HL, mean = 22 (21); head length 35–41% SL, mean = 38 (39); body depth at pectoral-fin base 21–32% SL, mean = 27 (31); caudal-peduncle depth 12–15% SL, mean = 13 (14). Lower jaw extending anteriorly beyond upper jaw, distance from tip of lower jaw to orbit 18–28% HL, mean = 23% HL (22), difference between that measurement and snout length (tip of upper jaw to orbit) 1–7% HL, mean = 4 (2). Both jaws with multiple rows of small conical teeth; no enlarged canines, but teeth near premaxillary symphysis largest; thick chevron-shaped patch of teeth on vomer; elongate patch of teeth on each palatine, patch tapering posteriorly.

Coloration.—In life background tan, straw colored, or brown; some specimens with hint of red coloration on trunk and hint of yellow on head. Pectoral and vertical fins usually same

color as or darker than background color; in young adults pectoral and vertical fins with very narrow but distinctive yellow edge; in large adults those fins with very thin black distal edge. In preservative, head and trunk tan to brown. Pigment posterior to eye typically comprising three or four dark spots or elongate blotches, third—and sometimes first—equal in size to or larger than diameter of pupil; elongate blotches sometimes joined to form postorbital stripe. Interorbital region usually with two sets of bilaterally paired spots, first pair just posterior to middle of orbit, second following posteriorly; spots on each side directly on or abutting orbital rim and sometimes joined to form stripe (Figs. 3B, 4). Trunk with numerous dark spots, size of spots variable but decreasing in relative size with increasing standard length. Belly usually without spots but belly spots present in some specimens. Caudal fin usually without spots, but one or two spots sometimes present on base of fin. A few small spots sometimes present on soft dorsal and anal fins.

Smallest genetically identified specimens of *R. subbifrenatus* (17.0 and 23.0 mm SL) with distinctive color pattern (Fig. 4, 23 mm SL). Although similar to larger *R. subbifrenatus* in having prominent, somewhat elongate spots of pigment behind middle of eye and dark areas on vertical fins, other aspects of coloration different: thin white stripe extending from lower portion of eye posteriorly to caudal peduncle; anteriorly, this stripe bordering ventral margin of dark spots behind middle of eye; posteriorly, white stripe separating brownish green trunk pigment from yellow/gold pigment on abdomen. Alternating pale and dark pattern of pigment on ventral fins as follows: yellow stripe of pigment present along base of dorsal fin, a similar yellow stripe present along base of anal fin, and two angled yellow stripes (one dorsal and one ventral) present on caudal fin (caudal fin damaged in Belize specimen but dorsal yellow stripe visible); those yellow stripes followed distally by broad stripes of darker (tan) pigment, and edges of vertical fins yellow. Overall, 23.0 mm SL specimen with more yellow pigment than larger *R. subbifrenatus*, and 17.0 mm SL specimen with much stronger yellow coloration than 23.0 mm SL specimen. Another 17.0 mm SL (preserved) specimen, not analyzed genetically (Fig. 5B), exhibiting remnants of dark juvenile body stripe and alternating pale and dark pattern on vertical fins; this specimen identified as *R. subbifrenatus* based on presence of the same pattern of vertical-fin pigment as in genetically identified 17 and 23 mm SL specimens. Slightly larger specimens (24.0 and 27.0 mm SL, Fig. 4) with pigment typical of adult *R. subbifrenatus*. Trunk spots arranged roughly in horizontal rows posteriorly, lowest row comprising spots much smaller in size than upper rows. Second dorsal, caudal, and anal fins with very thin yellow edge; lower portion of cheek with hints of yellow pigment, posterior portion of head and pectoral-fin base with hints of red pigment. A 26 mm SL specimen from Brazil (GCRL 9461) with pigment behind eye in discrete spots on left side of body, forming a stripe on right side. Elongate blotches or stripes of pigment behind eye also present in other small (<50 mm SL) specimens.

