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Halichoeres gurrobyi, a new labrid fish (Teleostei: Labridae) from Mauritius in the southwestern Indian Ocean, with a review of the *H. zeylonicus* species complex

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Abstract

The new labrid fish species, *Halichoeres gurrobyi* n. sp., is described from specimens collected in Mauritius, in the southwestern Indian Ocean. The new species is part of the yellow-striped initial-phase species complex of *Halichoeres*, comprising several species found in the Indo-Pacific, including the type species for the genus *Halichoeres* Rüppell. Two of the closest relatives of *H. gurrobyi* also occur in Mauritius, i.e. *H. zeylonicus* (the southwestern Indian Ocean [SWIO] genovariant) and the rare deep-reef *H. pelicieri*. The initial-phases of these species are similar and have been confused, but DNA barcoding clearly shows three distinct DNA lineages in the SWIO and helps resolve the diagnostic characters. The terminal-phase (TP) male of the new species is unknown. The new species is 9% divergent in the sequence of the mtDNA-barcode marker COI (minimum interspecific divergence, pairwise; 9.6% K2P distance) from its nearest relative, *H. pelicieri*. A neighbor-joining tree of COI mtDNA sequences is presented for the species complex.

Key words: coral-reef fishes, ichthyology, new species, taxonomy, systematics, wrasse, Africa, DNA barcoding.

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Introduction

The labrid genus *Halichoeres* Rüppell is a large polyphyletic collection of species and will doubtless be subdivided (Barber & Bellwood 2005, Westneat & Alfaro 2005, Victor *et al*. 2013). Nevertheless, the type species for the genus is *Halichoeres zeylonicus* (Bennett), type location Sri Lanka (Parenti & Randall 2000, Eschmeyer *et al*. 2016), and the *H. zeylonicus* species complex should thus remain in *Halichoeres* after revision. The species in this complex share a yellow-striped initial phase (IP) with a variable black spot at the caudal-fin base.

Sequencing of the "barcode" mtDNA marker COI can be useful in distinguishing among look-alike fishes and uniting different life stages of a species (e.g. Steinke *et al*. 2009, Victor *et al*. 2009). In addition, the results can assist in taxonomic decisions: if two populations share DNA haplotypes then it suggests there is gene flow or a recent split of incipient species with insufficient time to develop non-overlapping sets of haplotypes. In that situation, the case for two populations being different species needs to be very well documented, especially assessing the consistency of the phenotypic differences and thorough sampling of the geographic range of the two phenotypes. Conversely, if two populations have divergent mtDNA lineages, it indicates there has been some reproductive isolation and the populations may be different species if sufficient phenotypic differences can be documented to satisfy other ichthyologists; if not, then they should be considered genovariant populations of the same species (Victor 2015). In this study, I use mtDNA barcoding to distinguish members of the *H. zeylonicus* species complex and characterize a new species from Mauritius.

Materials and Methods

Specimens have been examined from the Bernice P. Bishop Museum, Honolulu (BPBM). In addition, ethanol-preserved specimens (or tissues) of comparison species were collected by the author and various contributors for DNA sequencing from Bali and Lombok (Indonesia), Australia (GBR), Korea, India, Réunion, Madagascar, Mozambique, and South Africa, as well as obtained via the aquarium trade from the Philippines, Maldives, Madagascar, and Mauritius (see Appendix 1).

DNA extractions were performed with the NucleoSpin96 (Machery-Nagel) kit according to manufacturer specifications under automation with a Biomek NX liquid-handling station (Beckman-Coulter) equipped with a filtration manifold. A 652-bp segment was amplified from the 5′ region of the mitochondrial COI gene using a variety of primers (Ivanova *et al.* 2007). PCR amplifications were performed in 12.5 µl volume including 6.25 µl of 10% trehalose, 2 µl of ultra pure water, 1.25 µl of 10× PCR buffer (10mM KCl, 10mM $(NH_4)_2SO_4$, 20mM Tris-HCl (pH8.8), 2mM $MgSO_4$, 0.1% Triton X-100), 0.625 µl of $MgCl_2$ (50mM), 0.125 µl of each primer (0.01mM), 0.0625 µl of each dNTP (10mM), 0.0625 µl of *Taq* DNA polymerase (New England Biolabs), and 2 µl of template DNA. The PCR conditions consisted of 94°C for 2 min., 35 cycles of 94°C for 30 sec., 52°C for 40 sec., and 72°C for 1 min., with a final extension at 72°C for 10 min. Specimen information and barcode sequence data from this study were compiled using the Barcode of Life Data Systems (Ratnasingham & Hebert 2007). The sequence data is publicly accessible on BOLD and GenBank. Sequence divergences were calculated using BOLD with the Kimura 2-parameter (K2P) model generating a mid-point rooted neighbor-joining (NJ) phenogram to provide a graphic representation of the species' sequence divergence. Genetic distances were calculated by the BOLD algorithm, both as uncorrected p-distances and as K2P distances.

The length of specimens is given as standard length (SL), measured from the median anterior end of the upper lip to the base of the caudal fin (posterior end of the hypural plate); body depth is the greatest depth from the base of the dorsal-fin spines to the ventral edge of the abdomen (correcting for any malformation of preservation); body width is measured just posterior to the gill opening; head length from the front of the upper lip to the posterior end of the opercular flap; orbit diameter is the greatest fleshy diameter of the orbital rim, and interorbital width the least bony width; snout length is measured from the median anterior point of the upper lip to the nearest fleshy rim of the orbit; caudal-peduncle depth is the least depth, and caudal-peduncle length the horizontal distance between verticals at the rear base of the anal fin and the caudal-fin base; predorsal, prepelvic and preanal lengths are oblique measurements; lengths of spines and rays are measured to their extreme bases; caudal-fin and pectoral-fin lengths are the length of the longest ray; pelvic-fin length is measured from the base of the pelvic spine to the tip of the longest soft ray. The upper rudimentary pectoral-fin ray is included in the count. Lateral-line scale counts include the last pored scale that overlaps the end of the hypural plate as +1. The count of gill rakers is made on the first gill arch and includes all rudiments. Proportional measurements in the text are rounded to the nearest 0.1. The counts and measurements for the paratype are shown in parentheses following data for the holotype. Proportional morphological measurements as percentages of the standard length are presented in Table 1.

Figure 1. *Halichoeres gurrobyi*, fresh holotype, BPBM 41277, 41.5 mm SL, Mauritius (B.C. Victor).

Halichoeres gurrobyi, n. sp.

Blacksaddle Wrasse

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Figures 1–4, Table 1.

Holotype. BPBM 41277, 41.5 mm SL, Grand Bay, Mauritius, 12–22 m, Chabiraj (Yam) Gurroby, Suresh Lilloo, Mohesh Gurroby, and Abhishekh Lillloo, Dec. 16, 2014.

Paratype. BPBM 41278, 72.0 mm SL, same collection data, about April 8, 2015.

