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## *Cirrhilabrus marinda*, a new species of wrasse (Pisces: Labridae) from eastern Indonesia, Papua New Guinea, and Vanuatu

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### Abstract

A new species of labrid, *Cirrhilabrus marinda*, is described from 29 type specimens, 17.4–45.9 mm SL, collected at Ayau Atoll, West Papua Province, Indonesia and 7 non-type specimens, 32.0–67.0 mm SL, from Halmahera, Indonesia and the vicinity of Espiritu Santo, Vanuatu. The new taxon is closely related to *Cirrhilabrus condei* of Indonesia (West Papua), Papua New Guinea, Solomon Islands, Coral Sea, and the northern Great Barrier Reef, mainly differing in the shape and colouration of the male dorsal fin. The spinous dorsal fin of *C. marinda* is mostly black and noticeably taller than the soft portion in comparison with *C. condei*, which has a more uniform fin profile with black colouration restricted to the outer fin margin. The population of *C. marinda* from Ayau Atoll differs from conspecific populations in other regions and from *C. condei* in having an exceptionally small maximum size of approximately 46 mm SL, with mature females as small as 30.4 mm SL. The two species are broadly sympatric, but do not share the same habitat; *C. marinda* prefer deeper offshore sand habitats. The barcode (COI) mitochondrial DNA sequences of the new species are the same as *C. condei*, apparently a case of phenotypic divergence outpacing changes in mitochondrial genotype. As in other reported cases of this phenomenon, the phenotypic differences are in the male mating display, which would be expected in the early stages of species divergence.

**Key words:** coral reef fishes, taxonomy, systematics, Indo-Pacific Ocean, DNA barcoding, phenovariant.

## Introduction

The labrid genus *Cirrhilabrus* Temminck & Schlegel 1845 is widely distributed on coral reefs of the tropical Indo-west Pacific region. These fishes, commonly known as fairy wrasses, are well known to divers, due to their abundance and remarkable male colour patterns, which are especially intensified during courtship and spawning. Spawning generally occurs daily, most commonly about 1–2 hours before sunset. The colourful terminal-phase males are typically far outnumbered by the much smaller and relatively drab-coloured initial phase females. Taxonomically, the group was poorly known, with only a few species described prior to the “scuba revolution” among researchers that began to gain serious momentum in the 1960s. Indeed, only six of the numerous species now considered as valid were described prior to that period. The genus is now the second largest in the family (after *Halichoeres* Rüppell 1835), with 51 currently recognized species (Table 1). The Bishop Museum ichthyologist, John E. Randall, has played a major role in advancing our knowledge of this group, having described 30 species, usually in conjunction with various coauthors. The present paper describes a new species that was initially identified as *C. condei* Allen & Randall 1996, but consistent differences in the shape and colouration of the male dorsal fin aroused our suspicion that two species with broadly sympatric ranges in the New Guinea region were involved.

## Materials and Methods

Counts of fin spines are given in Roman numerals and soft rays in Arabic numerals. Pectoral-ray counts include the rudimentary upper ray. The lateral line is interrupted; the count of the anterior part is given first, followed by a plus sign and the peduncular part. Only lateral-line scales with tubes are counted. All the tubed scales of the peduncular part are counted, even though one is usually located posterior to the base of the caudal fin. Gill-raker counts include all rudiments. Because it may be difficult to determine which raker is at the angle, only the total gill-raker count is given.

Lengths of specimens are given as standard length (SL), the straight-line measurement from the front of the upper lip to the base of the caudal fin (end of hypural plate). Measurements in Table 2 are given as percentages of the standard length. Head length is the distance from the front of the upper lip to the posterior end of the opercular membrane. Body depth is the greatest depth to the base of the dorsal fin (adjusting for any malformation of the abdomen due to preservation). Body width is measured just posterior to the opercular flap. Snout length is taken from the front of the upper lip to the fleshy edge of the orbit (if the upper jaw is protruded, it is pressed back to the nonprotractile position before the measurement is taken). Orbit diameter is the greatest fleshy diameter. Interorbital width is the least bony width. Caudal peduncle depth is the least depth; caudal peduncle length is the horizontal measurement between verticals at the rear base of the anal fin and the caudal-fin base. Measurements of fin spines and rays are taken to the extreme base of these elements. Pectoral-fin length is taken from the tip of the longest ray to the base of this ray. Pelvic-fin length is measured from the base of the spine to the tip of the longest ray.