Largest genetically analyzed *R. subbifrenatus* (130 mm SL, Fig. 4) with dark spotting restricted to anterior portion of trunk and head; all spots relatively small. Pectoral, second dorsal, caudal, and anal fins conspicuously darker than trunk basally, with paler band distally, and with very thin black distal edge. Another large specimen in *R. subbifrenatus* genetic lineage (110 mm SL) nearly identical to the 130 mm SL

specimen in pattern of pigment, but vertical fins paler and posterior portion of trunk with pale swath. A 105 mm SL specimen similar, but retaining some small spots posteriorly on body and with some fairly large spots on head behind eye.

Distribution.—Antigua, Bahamas, Belize, Brazil, Colombia, Cuba, Curacao, Dominica, Dominican Republic, Equatorial Guinea, Fernando Poo, Florida, Grand Cayman, Grenadines, Haiti, Honduras, Jamaica, Mexico, Navassa, Nigeria, Panama, Puerto Rico, Tobago, Turks and Caicos, U.S. Virgin Islands, and Venezuela (Fig. 6). See “Remarks” for comments on identification of specimens from Brazil, Nigeria, and Fernando Poo.

Habitat.—*Rypticus subbifrenatus* inhabits clear tropical waters to depths of 26 m, but it is found most commonly at 1–2 m (Fig. 7). Mean maximum depth of specimens examined herein is 5 m, and only six specimens were captured deeper than 15 m. *Rypticus subbifrenatus* lives in tide pools, among coral rubble, in patch reefs and shallow spur and groove reef areas, and occasionally it may be found on steep vertical walls.

Remarks.—Gill (1861) indicated that *R. subbifrenatus* has 26 dorsal-fin elements and 16 pectoral-fin rays, features that best match our dark-finned genetic lineage of *Rypticus*. Herein we recognize that lineage as *R. subbifrenatus* Gill. The species designation is further corroborated by the species name, *subbifrenatus*, which is from the Latin meaning “almost two bridles” and presumably refers to the two rows of spots on the head, one behind the middle of the eye, the other extending posteriorly from the posterodorsal margin of the eye. Those spots are coalesced in some young *R. subbifrenatus* such that they form lines or stripes (like bridles), but are not coalesced in young *R. carpenteri* (Fig. 4). Gill (1861) did not provide the length of his specimen, but the pattern of head pigment described and the specific epithet suggest it was a young specimen.

There is one synonym of *R. subbifrenatus*, *Rhypticus nigromaculatus*, which Steindachner (1867) described as having 26–27 total dorsal elements. Those counts are typical of *R. subbifrenatus*. We examined photographs of the holotype of *R. nigromaculatus* (NMW 57867), and although pigment is largely faded, several relatively large spots are present in a row behind the eye, and there is at least some dark pigment on the distal portion of the caudal fin. Both of those features best match *R. subbifrenatus*, and we concur with Courtenay (1967) that *R. nigromaculatus* is a synonym of *R. subbifrenatus*.

Two spotted soapfish specimens from Nigeria (USNM 201597 and USNM 330395) have counts that suggest they are *R. subbifrenatus* (although one has 17 pectoral-fin rays—a higher count than we observed in our other material), and the pigment pattern in the larger specimen (110 mm SL) is typical of large *R. subbifrenatus* described above. Pigment behind the eye in the smaller specimen (53.0 mm SL) is in the form of short stripes and oblong blotches, which is typical of some *R. subbifrenatus* but not *R. carpenteri*, and spots are present on the belly—atypical of *R. subbifrenatus* but present occasionally (e.g., Fig. 4, 34 mm SL). Likewise, a single specimen from Fernando Poo (ANSP 109203) has a stripe behind the eye and spots on the belly. The vertical fins are dark as in *R. subbifrenatus*. Two additional specimens from offshore and coastal Brazil (CIUFES 0872, 50 mm SL,

and CIUFES 0204, 40 mm SL, respectively) also are likely *R. subbifrenatus* based on counts, especially the high total dorsal count (27). The 50 mm specimen has large spots behind the eye similar to those of *R. subbifrenatus*, but in the 40 mm specimen the spots are joined as a thick dark line that continues anteriorly in front of the eye to the lips. Although some *R. subbifrenatus* have a dark stripe from the lips to the eye, none has the condition as prominent as in this specimen from Brazil. Eastern Atlantic and Brazilian populations warrant further investigation, including morphological and genetic, to determine if they represent *R. subbifrenatus* or undescribed species.