Diagnosis. Dorsal-fin rays IX,11 (12); anal-fin rays III,11; pectoral-fin rays 13; lateral-line scales 27 (+1 on caudal-fin base), single small pore per scale; suborbital pores 6–7; gill rakers 19–21; a single pair of large, projecting, and slightly recurved canine teeth anteriorly in each jaw, the lowers curving forward and fitting between uppers when mouth closed, second canines about half size of first, followed by rows of mostly caniniform teeth, no canine posteriorly at corner of mouth; elongate body, body depth 4.5–5.0 in SL; body width 1.7–2.3 in depth; caudal fin slightly rounded to truncate in IP; color pattern of IP comprises yellow stripes on a pale background, on holotype three lateral stripes and a fourth along dorsal-fin base, on paratype two midlateral stripes plus dorsal-fin base stripe; large black blotch on caudal peduncle and caudal-fin base, saddle-like in paratype and larger specimens; small black spot at upper rim of pectoral-fin base; fins translucent except yellow band along distal dorsal fin and posterior margin of caudal fin. Colors of TP male unknown.

Figure 2. *Halichoeres gurrobyi*, BPBM 41278, preserved paratype, 72 mm SL, Mauritius (B.C. Victor).

Figure 3. *Halichoeres gurrobyi*, live individual, approx. 90 mm SL, specimen not retained, Mauritius (Meneeka Gurroby).

Description. Dorsal-fin rays IX,11 (12); anal-fin rays III,11, all soft dorsal and anal-fin segmented rays branched, last split to base; pectoral-fin rays 13, first rudimentary, second unbranched; pelvic-fin rays I,5; segmented caudal-fin rays 17, upper two and lower three unbranched, 4–5 upper and lower procurrent rays; pored lateral-line scales 27 (+1 on caudal-fin base); gill rakers 21 (19).

Body elongate, body depth 4.5 (5.0) in SL, and compressed, body width 1.7 (2.3) in depth; head length 3.0 (3.1) in SL; snout pointed, its length 3.7 (3.5) in HL; orbit diameter 3.9 (5.0) in HL; interorbital space broadly convex, least bony width 5.7 (5.7) in HL; caudal peduncle relatively wide and short, least depth 2.7 (2.6) in HL, caudal-peduncle length 2.6 (2.8) in HL.

Mouth small, terminal, rear end of maxilla ending before anterior margin of orbit. A pair of large, moderately projecting, and slightly recurved canine teeth anteriorly in each jaw, the lower pair curving forward and fitting between uppers when mouth closed; second canines about half size of first canines, followed by a row of decreasing-sized caniniform teeth, in upper jaw 5–6 followed by two or three molariform small teeth, in lower jaw 4–5 followed by two or three peg-like, almost incisiform, small teeth; second inner row of short embedded teeth in most anterior portion of upper and lower laws; no canine tooth posteriorly on upper jaw (but specimens are small). Upper preopercular margin free nearly to level of lower edge of orbit; lower margin free anterior to a vertical through anterior nostril. Gill rakers short, longest on first arch (at angle) about one-quarter length of longest gill filament. Nostrils small, in front of anterior edge of orbit. Pores on lower half of head comprise one over rear maxilla, then two anterior to orbit, followed by a curving suborbital series (counting up to rear mid-eye level) numbering 6–7 in single series; preopercular pores in a curved series after start of free edge near mandible, numbering 9 or 10 up to rear mid-eye level, with additional row of four pores along actual margin of lower preopercle.

Scales thin and cycloid; scales on side of thorax less than half as high as largest scales on side of body, becoming still smaller ventroanteriorly; head naked except for small partially embedded scales on nape in irregular rows but sparing midline in front of dorsal fin; fins naked except for several progressively smaller scales on basal region of caudal fin and mid-ventral scale projecting posteriorly from base of pelvic fins. Lateral line continuous, nearly following contour of back to about 19th pored scale, below base of about eighth dorsal-fin soft ray, where deflected sharply ventrally to straight peduncular portion; single small pore per scale, on short oblique tubule on at least first 16 scales and on slanting portion, then at end of short horizontal tubules, last pored scale on caudal-fin

TABLE 1

Proportional measurements of type specimens of *Halichoeres gurrobyi*, n. sp. as percentages of the standard length

	holotype	paratype
	BPBM 41277	BPBM 41278
Standard length (mm)	41.5	72.0
Body depth	22.2	20.1
Body width	12.8	8.6
Head length	33.0	32.6
Snout length	8.9	9.4
Orbit diameter	8.4	6.5
Interorbital width	5.8	5.7
Caudal-peduncle depth	12.3	12.6
Caudal-peduncle length	12.5	11.7
Predorsal length	33.0	31.0
Preanal length	51.6	55.4
Prepelvic length	33.5	33.9
Base of dorsal fin	53.3	57.5
First dorsal-fin spine	5.1	5.8
Ninth dorsal-fin spine	10.4	8.2
Longest dorsal-fin ray	12.3	13.2
Base of anal fin	33.0	34.0
First anal-fin spine	3.1	3.3
Second anal-fin spine	5.5	4.7
Third anal-fin spine	8.9	7.2
Longest anal-fin ray	10.1	11.4
Caudal-fin length	22.7	19.9
Pectoral-fin length	21.0	16.8
Pelvic-spine length	9.2	6.8
Pelvic-fin length	13.0	13.3

base. Origin of dorsal fin just anterior to vertical through pectoral-fn base; dorsal-fin spines progressively longer, first 6.5 (5.6) and ninth 3.2 (4.0) in HL; longest dorsal-fin soft ray 2.7 (2.5) in HL; origin of anal fin below base of last dorsal-fin spine; first anal-fin spine very short, 10.5 (9.8) in HL; second anal-fin spine 6.0 (6.9) in HL; third anal-fin spine 3.7 (4.5) in HL; longest anal-fin soft ray 3.3 (2.9) in HL; caudal fin slightly rounded to truncate (in IP), caudal-fin length 1.5 (1.6) in HL; about third pectoral-fin ray longest, 1.6 (1.9) in HL; pelvic fins short, 2.5 (2.4) in HL.

Color in life. (Figs. 1, 3 & 4) Color pattern of IP consists of yellow stripes on a pale background. On holotype, there are two major midlateral stripes on head and body, meeting on snout and covering lips; an additional thin yellow stripe along lower body and another along base of dorsal fin extending forward onto head; on larger paratype, there is no ventral body stripe. A large black blotch extends over entire caudal peduncle and base of caudal fin on holotype, blotch becoming saddle-like, sparing ventral edge of peduncle, on larger paratype. Fins translucent except for distal yellow band along dorsal fin and yellow margin on posterior caudal fin; also mottled orange and brown on the central caudal fin of holotype. A small black spot on upper rim of pectoral-fin base. Iris yellow-orange.

It is unknown what the TP stage looks like, since the largest individual collected, at about 90 mm SL (Fig. 3), is a more colorful version of the IP and the usual pattern among these labrids is to have a completely different TP color pattern with flashy colors and intricate sets of colorful bands and spots. It is likely that this large individual is a transitional stage. The fish has the basic IP color pattern with a bright yellow cheek formed by the merging of the yellow stripes, outlined above and below by turquoise bands, a general turquoise wash over the ventral body and caudal fin, and a bright yellow posterior margin of the caudal fin. Unlike the general pattern in related wrasses, the black caudal saddle is as large, or even slightly larger, than in earlier stages.

Color in alcohol. (Fig. 2) IP head and body tan dorsally grading to white ventrally, lateral stripes dark brown (lowest stripe of holotype not apparent in preservative), caudal-peduncle blotch black; a small black spot at upper rim of pectoral-fin base. Fins are translucent, except dark markings in central caudal fin of holotype.

Etymology. Named for Chabiraj (Yam) Gurroby, in recognition of his 35 years of efforts in observing and collecting the fishes of Mauritius. He operates Ornamental Marine World Ltd. with his children Mohesh and Meneeka Gurroby.