Data in parentheses in the descriptions refer to paratypes, if differing from the holotype. Type specimens are deposited at Bernice P. Bishop Museum, Honolulu (BPBM), Museum Zoologicum Bogoriense, Cibinong, Java, Indonesia (MZB), United States National Museum of Natural History, Washington, D.C. (USNM), and Western Australian Museum, Perth (WAM).

Specimens of the new species were sequenced for the cytochrome c oxidase I (CO1) DNA barcoding fragment (Ward *et al.* 2009) and those sequences were compared with sequences available for the closely related species *C. condei* and other congeners, with *Paracheilinus flavianalis* used as the outgroup for the analysis. DNA extractions, PCR reactions, and sequencing followed the protocols described in Allen *et al.* (2013). The PCR product was sequenced at the University of California, Berkeley sequencing facility. Forward and reverse sequences were proofread in Geneious R7 (Kearse *et al.* 2012) then aligned using MUSCLE (Edgar 2004). Three methods were used to generate tree reconstructions: neighbor joining and maximum likelihood using MEGA5 (Tamura *et al.* 2011) and Bayesian inference using MRBAYES 3.2 (Ronquist & Hulsenbeck 2003). Neighbor joining was used

TABLE 1

Valid species of *Cirrhilabrus*, in chronological order of date described

species	author & date	species distribution
1 <i>cyanopleura</i>	(Bleeker 1851)	Andaman Sea to Bali
2 <i>solorensis</i>	Bleeker 1853	Indonesia
3 <i>temminckii</i>	Bleeker 1853	S Japan to W Australia
4 <i>jordani</i>	Snyder 1904	Hawaiian Islands
5 <i>ryukyuensis</i>	Ishigawa 1904	S Japan to Indonesia
6 <i>exquisitus</i>	Smith 1957	Indo-Pacific
7 <i>blatteus</i>	Springer & Randall 1974	Red Sea
8 <i>rubriventralis</i>	Springer & Randall 1974	Red Sea
9 <i>filamentosus</i>	(Klausewitz 1976)	Indonesia
10 <i>melanomarginatus</i>	Randall & Shen 1978	Taiwan, Philippines, S China Sea
11 <i>rubripinnis</i>	Randall & Carpenter 1980	Sabah, Philippines
12 <i>flavidorsalis</i>	Randall & Carpenter 1980	Philippines & E Indonesia
13 <i>lubbocki</i>	Randall & Carpenter 1980	Philippines, Indonesia
14 <i>laboutei</i>	Randall & Lubbock 1982	SW Pacific
15 <i>lineatus</i>	Randall & Lubbock 1982	SW Pacific
16 <i>roseafascia</i>	Randall & Lubbock 1982	SW Pacific
17 <i>rubrisquamis</i>	Randall & Emery 1983	Maldives, Chagos Archipelago
18 <i>sanguineus</i>	Cornic 1987	Mauritius
19 <i>balteatus</i>	Randall 1988	Marshall Islands
20 <i>johnsoni</i>	Randall 1988	Marshall & Caroline Islands
21 <i>luteovittatus</i>	Randall 1988	Marshall & Caroline Islands
22 <i>rhomboidalis</i>	Randall 1988	Marshall & Caroline Islands
23 <i>scottorum</i>	Randall & Pyle 1988	Coral Sea to Pitcairn Island
24 <i>punctatus</i>	Randall & Kuitert 1989	Fiji & Tonga to E Australia
25 <i>lunatus</i>	Randall & Masuda 1991	S Japan
26 <i>lanceolatus</i>	Randall & Masuda 1991	S Japan
27 <i>katherinae</i>	Randall 1992	Japan, Mariana & Caroline Islands
28 <i>rubrimarginatus</i>	Randall 1992	Ryukyu Islands to Fiji-Tonga
29 <i>randalli</i>	Allen 1995	NW Australia to E Lesser Sunda Islands
30 <i>condei</i>	Allen & Randall 1996	New Guinea to northern GBR
31 <i>pylei</i>	Allen & Randall 1996	New Guinea
32 <i>walindi</i>	Allen & Randall 1996	N Papua New Guinea
33 <i>adornatus</i>	Randall & Kunzmann 1998	Sumatra
34 <i>aurantidorsalis</i>	Allen & Kuitert 1999	Tomini Bay, Indonesia
35 <i>tonozukai</i>	Allen & Kuitert 1999	E Indonesia
36 <i>morrisoni</i>	Allen 1999	Timor Sea
37 <i>joanallenae</i>	Allen 2000	NW Sumatra
38 <i>katoi</i>	Senou & Hirata 2000	Japan
39 <i>claire</i>	Randall & Pyle 2001	Cook Islands
40 <i>earlei</i>	Randall & Pyle 2001	W Caroline Islands
41 <i>walshi</i>	Randall & Pyle 2001	Samoa
42 <i>bathyphilus</i>	Randall & Nagareda 2002	Coral Sea
43 <i>marjorie</i>	Allen, Randall & Carlson 2003	Fiji
44 <i>brunneus</i>	Allen 2006	Sabah, Philippines & Indonesia
45 <i>cenderawasih</i>	Allen & Erdmann 2006	Cenderawasih Bay, W New Guinea
46 <i>beauperryi</i>	Allen, Drew & Barber 2008	Papua New Guinea and Solomon Is.
47 <i>naokoae</i>	Randall & Tanaka 2009	Sumatra
48 <i>nahackyi</i>	Walsh & Tanaka 2012	Fiji & Tonga
49 <i>humanni</i>	Allen & Erdmann 2012	E Lesser Sunda Islands, Indonesia
50 <i>squirei</i>	Walsh 2014	Great Barrier Reef & Coral Sea
51 <i>marinda</i>	Allen, Erdmann & Dailami 2015	E Indonesia to Vanuatu