DISCUSSION

Comparisons among *R. carpenteri* and *R. subbifrenatus*.—*Rypticus carpenteri* and *R. subbifrenatus* are generally easily distinguished by the color of the pectoral and vertical fins—pale (yellow in life) in *R. carpenteri*, tan to dark brown (in life and preservative) in *R. subbifrenatus* (Figs. 2, 4). Pigment on the head posterior to a horizontal through the eye is also distinctive: in *R. carpenteri*, the spots behind the eye are almost always round and smaller than the pupil, whereas in *R. subbifrenatus* the spots may be round or elongate (or joined to form a stripe), and at least one spot is typically equal in size to or larger than the diameter of the pupil. In specimens of *R. subbifrenatus* between approximately 70 and 90 mm SL, all spots behind the eye may be smaller than the pupil, but they are still considerably larger than the spots behind the eye in comparable-size specimens of *R. carpenteri* (e.g., compare size of spots in 75 mm SL specimen of *R. subbifrenatus* and 68 and 86 mm SL specimens of *R. carpenteri* in Fig. 4). In the largest specimens of *R. subbifrenatus* (110–130 mm SL), all spots on the head are smaller than the pupil, but there are no specimens of *R. carpenteri* of similar size for comparative purposes. Interorbital pigment also is useful in separating the species: *R. carpenteri* usually has one pair of spots near the posterior end of the interorbital region that is set slightly apart from the orbital rim; *R. subbifrenatus* usually has two pairs of spots (sometimes joined as a stripe) just posterior to the middle of the orbit that are directly on or abut the orbital rim (Fig. 3). *Rypticus carpenteri* usually has dark pigment spots on the belly, whereas *R. subbifrenatus* does not, but some small specimens of *R. carpenteri* lack belly spots, and a few of our specimens of *R. subbifrenatus* have them (Fig. 4). Likewise, *R. carpenteri* usually has small to tiny dark spots on the caudal fin, whereas *R. subbifrenatus* typically does not.

Rypticus carpenteri almost always has four dorsal spines vs. three or four (nearly bimodal) in *R. subbifrenatus*. Other counts useful in distinguishing the species are total dorsal-fin elements (modally 25 in *R. carpenteri*, modally 26 in *R. subbifrenatus*), pectoral-fin rays (modally 15 in *R. carpenteri*, modally 16 in *R. subbifrenatus*), and total caudal-fin rays (modally 23 in *R. carpenteri*, modally 25 in *R. subbifrenatus*). Two morphometric features help separate the species: anterior projection of lower jaw relative to upper jaw (average difference between distance from tip of lower jaw to orbit and tip of upper jaw to orbit 5% HL in *R. carpenteri*, 4% in *R. subbifrenatus*); and depth of caudal peduncle (average depth 11% SL in *R. carpenteri*, 13% in *R. subbifrenatus*).

Rypticus carpenteri may attain a smaller maximum size than *R. subbifrenatus*; the largest specimens of the former examined are between 80 and 90 mm SL, whereas several of

the latter examined are >100 mm SL. The largest *R. carpenteri* retain dark spots on the entire trunk, but the largest *R. subbifrenatus* have them only on the head and anterior portion of the trunk. Body spots in *R. subbifrenatus* begin disappearing at ca. 80 mm SL, so it is not known if larger specimens of *R. carpenteri* (if they exist) would also lose body spots. When the posterior body spots in *R. subbifrenatus* disappear, the pattern of pigment behind the middle of the eye also changes: there are typically no large, pupil-size spots. Species identification is still relatively easy based on the dark body and median fins.

Subadults of *R. carpenteri* and *R. subbifrenatus* are easily distinguished by the size and configuration of the dark spots behind the middle of the eye (small round spots in *R. carpenteri*, elongate dark spots/stripes in *R. subbifrenatus*) and by color pattern of the vertical fins (yellow [pale in preservative] in *R. carpenteri*, with alternating yellow [pale in preservative] and dark stripes in *R. subbifrenatus*—Fig. 4, 22 and 23 mm SL specimens). Dark trunk spots are relatively larger in smaller specimens than in larger ones in both species. As in larger specimens, young specimens of *R. carpenteri* also typically have small pigment spots on the belly, caudal peduncle, and sometimes caudal fin, whereas those of *R. subbifrenatus* usually do not.