Figure 4. *Halichoeres gurrobyi*, live in aquarium, Mauritius (Meneeka Gurroby).

Distribution. The new species is described from specimens from Mauritius only.

Barcode DNA sequence. A 652-nucleotide sequence of the segment of the mitochondrial COI gene used for barcoding by the BOLD informatics database (Ratnasingham & Hebert 2007) was obtained for the holotype. Following the database management recommendation of the BOLD, the sequence of the holotype (GenBank accession number KT352030) is presented here as well:

CCTTTATTTAGTATTCGGCGCCTGAGCCGGGATGGTAGGCACAGCCCTAAGCTTGCTTATTCGGGCT
GAACTAAGCCAACCCGGGGCTCTCCTTGGAGACGACCAGATTTATAATGTAATCGTTACAGCCCATG
CATTCGTAATAATTTTCTTCATGGTTATACCTATCATGATCGGCGGATTTGGAAACTGACTGATTCCCC
TTATGATTGGAGCCCCAGACATGGCCTTTCCTCGTATGAACAACATGAGCTTTTGACTCTTGCCCCC
CTCTTTCTTACTTCTACTCGCCTCCTCAGGCGTAGAGGCAGGAGCTGGCACTGGTTGAACAGTTTAT
CCCCCACTGGCAGGCAACTTAGCCCATGCCGGGGCATCCGTTGACCTCACAATCTTCTCCCTCCACT
TAGCTGGTATTTCATCAATTTTAGGGGCCATTAATTTTATTACAACCATTGTTAACATGAAACCTCCAG
CTATCTC CCAATATCAAACCCCGCTCTTTGTTTGGGCTGTCCTAATTACAGCAGTTCTACTTCTTCTC
TCACTACCCGTCCTTGCTGCCGGAATCACAATACTGCTGACAGACCGAAACCTAAATACAACATTTT
TTGACCCCGCAGGAGGAGGAGATCCAATTCTGTATCAACACTTA

DNA Analysis. The neighbor-joining phenetic tree based on the COI mtDNA sequences of a variety of Indo-Pacific labrids with striped initial phases, following the Kimura two-parameter model (K2P) generated by BOLD (Barcode of Life Database), shows deep divergences between species and relatively small differences within species, except for two divergent lineages representing *H. zeylonicus* from different regions of the Indian Ocean (Fig. 5). As a broad generality, among most reef fishes the minimum interspecific distance between close congeners is often up to an order of magnitude greater than the maximum intraspecific distance, which is precisely what makes the barcode database particularly useful. It appears that the majority of reef fish species (with many exceptions) differ by more than 2% from their nearest relatives (Steinke *et al*. 2009, Ward *et al.* 2009, Victor 2015).

The genetic results show that the new species *H. gurrobyi*, falls within a clade of species related to *H. zeylonicus*, with its nearest neighbor being *H. pelicieri*, interestingly another Mascarene endemic species. The two species diverge by 9% in the COI sequence (minimum interspecific difference; uncorrected pairwise; 9.6% by K2P). An adjacent clade includes the genera *Leptojulis* and *Parajulis*, and several other *Halichoeres* species are more distantly related.

Comparisons. All of the members of the broad grouping of species allied to *H. zeylonicus* have an initial phase with some variation of yellow stripes and a dark spot on the base of the tail. Some members have only a trace of a dark spot on the tail, and some have dark stripes with only occasional individuals with dusky yellow stripes (see Kuiter 2010). Fortunately, the IP of *H. gurrobyi* is easily distinguished by the large size of the tail spot, which is a saddle-like blotch occupying most of the caudal peduncle, even in the largest specimen, which may represent a transitional stage or even the TP. In addition, all IP stages of *H. gurrobyi* have two major mid-lateral yellow stripes, a pattern only shared with some IP *H. leptotaenia* (endemic to the Persian Gulf; Randall & Earle [1994]), vs. a less prominent lower mid-lateral stripe in *H. pelicieri* or only a single mid-lateral stripe in the other members of the complex.

It is difficult to distinguish the IP of the relatives of *H. gurrobyi*: indeed, without DNA barcodes, the identity of IP fish in zones of overlap are tentative. There is an apparently diagnostic difference between the two species occurring along with *H. gurrobyi* in Mauritius (*H. pelicieri* and *H. zeylonicus*), but the differences, if any, between juvenile and IP *H. zeylonicus* and *H. hartzfeldii*, which overlap in southern Indonesia, need to be confirmed.

Halichoeres pelicieri vs. *H. zeylonicus*

There has been some confusion between IP *H. pelicieri* and *H. zeylonicus* in the southwestern Indian Ocean: indeed, there are reports of *H. pelicieri* from the African coast, but those are presently considered misidentifications of *H. zeylonicus* (discussed in Wickel *et al*. [2016]). Thus far, there seems to be no evidence that *H. pelicieri*