to calculate relationships between individuals based on genetic distance. The maximum likelihood analysis was used to assess the model of best fit for the nucleotide substitutions. The Bayesian Information Criterion (BIC) was used to rank the Hasegawa-Kishino-Yano (HKY) model with a discrete Gamma distribution (HKY+G) to derive the best fit to the data. This model assumes different rates of transitions and transversions as well as different nucleotide frequencies, and was chosen as the appropriate model of evolution as determined in MEGA5 (Tamura *et al.* 2011). Bootstrap support was determined using 1000 replicates in MEGA5. For the Bayesian analysis we used a Markov Chain Monte Carlo (MCMC) approach with four chains. Analyses were run for 20,000,000 generations. After 20,000,000 generations, the resulting tree was checked for convergence using Tracer v1.5 (Rambaut & Drummond 2009).



**Figure 1.** *Cirrhilabrus marinda*, freshly captured (anesthetised) holotype, MZB 22718, 45.9 mm SL, Ayau Atoll, West Papua Province, Indonesia (G.R. Allen).

### ***Cirrhilabrus marinda* Allen, Erdmann & Dailami, n. sp.**

Sailfin Fairy-wrasse

Figures 1–4 & 7–8; Table 2.

**Holotype.** MZB 22718, male, 45.9 mm SL, Ayau Atoll, 0° 20.792'N, 131° 01.495'E, Raja Ampat Islands, West Papua Province, Indonesia, rubble bottom on outer reef, 30 m, rotenone, M.V. Erdmann, 18 February 2015.

**Paratypes.** (all collected with holotype) BPBM 41211, 6 specimens, 17.4–42.4 mm SL; MZB 22719, 7 specimens, 21.5–45.3 mm SL; USNM 432484, 8 specimens, 19.6–45.2 mm SL; WAM P.34338-001, 8 specimens, 22.7–45.7 mm SL.