Juveniles of both species apparently have a brown stripe extending from the tips of the jaws to near the distal end of the caudal fin (Fig. 5A, remnant of stripe visible in Fig. 5B, C). Large juveniles (16–17 mm SL, Fig. 5B, C) can be distinguished by the pattern of pigment on the vertical fins: in *R. carpenteri* those fins are pale (yellow in life), whereas in *R. subbifrenatus* they have alternating pale/dark areas (the pale areas yellow in slightly larger specimens, i.e., Fig. 4, 23 mm SL). Although it appears from Figure 5 that the dark head and body spots appear earlier in development in *R. carpenteri* (present in 16 mm SL juvenile, Fig. 5C) than in *R. subbifrenatus* (absent in 17 mm SL juvenile, Fig. 5B), another 17 mm SL juvenile of *R. subbifrenatus* (USNM 401280) has dark head and body spots.

Rypticus carpenteri and *R. subbifrenatus* have overlapping depth distributions, but *R. carpenteri* typically inhabits deeper water (Fig. 7). *Rypticus carpenteri* has been collected at depths up to 40 m (mean maximum depth = 17 m), whereas *R. subbifrenatus* has been taken only as deep as 26 m (mean maximum depth = 5 m). Most specimens of *R. carpenteri* examined were taken in areas with vertical relief (walls, steep slopes), whereas most *R. subbifrenatus* were taken in shallow patch reefs, coral rubble, and tide pools. The habitats are not exclusive, however, as some *R. carpenteri* are found in flat shallow areas (e.g., USNM 401039, BLZ 8047, was taken among coral heads in 0–3 m around Carrie Bow Cay, Belize), and some *R. subbifrenatus* are found on vertical walls (e.g., USNM 318523, two specimens were taken on a vertical wall off Saint Giles Islands, Tobago).

The utility of DNA barcoding in systematic studies.—Comparative morphological investigation supports dividing *R. subbifrenatus* into two species that correspond to two genetic lineages recovered through DNA (COI) analysis. This discovery serves as an example of the value of incorporating DNA techniques in species-level systematic studies. The new species has been confused with *R. subbifrenatus* for over 100 years, and may have continued to go unnoticed indefinitely. Without genetic data suggesting that we take another look, there was little reason to further examine the

taxonomy of *R. subbifrenatus*. Inclusion of DNA data should continue to be valuable in taxonomic studies of *Rypticus*; for example, species identification of larvae and juveniles is problematic because young stages lack diagnostic morphological features of adults. One larval and one juvenile specimen of *Rypticus* from Belize analyzed genetically (BLZ 7751 and BLZ 6441 in Fig. 1, respectively) have very similar COI sequences but match no species in our COI data set or in the Barcode of Life Data Systems (BOLD) database. They do not appear to be *R. bornoi*, *R. carpenteri*, *R. saponaceus*, or *R. subbifrenatus*, which are accounted for in our DNA data (Fig. 1), and they are likely not *R. maculatus*, which occurs along the southeast and Gulf coasts of the U.S. and extends south only to the northern Gulf of Mexico. Those specimens therefore represent young *R. bistrispinus*, *R. randalli*, or an undescribed species. Additional material for genetic analysis is needed.