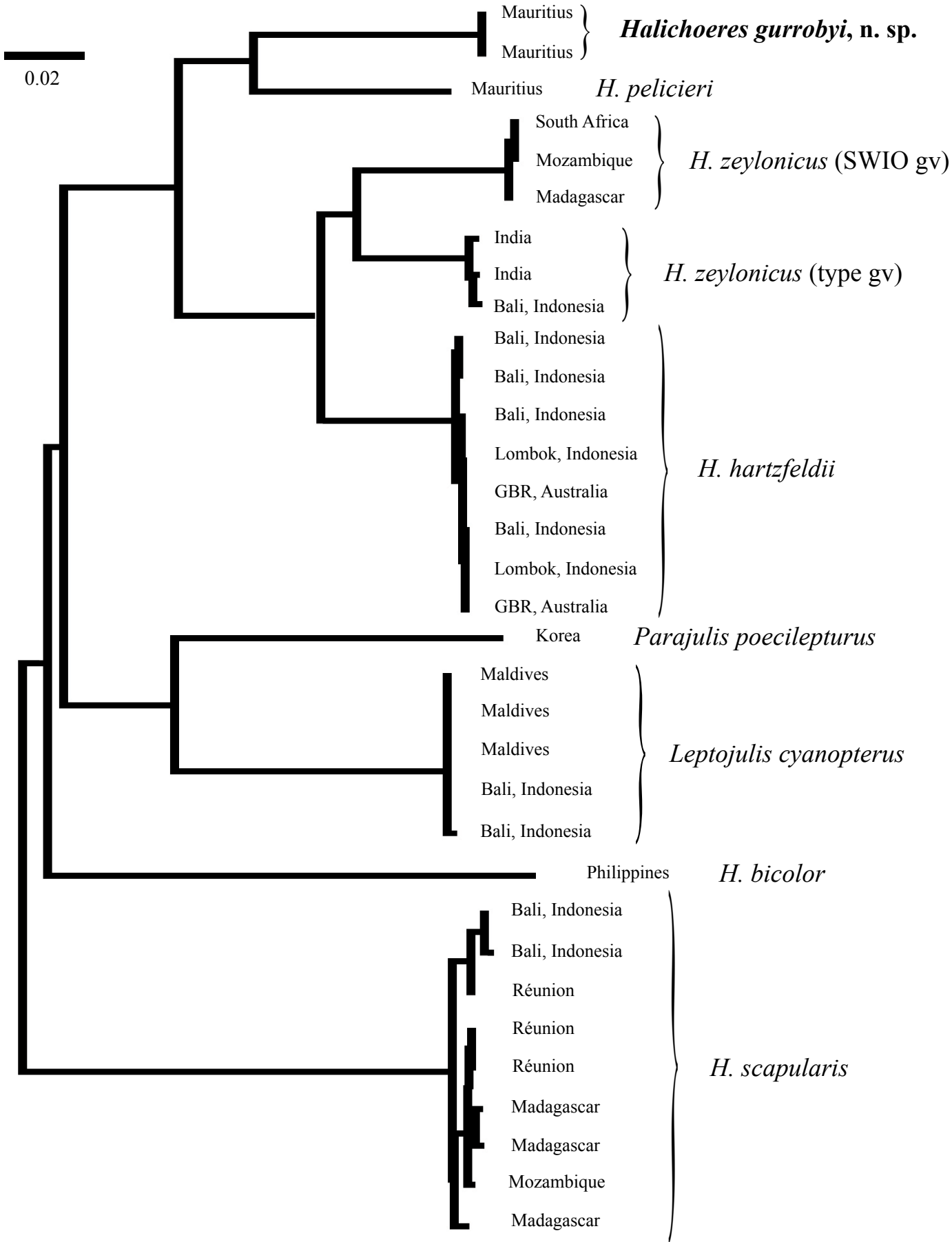

Figure 5. The neighbor-joining phenetic tree of various striped initial-phase species of Indo-Pacific labrids following the Kimura two-parameter model (K2P) generated by BOLD (Barcode of Life Database). The scale bar at left represents a 2% sequence difference. Collection locations for specimens are indicated. GenBank accession numbers and collection data for the sequences in the tree are listed in Appendix 1. gv=genovariant lineage (type population or SWIO lineage).

Figure 6. *Halichoeres pelicieri* above: live in aquarium, from Mauritius (V. Altimirano); below: fresh, same specimen, 56 mm SL, DNA-barcode identified and sequence presented in tree in Fig. 5 (B.C. Victor).

occurs outside of the type location of Mauritius (Randall & Smith 1982, Fricke 1999) and Réunion (Wickel *et al*. 2016). In contrast, *H. zeylonicus* occurs throughout the SWIO, including Mauritius.

Comparisons of DNA-identified specimens, along with other available photographs, show a difference between IP *H. pelicieri* and *H. zeylonicus*. A specimen of DNA-identified IP *H. pelicieri* from Mauritius (Fig. 6) matches the photographs from the description of the species, also from Mauritius (Figs. 7 & 8 lower). Notable features are a broad yellow midlateral stripe ending in a dark spot on the base of the caudal fin, with an additional thin yellow stripe below the lateral midline in all but the largest IP fish (i.e. Fig. 7 bottom; which is perhaps transitional). This lower stripe is apparently absent on IP *H. zeylonicus* (Fig. 9; DNA-identified). In addition, the larger yellow stripe continues across the snout at about the same level, at mid-pupil level, in *H. pelicieri* vs. elevated on the snout, above mid-pupil, in *H. zeylonicus*, particularly in larger IP individuals (as in Fig. 9; it is uncertain if this character applies to very small fish). Lastly, the dark tail spot is often wider than the adjacent stripe in *H. pelicieri* (e.g. Fig. 8 upper) vs. always narrower (or sometimes the same) than the stripe in *H. zeylonicus* (Figs. 9 & 10).

The juvenile of *H. pelicieri* apparently has not been photographed; the photograph in Fig. C in Kuiter (2010, p. 274) appears to be another wrasse– the eye is relatively small, consistent with a specimen of about 50 mm SL, but it does not share the markings of the similar-sized *H. pelicieri* identified here.

It is also not entirely resolved what the diagnostic differences are for the TP of *H. pelicieri* vs. *H. zeylonicus*. There is a verbal description of the TP *H. pelicieri* in Randall & Smith (1982), based on a large paratype when fresh and an underwater photograph of a similar-sized TP male by D. Pelicier in that paper; the authors then

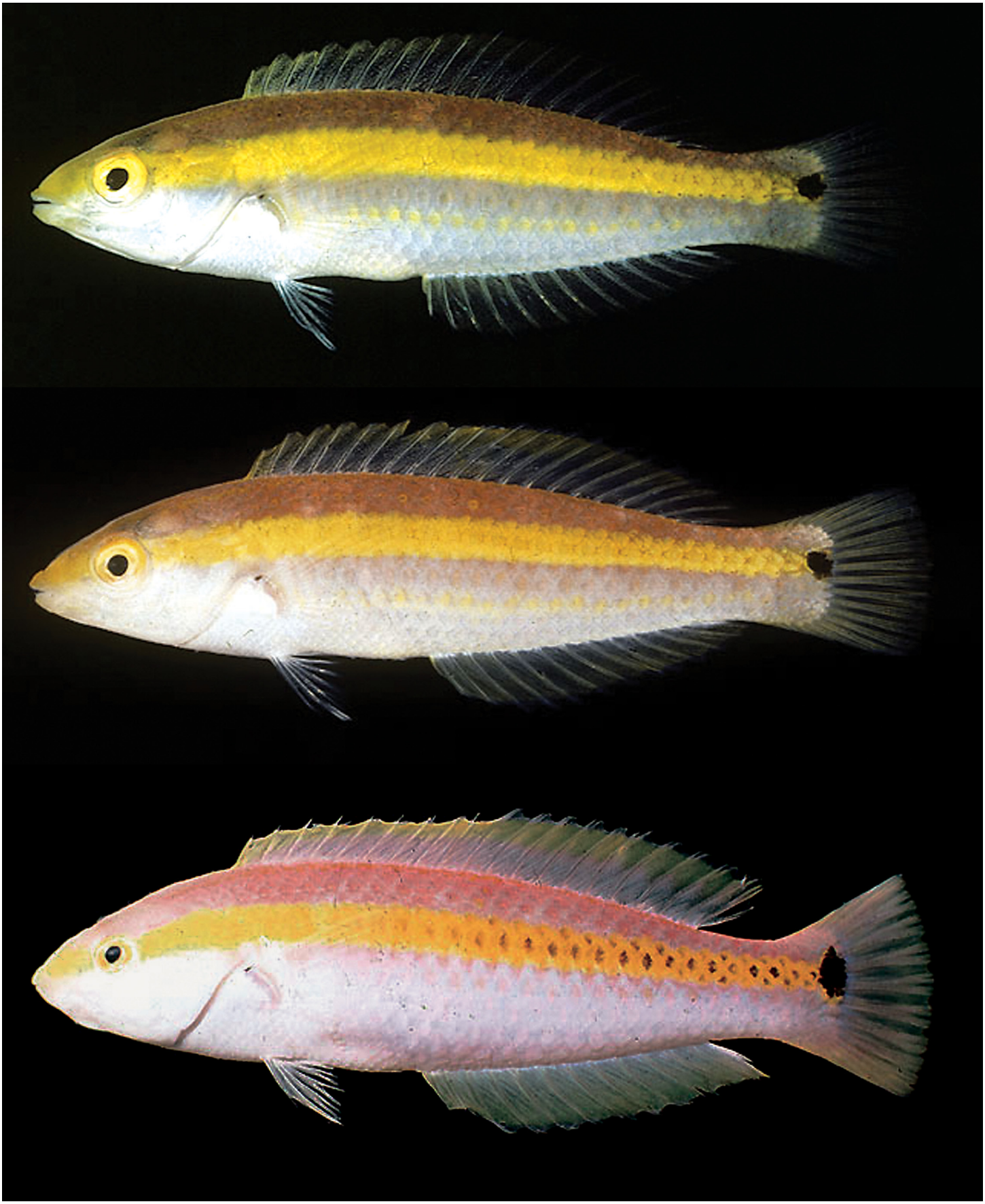

Figure 7. *Halichoeres pelicieri*, fresh photographs, Mauritius- top: 49 mm SL (D. Pelicier); middle: BPBM 22908, 50 mm SL (J.E. Randall); bottom: holotype, BPBM 17349, 86 mm SL (D. Pelicier).