**Non-type specimens.** BPBM 40767, 4 specimens, 32.0–43.0 mm SL, Tutuba Island, 15° 32' 35.23''S, 167° 16' 49.65''E, Vanuatu; BPBM 40774, 3 specimens, 50.0–67.0 mm SL, Perumamasa Islet, 15° 36.770'S, 167° 08.797'E, Aore Island, Vanuatu; WAM P.32979-001, 59.3 mm SL, Morotai Island, 2° 17.224'N, 128° 09.732'E, Halmahera, Maluku Province, Indonesia.



**Diagnosis.** Dorsal-fin rays XI,9; anal-fin rays III,9; pectoral-fin rays usually 15 (occasionally 16); lateral-line scales 15–17 + 6–9; median predorsal scales 4–6; single horizontal scale rows on cheek below eye; gill rakers 13–16 (usually 14); body depth 2.9–3.5 in SL; head length 2.8–3.1 in SL; snout length 3.7–4.5 in HL; caudal fin rounded; pelvic fins of male elongate, reaching posteriorly to about middle of anal fin, 2.2–2.9 in SL; male in life mainly bright red to orange on upper one half to two-thirds of head and body, usually with orange wash on nape and diffuse orange zone between dorsal-fin origin and upper pectoral-fin base; head and body abruptly white to pale greyish on lower third; dorsal fin with white basal stripe and broad black band covering most of spinous part of fin, tapering in width posteriorly to end of soft dorsal, outer half of soft dorsal translucent yellowish with row of blue spots between black and translucent portions; anal fin white basally and remainder of fin bright red except row of blue spots between white and red portions and narrow blue outer margin; caudal fin red medially with 2–3 transverse rows of small blue spots, dorsalmost and ventralmost fourths of fin yellowish; female and juvenile in life mainly yellowish anteriorly on head and body, grading to pinkish on remainder of body except belly and lower half of head whitish; about 6–7 narrow white to bluish stripes on upper half of head (including snout), continuing on side of body (corresponding with lateral scale rows) to caudal-fin base; fins mainly pale grey to pinkish except dorsal fin with broad yellow basal stripe and dark grey to blackish on remainder of spinous portion.

**Description.** (meristic and morphometric data from 20 specimens, 28.0–59.3 mm SL) Dorsal-fin rays XI,9; anal-fin rays III,9; all dorsal and anal soft rays branched except first, last ray branched to base; pectoral-fin rays 15 (except 16 in two paratypes), the upper two unbranched; pelvic rays I,5; principal caudal-fin rays 13, uppermost and lowermost rays unbranched; upper and lower procurrent caudal-fin rays 3 (3–5), posteriormost segmented; lateral-line interrupted, pored scales 17 + 9 (15–17 + 6–9); scales above lateral line to origin of dorsal fin 2; scales below lateral line to anus 6; median predorsal scales 5 (4–6); median preventral scales 5 (5–6); single horizontal scale row on cheek; circumpeduncular scales 16 (15–16); gill rakers 14 (except 2 paratypes with 13, one with 15, and two with 16); pseudobranchial filaments 11 (10–12); branchiostegal rays 5.