DNA barcoding has received considerable negative publicity since its debut in 2003, and Mitchell (2011:67) noted that it “is all too often derided by taxonomists with little understanding of how far this emerging subdiscipline of systematics has progressed since it was proposed” Recently the value of DNA barcoding in any taxonomic endeavor has been questioned. Ebach and de Carvalho (2010:167) stated: “Those who want barcoding are the end-users, usually an industry, government, or biodiversity management organization, rather than taxonomists.” Ebach (2011:1) stated: “. . . barcoding is not something that would attract taxonomists . . . and . . . nowhere do we find its uses for taxonomy” While the focus of those authors’ attacks was their perception of a barcoding “business enterprise” taking over traditional morphology-based systematics, and we share their and many others’ concern about the demise of traditional taxonomy and decline in taxonomic specialists (Wilson, 1971; de Carvalho et al., 2008; Boero, 2010; de Carvalho and Ebach, 2010), they failed to recognize or at least acknowledge the utility of DNA barcoding in taxonomic studies. If results from DNA barcoding are used to direct subsequent morphological work rather than serve as end points, they can be of great value. Specifically, when incongruences between barcoding data and current species classification exist—for example, there are more or fewer genetic lineages than known species—systematists should further investigate the organisms involved. Through subsequent comparative morphological examination of DNA voucher material, long-standing taxonomic issues may be clarified and new species identified (Victor, 2007, 2010; Baldwin et al., 2009, 2011; Tornabene et al., 2010; this study). One value of DNA barcoding data in taxonomic studies is thus its ability to highlight where potential taxonomic issues exist. Used as a tool to direct subsequent morphological research, DNA barcoding should not engender criticism and can greatly streamline efforts to provide accurate estimates of species diversity.

One issue is whether or not “extra” genetic lineages identified through DNA barcoding that have not been sufficiently investigated using traditional systematic methods appropriate for the organisms under study should be called “species.” Hebert et al. (2004) divided a single species of the butterfly genus *Astraptes* into ten species based on DNA barcoding and certain life history attributes. They (2004:14816) asked: “Should the 10 species of *A. fulgerator* identified in this study be formally described despite their

morphological similarity? Yes” They did not describe the ten new species, however, and the ten genetic lineages continued to be referenced in the literature by acronyms that Hebert et al. (2004) derived from certain life-history attributes. Brower (2010), clearly frustrated with the attention in the literature the nameless species were receiving as an example of barcoding success, took the unorthodox step of naming ten new *Astraptes* species solely on the basis of small nucleotide differences in their DNA barcodes. No material was examined. Brower’s own (2006) analysis of the Hebert et al. (2004) data set suggested that there may be at least three but not more than six or seven species, and he remained skeptical about the existence of ten. Ostensibly to make a point and acknowledging that he is not even an expert on the butterfly group in question, Brower (2010) carried through with the species descriptions “as a service to taxonomy.”

New fish species also have been recognized based on genetic data without subsequently being named, diagnosed, and described—for example, a skate of the genus *Bathyraja* (Smith et al., 2008), a shark of the genus *Sphyrna* (Quattro et al., 2006), a dory of the genus *Zeus* (Teletchea et al., 2008; Ward et al., 2008), and a scabbardfish of the genus *Lepidopus* (Ward et al., 2008). Whether those species are in the process of being described or whether they will suffer the same fate as *Astraptes* is unknown. But if there is reluctance among investigators to conduct subsequent morphological investigation, it is hardly surprising considering that reconciling genetic data with morphology and describing new species is time consuming, especially in speciose groups with long histories of literature and synonymies. And support for such detailed taxonomic work continues to dwindle, in part because species-level systematic work rarely results in publications in journals with high impact factors (IF). The Cited Half Life (CHL), another index of scientific performance, reflects how long the average article of a journal continues to be cited. As noted by Boero (2010), it is infinite for a paper containing the description of a new species, yet this measure has been disregarded at many institutions in favor of IF.

Teletchea (2010) noted that replacing traditional morphology-based classifications with systems based solely on molecular data is unlikely, and that in the future taxonomy will involve integrating morphological and molecular data. There is a great need globally to train a new generation of systematists so that current knowledge of organismic diversity is not discarded (Lipscomb et al., 2003). Taxonomists who have the systematic expertise needed to ground-truth molecular data by providing accurate species identifications, reconcile genetic data and current species concepts when they conflict, and describe new species as appropriate are in great demand now and will continue to be so in the future. The molecular revolution has increased, not decreased, the need to support taxonomy and taxonomists.