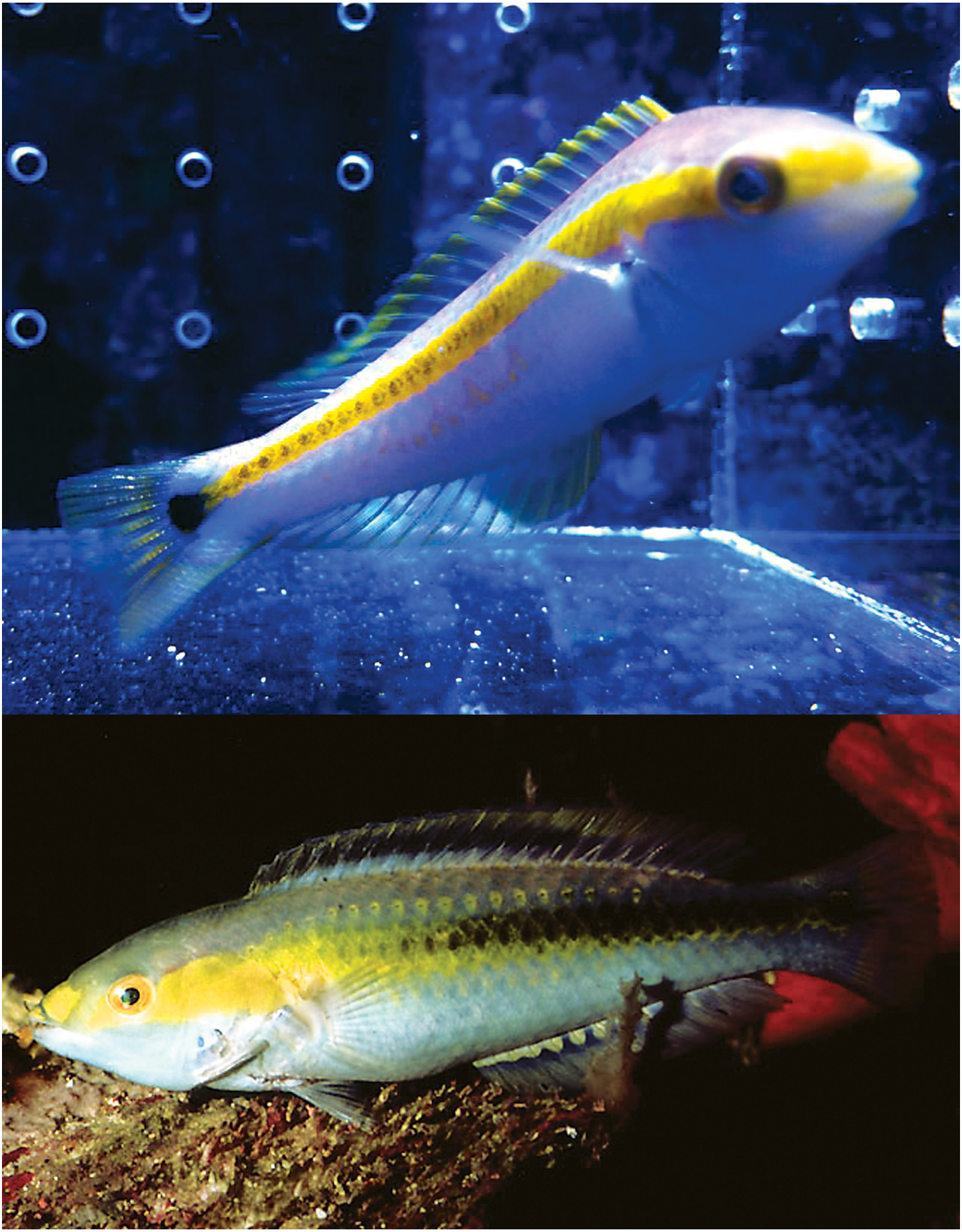

Figure 8. *Halichoeres pelicieri*, live photographs, upper: aquarium photograph (unknown photographer, www.reefaction.com); lower: male, Mauritius (D. Pelicier).