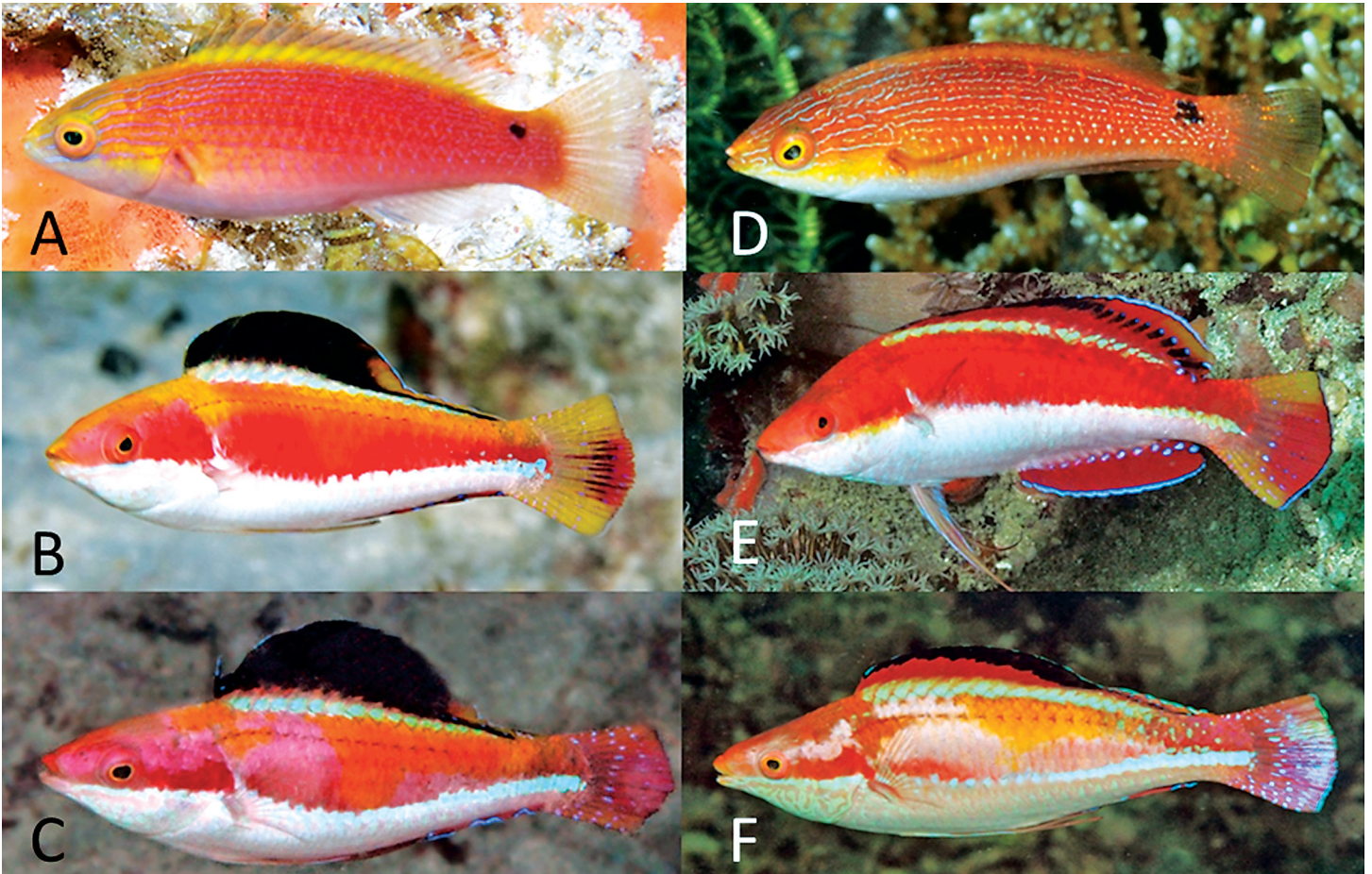
Greatest body depth 3.1 (2.8–3.5) in SL; body compressed, width 2.0 (1.9–2.2) in depth; dorsal profile of head nearly straight, becoming slightly convex on nape; HL 3.0 (2.8–23.1) in SL; snout length 3.7 (3.7–4.8) in HL; orbit diameter 3.7 (3.2–4.2) in HL; interorbital width 4.3 (3.2–4.5) in HL; caudal-peduncle depth 2.4 (2.2–2.8) in HL; caudal-peduncle length 1.6 (1.6–2.5) in HL.

Mouth small, terminal and oblique, maxilla reaching vertical at anterior nostril, upper-jaw length 4.1 (4.2–5.3) in HL; dentition typical of the genus with three pairs of canine teeth at front corner, gradually longer and more



**Figure 2.** *Cirrhilabrus marinda*, preserved holotype, MZB 22718, 45.9 mm SL, Ayau Atoll, West Papua Province, Indonesia (G.R. Allen).