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LITERATURE CITED

- Baldwin, C. C., C. I. Castillo, L. A. Weigt, and B. C. Victor.** 2011. Seven new species within western Atlantic *Starksia atlantica*, *S. lepicoelia*, and *S. sluiteri* (Teleostei: Labrisomidae), with comments on congruence of DNA barcodes and species. *ZooKeys* 79:21–72.
- Baldwin, C. C., L. A. Weigt, D. G. Smith, and J. H. Mounts.** 2009. Reconciling genetic lineages with species in western Atlantic *Coryphopterus* (Teleostei: Gobiidae), p. 113–140. *In: Proceedings of the Smithsonian Marine Science Symposium*. M. A. Lang, I. G. Macintyre, and K. Rützler (eds.). Smithsonian Contributions to the Marine Sciences 38.
- Boero, F.** 2010. The study of species in the era of biodiversity: a tale of stupidity. *Diversity* 2010:115–126.
- Böhlke, J. E., and C. C. G. Chaplin.** 1968. *Fishes of the Bahamas and Adjacent Tropical Waters*. Second edition. University of Texas Press, Austin.
- Brower, A. V. Z.** 2006. Problems with DNA barcodes for species delimitation: “ten species” of *Astrartes fulgerator* reassessed (Lepidoptera: Hesperidae). *Systematics and Biodiversity* 4:127–132.
- Brower, A. V. Z.** 2010. Alleviating the taxonomic impediment of DNA barcoding and setting a bad precedent: names for ten species of ‘*Astrartes fulgerator*’ (Lepidoptera: Hesperidae: Eudaminae) with DNA-based diagnoses. *Systematics and Biodiversity* 8:485–491.
- Carvalho, M. R. de., F. A. Bockmann, D. S. Amorim, and C. R. F. Brandão.** 2008. Systematics must embrace comparative biology and evolution, not speed and automation. *Evolutionary Biology* 35:150–157.
- Carvalho, M. R. de., and M. C. Ebach.** 2010. Death of the specialist, rise of the machinist. *History and Philosophy of the Life Sciences* 31:461–464.
- Courtenay, W. R., Jr.** 1967. Atlantic fishes of the genus *Rypticus* (Grammistidae). *Proceedings of the Academy of Natural Sciences of Philadelphia* 119:241–293.
- Ebach, M. C.** 2011. Taxonomy and the DNA barcoding enterprise. *Zootaxa* 2742:67–68.
- Ebach, M. C., and M. R. de Carvalho.** 2010. Anti-intellectualism in the DNA barcoding enterprise. *Zoologia* 27:165–178.
- Gill, T. N.** 1861. Synopsis generum Rhyptici et affinium. *Proceedings of the Academy of Natural Sciences of Philadelphia* 13:52–54.
- Guimarães, R. Z. P.** 1999. Revision, phylogeny and comments on biogeography of soapfishes of the genus *Rypticus* (Teleostei: Serranidae). *Bulletin of Marine Science* 65:337–379.
- Hebert, P. D. N., A. Cywinska, S. L. Ball, and J. R. DeWaard.** 2003. Biological identifications through DNA barcodes. *Proceedings of the Royal Society of London B* 270:313–321.
- Hebert, P. D. N., E. H. Penton, J. M. Burns, D. H. Janze, and W. Hallwachs.** 2004. Ten species in one: DNA barcoding reveals cryptic species in the neotropical skipper butterfly *Astrartes fulgerator*. *Proceedings of the National Academy of Sciences of the United States of America* 101:14812–14817.
- Heemstra, P. C., W. D. Anderson, Jr., and P. S. Lobel.** 2002. Serranidae: groupers (seabasses, creolefish, coney, hinds, hamlets, anthiines, and soapfishes), p. 1308–1369. *In: The Living Marine Resources of the Western Central Atlantic*. Volume 2: Bony fishes part 1 (Acipenseridae to Grammatidae). K. E. Carpenter (ed.). FAO Species Identification Guide for Fishery Purposes and American Society of Ichthyologists and Herpetologists Special Publication No. 5. FAO, Rome.
- Hubbs, C. L., and K. F. Lagler.** 1958. *Fishes of the Great Lakes Region*. *Bulletin of the Cranbrook Institute of Science* 26:1–213.
- Humann, P., and N. DeLoach.** 2002. *Reef Fish Identification*. Third edition. New World Publications, Jacksonville, Florida.
- Kells, V., and K. Carpenter.** 2011. *A Field Guide to Coastal Fishes from Maine to Texas*. The Johnson Hopkins University Press, Baltimore, Maryland.
- Kimura, M.** 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *Journal of Molecular Evolution* 16:111–120.
- Lipscomb, D., N. Platnick, and Q. Wheeler.** 2003. The intellectual content of taxonomy: a comment on DNA taxonomy. *Trends in Ecology and Evolution* 18:65–66.
- Mitchell, A.** 2011. DNA barcoding is useful for taxonomy: a reply to Ebach. *Zootaxa* 2772:67–68.
- Quattro, J. M., D. S. Stoner, W. B. Driggers, C. A. Anderson, K. A. Priede, E. C. Hoppmann, N. H. Campbell, K. M. Duncan, and J. M. Grady.** 2006. Genetic evidence of cryptic speciation within hammerhead sharks (Genus *Sphyrna*). *Marine Biology* 148:1143–1145.
- Saitou, N., and M. Nei.** 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. *Molecular Biology and Evolution* 4:406–425.
- Schultz, L. P., and E. D. Reid.** 1939. A revision of the soapfishes of the genus *Rypticus*. *Proceedings of the U.S. National Museum* 87:261–270.
- Seutin, G., P. Bagley, and B. N. White.** 1991. Preservation of avian blood and tissue samples for DNA analyses. *Canadian Journal of Zoology* 69:82–90.
- Smith, C. L.** 1997. *National Audubon Society Field Guide to Tropical Marine Fishes*. Alfred A. Knopf, New York.