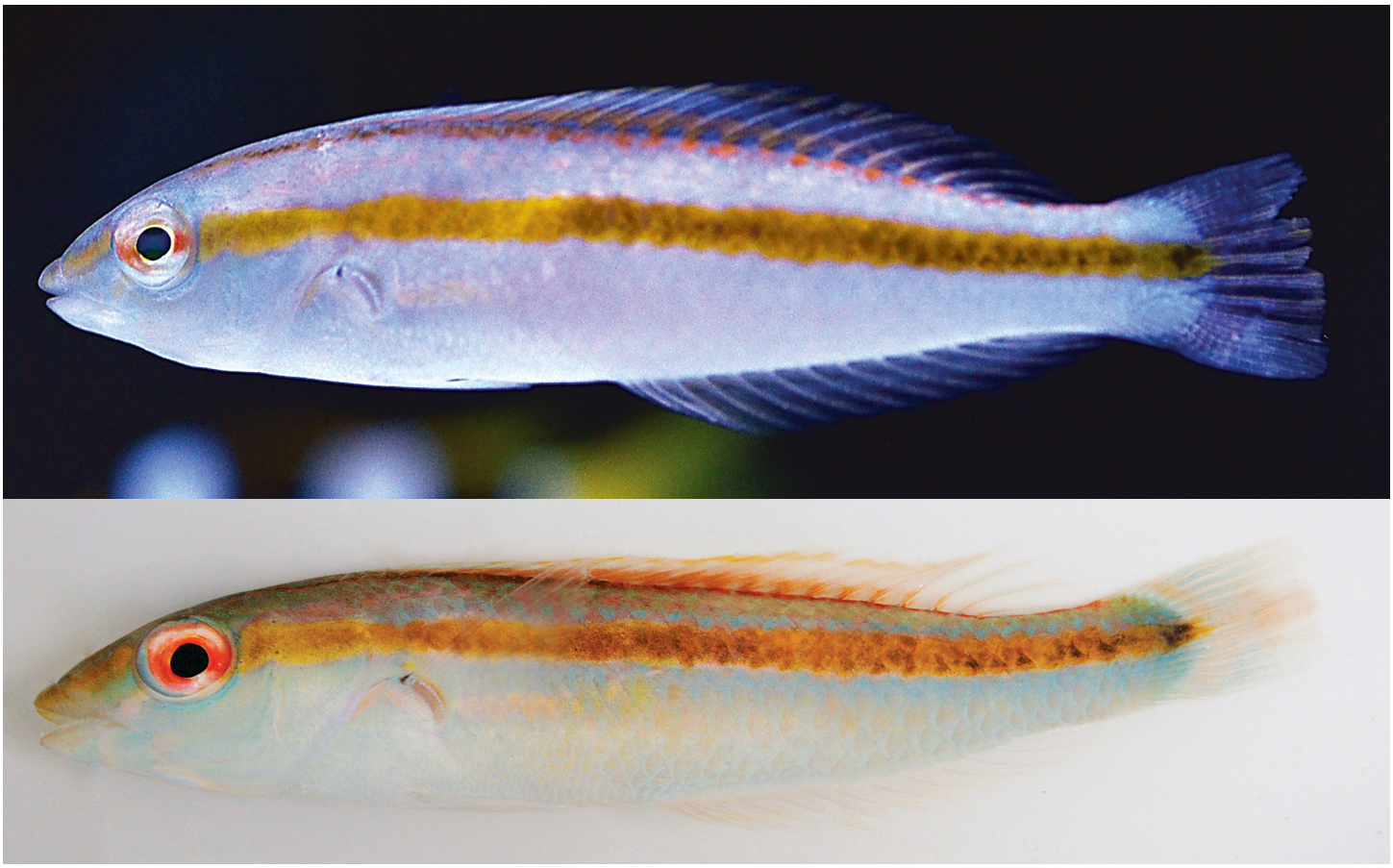

Figure 9. *Halichoeres zeylonicus* above: live in aquarium, from Madagascar (V. Altimirano); below: fresh, same specimen, 63 mm SL, DNA-barcode identified (SWIO gv) and sequence presented in tree in Fig. 5 (B.C. Victor).

compare TP color patterns, but based on Indian *H. zeylonicus* males (their Plate 5B and Fig. 11 top here). The differences are less clear when comparing to the darker TP *H. zeylonicus* morph found in the SWIO and Bali (Fig. 12). Randall & Smith (1982) emphasize 1) the blackish band in the dorsal fin of TP *H. pelicieri*, but that can also be found on TP *H. zeylonicus* (Fig. 12); 2) the persistence of the midlateral yellow stripe in TP *H. zeylonicus* (as in Fig. 11), but that is also not as evident on the darker morph of H *zeylonicus* (Fig. 12); and 3) the absence of the prominent mid-body black spot in TP *H. pelicieri*, but that can also be indistinct on darker TP *H. zeylonicus* (Fig. 12). The underwater photograph of the TP *H. pelicieri* by D. Pelicier in Randall & Smith (1982) does show a clearly rounded caudal fin outline vs. double emarginate in most TP *H. zeylonicus*. Additional specimens and photographs are needed to resolve these differences.

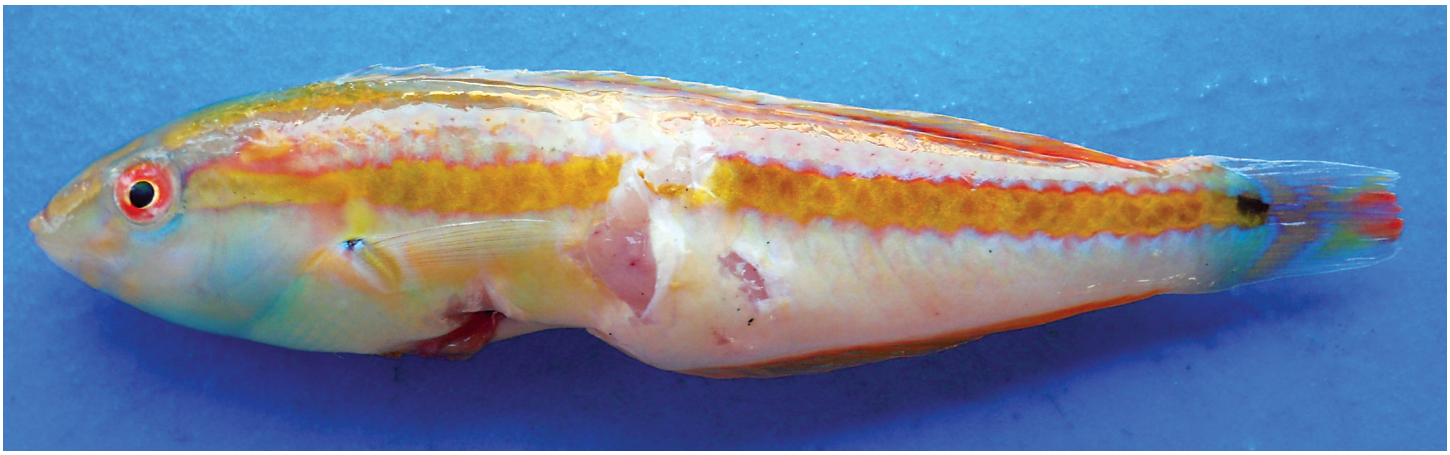

Figure 10. *Halichoeres zeylonicus*, fresh, Pomene, Mozambique, DNA-barcode identified (SWIO gv) and sequence presented in tree in Fig. 5 (A.D. Connell).

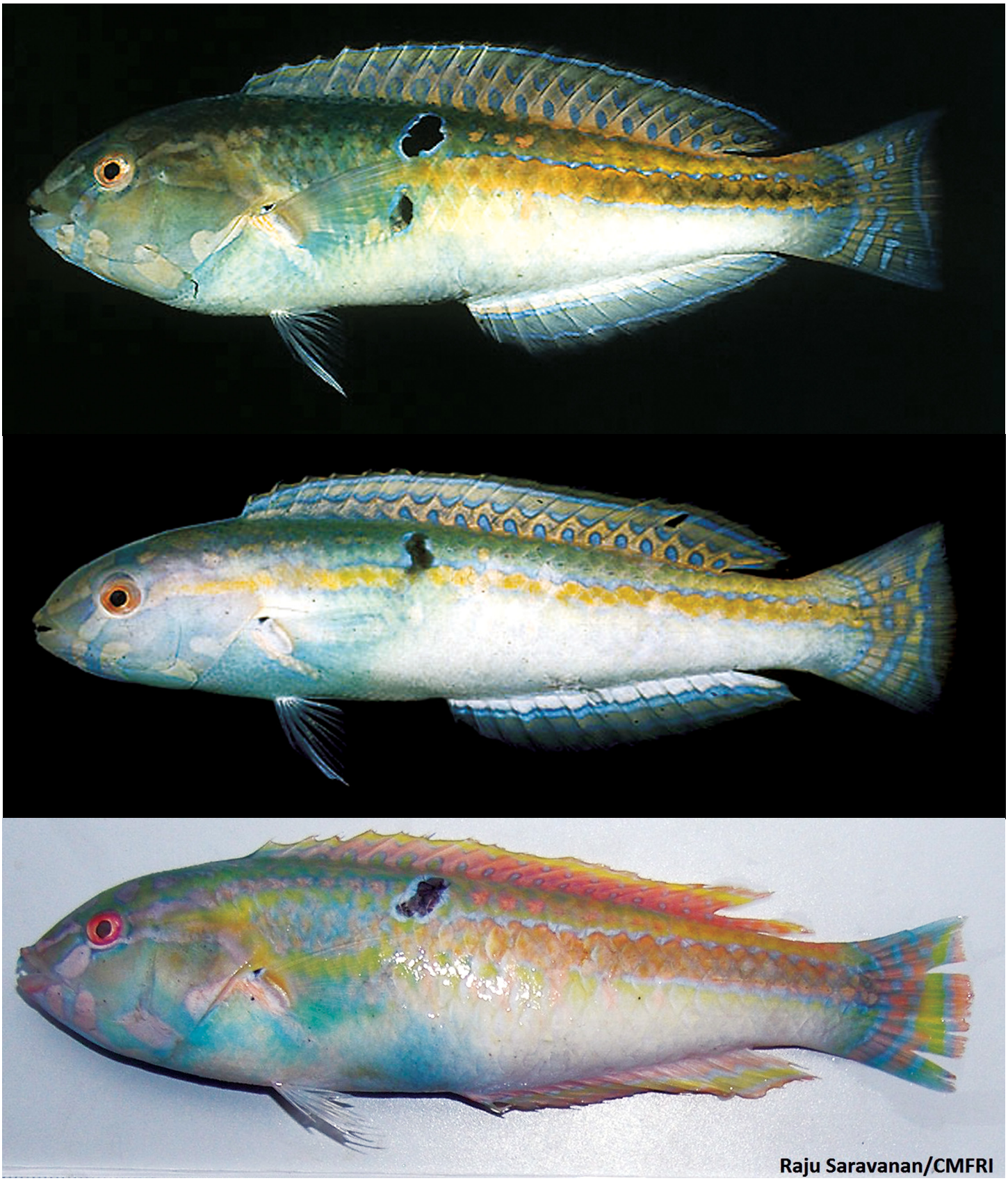

Figure 11. *Halichoeres zeylonicus*, fresh photographs of TP males, all from near type location (Sri Lanka), top: BPBM 20575, 133 mm SL, Tuticorin, India (J.E. Randall); middle: 95 mm SL, Seychelles (J.E. Randall); bottom: 180 mm SL, Gulf of Mannar, India (R. Saravanan).

Figure 12. *Halichoeres zeylonicus,* (black-finned TP male phenotype), fresh photographs, TP males, top: SAIAB 80655, 167 mm SL, Tanga, Tanzania, DNA-barcode-identified as SWIO genovariant (K. Sink); middle: Mauritius (D. Pelicier); bottom: 180 mm SL, Bali, Indonesia, DNA-barcode-identified as type lineage (W.White).

Halichoeres zeylonicus* vs. *H. hartzfeldii

A review of available underwater photographs show a variety of IP color patterns on W. Pacific specimens, which mostly represent *H. hartzfeldii*; some of these apparently look the same as IP *H. zeylonicus* or *H. pelicieri*. Additional mtDNA sequencing of small specimens would be needed to establish the range of appearances of IP individuals of *H. hartzfeldii*.

A review of the available genetic and photographic evidence indicates that *H. zeylonicus* and *H. hartzfeldii* are different species with mostly allopatric ranges, overlapping only in Indonesia, specifically Bali (Kuiter 2010). *Halichoeres zeylonicus* is found throughout the Indian Ocean extending eastward to Bali, while *H. hartzfeldii* occurs widely in the western Pacific from Japan south to Australia and eastward to Micronesia and the Marshall Islands and to the southwest Pacific islands of New Caledonia and Samoa. There is presently some confusion in the literature of the relative ranges of *H. zeylonicus* and *H. hartzfeldii*, since some authors have considered the two synonyms or subspecies, which has compromised the records when different names are used for the same populations (see Eschmeyer *et al*. 2016). The two species have quite different mtDNA lineages (6.14% divergent pairwise; 6.5% by K2P) and consistently different TP-male color patterns. TP males of *H. zeylonicus* have a blue-edged black blotch above the lateral stripe at mid-body, while TP males of *H. hartzfeldii* have the blotch in and below the lateral stripe and, notably, additional blue-edged black spots along the upper edge of the lateral stripe on the rear body (Fig. 13).

A review of photographs from various sources shows that the *H. hartzfeldii* TP color pattern is found only in the western Pacific, i.e. Australia (http://www.surg.org.au by Ian Shaw; Fenton Walsh, unpublished), Indonesia (Bali, Lombok, Banda; Kuiter 2010, CSIRO, FishBase by J.E. Randall), Philippines (Smithsonian by J.T. Williams), Taiwan (Academia Sinica by K.T. Shao), Japan (Nishiyama & Motomura 2012), Guam (www.guamreeflife.com by D. Burdick), Kwajalein (www.underwaterkwaj.com by S. & J. Johnson), and Samoa (www.nps.gov by R.C. Wass). The *H. zeylonicus* TP color pattern is found throughout the Indian Ocean eastward to Bali, Indonesia (Bali specimen collected, photographed, and DNA-sequenced by William White [Fig. 10], also photographed by Kuiter [2010]). Kuiter (2010) and Allen & Erdmann (2012) report these ranges correctly and Randall & Smith (1982) and Randall (1995, 2005) make clear that the nominal species occupy these different ranges, but suggest the two may be subspecies. Most of the literature before 2001 conflates the two species to varying degrees: Randall *et al*. (1990) combined the ranges under the senior name *H. zeylonicus*; Randall *et al*. (1997) and Myers (1999) accepted the two species, but presumed *H. hartzfeldii* to extend over the entire range from the Red Sea to Samoa, i.e. co-occurring with *H. zeylonicus* in the Indian Ocean; Parenti & Randall (2000) continued to report *H. zeylonicus* over the entire range of the two species, but added *H. hartzfeldii* as an Indonesian species. Laboute & Grandperrin (2000) and Fricke & Kulbicki (2006) reported *H. zeylonicus* from New Caledonia, but Fricke *et al*. (2011) corrected the reports to *H. hartzfeldii*.

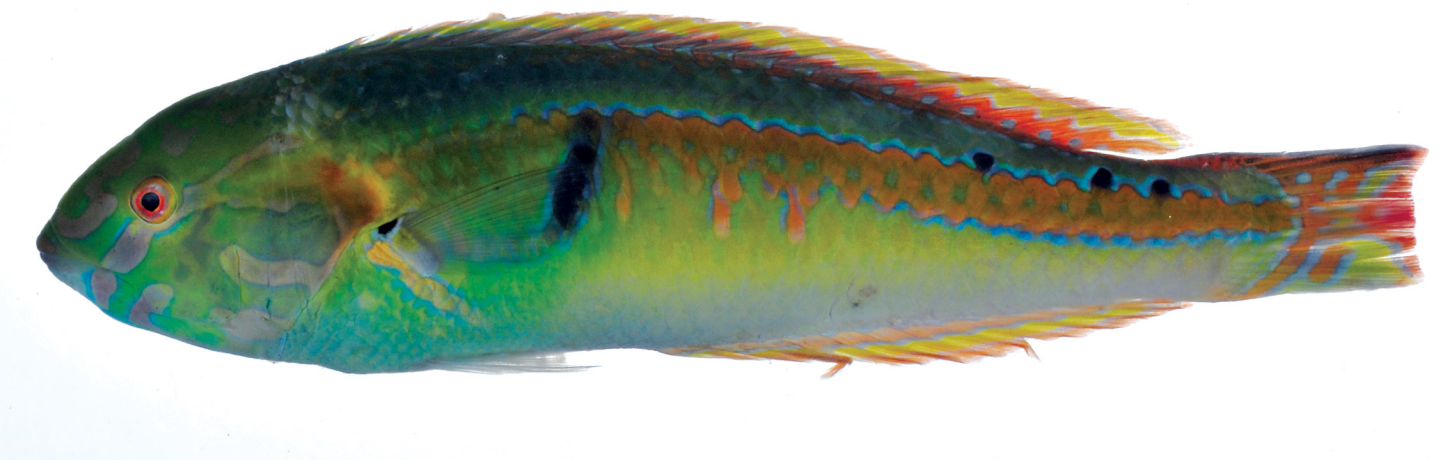

Figure 13. *Halichoeres hartzfeldii*, fresh TP male, USNM 408919, 158 mm SL, Luzon, Philippines, DNA-barcode identified (J.T. Williams).