- Smith, P., D. Steinke, S. Mcveagh, A. L. Stewart, C. Struthers, and C. Roberts.** 2008. Molecular analysis of Southern Ocean skates (*Bathyraja*) reveals a new species of Antarctic skate. *Journal of Fish Biology* 73:1170–1182.
- Steindachner, F.** 1867. Ichthyologische Notizen (VI). Sitzungsberichte der Kaiserlichen Akademie der Wissenschaften. Mathematisch-Naturwissenschaftliche Classe 56(1. Abth.):307–376.
- Swofford, D.** 2002. PAUP*: phylogenetic analysis using parsimony (*and other methods). Sinauer Associates, Sunderland, Massachusetts.
- Teletchea, F.** 2010. After 7 years and 1000 citations: comparative assessment of the DNA barcoding and the DNA taxonomy proposals for taxonomists and non-taxonomists. *Mitochondrial DNA* 21:206–226.
- Teletchea, F., J. Bernillon, M. Duffraisie, V. Laudet, and C. Hänni.** 2008. Molecular identification of vertebrate species by oligonucleotide microarray in food and forensic samples. *Journal of Applied Ecology* 45:967–975.
- Tornabene, L., C. C. Baldwin, L. A. Weigt, and F. Pezold.** 2010. Exploring the diversity of western Atlantic *Bathygobius* (Teleostei: Gobiidae) using mitochondrial cytochrome *c* oxidase-I, with descriptions of two new species. *Aqua* 16:141–170.
- Victor, B. C.** 2007. *Coryphopterus kuna*, a new goby (Perciformes: Gobiidae: Gobiinae) from the western Caribbean, with the identification of the late larval stage and an estimate of the pelagic larval duration. *Zootaxa* 1526:51–61.
- Victor, B. C.** 2010. The redcheek paradox: the mismatch between genetic and phenotypic divergence among deeply-divided mtDNA lineages in a coral-reef goby, with the description of two new cryptic species from the Caribbean Sea. *Journal of the Ocean Science Foundation* 2010:1–16.
- Ward, R. D., F. O. Costa, B. H. Holmes, and D. Steinke.** 2008. DNA barcoding shared fish species from the North Atlantic and Australasia: minimal divergence for most taxa but a likely two species for both *Zeus faber* (John dory) and *Lepidopus caudatus* (silver scabbardfish). *Aquatic Biology* 3:71–78.
- Williams, J. T., K. E. Carpenter, J. L. Van Tassell, P. Hoetjes, W. Toller, P. Etnoyer, and M. Smith.** 2010. Biodiversity assessment of the fishes of Saba Bank Atoll, Netherlands Antilles. *PLoS ONE* 5(5):e10676.
- Wilson, E. O.** 1971. The plight of taxonomy. *Ecology* 52:741.