Halichoeres zeylonicus genovariants

The population of *H. zeylonicus* in the southwestern Indian Ocean is genetically divergent from the northern and eastern population, which represent the type population (the type location is Sri Lanka). Specimens from Tanzania, Mozambique, South Africa, and Madagascar are in a mtDNA lineage 5.68% divergent from the lineage with specimens from India and Bali, Indonesia (pairwise comparison; BOLD:AAF7654 and BOLD:AAF7655 respectively). There are numerous photographs of TP *H. zeylonicus* from India and they all show fishes with orange to reddish background color on the dorsal fin (e.g. Fig 11), while the two available TP specimens with sequences from Tanzania and Mauritius have dark or black dorsal fins (Fig. 12). This suggested a color difference between the two lineages, however a subsequent photograph of the TP specimen that was sequenced from Bali also shows the same dark dorsal fin as the SWIO lineage (Fig. 12 bottom). Thus it appears there are no consistent differences in the appearance of the two populations and therefore no present basis for elevating the SWIO lineage to species status– in this case, the two populations represent genovariant populations of *H. zeylonicus* (*sensu* Victor 2015).

The yellow-striped-IP species complex

The set of related species in the clade associated with *Halichoeres zeylonicus* are linked by an IP color pattern including a mid-lateral yellowish stripe or two and a variable dark spot at the end of the stripe at the caudal-fin base. In addition, the known TP male color patterns usually include a mid-body black spot, often blue-edged. At present, this species complex contains a mostly allopatric set of five species: *H. zeylonicus* everywhere in the Indian Ocean (excluding the Persian Gulf), from the Red Sea eastward to Bali; *H. hartzfeldii* in the western Pacific Ocean, from Japan to Australia and eastward to the Marshall Islands and Samoa (and overlapping *H. zeylonicus* in Bali); *H. leptotaenia* endemic to the Persian Gulf; *H. pelicieri* endemic to Mauritius and Réunion; and *H. gurrobyi* endemic to Mauritius.

Interestingly, the related julidine *Leptojulis cyanopleura* shares both of these marking characters and, perhaps not coincidentally, falls in the same broad clade in a phenetic tree of mtDNA sequences, as well as in a multi-gene phylogenetic tree (Victor *et al*. 2013). Similarly, *Parajulis poecilepterus* shares these marking patterns as well; although the stripe on the IP is usually dark, it can sometimes be yellowish (e.g. Kuiter 2010, p. 259). *Parajulis* also falls in the same broad clade in the phenetic tree of mtDNA sequences (Victor *et al*. 2013). The nearest neighbor to the mtDNA COI clade containing *Parajulis* and *Leptojulis* in the BOLD database is *H. pelicieri*, which is intriguing, especially since a large proportion of the julidine wrasses have been barcoded in the BOLD database (at least 75% of the approximate 200 julidine species; Victor *et al*. [2013]). Given these relationships and the probable invalid status due to paraphyly of the monospecific genus *Parajulis*, and perhaps *Leptojulis* as well, all of these species may end up in a narrow *Halichoeres* after a more thorough phylogenetic analysis.

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Appendix 1. Specimen data and GenBank accession numbers for the mtDNA COI barcode sequences used to generate the phenogram in Fig. 5, following the order in the tree. Holotype in bold.

Genus	species	Collection site	Voucher	GenBank #	Collector/Source
Halichoeres	***gurrobyi*, n. sp.**	**Grand Bay, Mauritius**	**BPBM 41277**	**KT352030**	**Gurroby *et al*.**
Halichoeres	*gurrobyi*, n. sp.	Grand Bay, Mauritius	BPBM 41278	KU986291	Gurroby *et al*.
Halichoeres	*pelicieri*	Grand Bay, Mauritius	BPBM 41xx	KT352033	Gurroby *et al*.
Halichoeres	*zeylonicus*	KwaZulu, South Africa	ADC2013 220.34A2	KT352032	A. Connell/SAIAB
Halichoeres	*zeylonicus*	Pomene, Mozambique	ADC08 220.34A #1	JF493603	A. Connell/SAIAB
Halichoeres	*zeylonicus*	Madagascar	je14hp650	KT352031	J. Edward/aq. trade
Halichoeres	*zeylonicus*	Tamil Nadu, India	NBFGR:1333A	FJ158563	Lakra *et al*.
Halichoeres	*zeylonicus*	Tamil Nadu, India	NBFGR:1333B	FJ158564	Lakra *et al*.
Halichoeres	*zeylonicus*	Bali, Indonesia	ANFC KD903	JN313335	W. White/R. Ward
Halichoeres	*hartzfeldii*	Bali, Indonesia	bal11800plx134	KT352042	B. Victor
Halichoeres	*hartzfeldii*	Bali, Indonesia	bal11800plx130	KT352043	B. Victor
Halichoeres	*hartzfeldii*	Bali, Indonesia	bali11700clx127	KT352039	B. Victor
Halichoeres	*hartzfeldii*	Lombok, Indonesia	ANFC LM461	KX459126	W. White/R. Ward
Halichoeres	*hartzfeldii*	North Reef, GBR		DQ164159	D. Bellwood, JCU
Halichoeres	*hartzfeldii*	Bali, Indonesia	bal11600lx290	JQ839471	B. Victor
Halichoeres	*hartzfeldii*	Lombok, Indonesia	ANFC LM462	HQ564372	W. White/R. Ward
Halichoeres	*hartzfeldii*	Lizard Island, GBR		AY850748	Barber & Bellwood 2005
Parajulis	*poecilepterus*	Korea	NSMK:PI-000075	HM180591	Kim *et al*.
Leptojulis	*cyanopleura*	Maldives	je14lc590	KX459124	J. Edward/aq. trade
Leptojulis	*cyanopleura*	Maldives	je14lc550	KX459122	J. Edward/aq. trade
Leptojulis	*cyanopleura*	Maldives	je14lc770	KX459125	J. Edward/aq. trade
Leptojulis	*cyanopleura*	Bali, Indonesia	bal11700px124	JQ839546	B. Victor
Leptojulis	*cyanopleura*	Bali, Indonesia	bal11800l157	KX459127	B. Victor
Halichoeres	*bicolor*	Philippines, aquarium trade	aqhb	JX034554	B. Victor/aq. trade
Halichoeres	*scapularis*	Bali, Indonesia	bal11700h93	JQ839530	B. Victor
Halichoeres	*scapularis*	Bali, Indonesia	bal11400lx91	KX459123	B. Victor
Halichoeres	*scapularis*	Réunion	REU013-1	JF435007	N. Hubert *et al*.
Halichoeres	*scapularis*	Réunion	REU074-2	JF435005	N. Hubert *et al*.
Halichoeres	*scapularis*	Réunion	REU074-1	JF435006	N. Hubert *et al*.
Halichoeres	*scapularis*	Madagascar	NBE1266	JF435010	N. Hubert *et al*.
Halichoeres	*scapularis*	Madagascar	NBE1268	JF435008	N. Hubert *et al*.
Halichoeres	*scapularis*	Pomene, Mozambique	ADC08 220.35 #1	JF493604	A. Connell/SAIAB
Halichoeres	*scapularis*	Madagascar	NBE1267	JF435009	N. Hubert *et al*.