**Figure 3.** Comparison of live colour patterns of *Cirrhitlabrus marinda* (A-C) from Ayau Atoll, West Papua and *C. condei* (D-F) from Samarai Island, Papua New Guinea. A & D: initial phase female about 25 mm SL; B & E: terminal phase male about 45 and 60 mm SL; C & F: nuptial phase male about 45 and 65 mm SL (G.R. Allen).

laterally recurved proceeding posteriorly; series of about 18–20 small conical teeth medial to anterior canines and continuing on side of jaw; lower jaw with single stout pair of canines anteriorly, protruding obliquely outward and slightly lateral to medial pair of upper jaw; inner series of about 17–21 small conical teeth in lower jaw; tongue short with rounded anterior edge; gill rakers small, longest on first arch about one-third length of longest gill filaments of holotype.

Posterior margin of preopercle with 36 (28–38) small serrae; margin of posterior edge of preopercle free to level of middle of pupil (upper part of edge covered with scales); margin of ventral edge of preopercle free nearly to below anterior margin of pupil; anterior nostril very small, in short membranous tube with posterior flap, located anterior to upper edge of eye about one-half distance to snout tip; aperture of posterior nostril much larger than cephalic sensory pores, with a slight rim, located posterior and slightly dorsal to anterior nostril on a vertical with anterior margin of eye; pores of cephalic lateralis system adjacent to eye from behind middle of orbit to below front of orbit 10 (10–12); pores on side of snout anterior to eye 4; pores on posterior and ventral edges of preopercle 8 (7–9), continuing as a series of 4 pores on mandible to front of chin; single, tiny mid-interorbital pore; pores adjacent to upper edge of eye to front of anterior nostril 5; pores from upper margin of preopercle to upper rear corner of eye 5; and series of 8 (8–10) small pores on side of nape from anterior end of lateral line to front of most anterior predorsal scale.

Scales cycloid; head scaled except snout, interorbital region, lips, and chin, also broad (maximum width about equal to half width of adjacent cheek scale) naked flange on posterior and ventral edges of preopercle; cheek with single row of large cycloid scales; base of dorsal and anal fins with row of large, pointed elongate scales, one per membrane (except first and last scale generally covers two membranes), tallest slightly more than one-third length of adjacent dorsal fin spines (scales progressively shorter posteriorly on membranes of soft portion of fin); base of caudal fin with three enormous scales (about 4–5 times larger than body scales), middle one overlapping those



above and below, reaching about one-half distance to posterior margin of fin; pectoral fins naked; pelvic fins with a median ventral process of two elongate scales, the more pointed posterior scale about three-fourths length of pelvic spine and about equal in length to slender axillary scale above each pelvic fin.

Origin of dorsal fin above second lateral-line scale; first dorsal spine 3.1 (3.5–5.9) in HL; longest (seventh) dorsal spine 1.5 (1.5–2.0 and 2.3–2.6 respectively for male and female paratypes) in HL; interspinous membranes extending well above spine tips, supported by terminal cirrus projecting dorsally or posteriorly from behind each spine tip, each cirrus one-half spine length in adult males and slightly shorter in females; longest (first) dorsal soft ray 1.8 (1.7–2.3) in HL; origin of anal fin vertical with base of penultimate dorsal spine; first anal spine 7.5 (4.8–7.3) in HL; second anal spine 4.8 (3.2–4.8) in HL; third anal spine 3.4 (2.7–3.7) in HL; penultimate anal soft rays longest, 1.8 (1.7–2.4) in HL; caudal fin rounded, 3.8 (3.5–4.3) in SL; third and fourth pectoral-fin rays longest, 1.5 (1.4–1.8) in HL; origin of pelvic fins level with upper pectoral-fin base; pelvic fins of males elongate, reaching to about middle of anal fin, 2.2 (2.2–2.9 in male paratypes); pelvic fins of females and juveniles short, 5.7–6.3 in SL.

**Color of male in life.** (Figs. 1, 3B & C, 4) Upper one half to two-thirds of head and body mainly bright red to orange, usually with orange wash on nape and diffuse orange zone between dorsal-fin origin and upper pectoral-fin base; head and body abruptly white on lower third except some individuals pale grey on lower head with white stripe below eye and white spots on cheek; also some individuals with yellow-orange stripe across middle of opercle just below level of lower edge of eye; dorsal fin with white basal stripe and broad black band covering most of spinous part of fin, tapering in width posteriorly to end of soft dorsal, outer half of soft dorsal translucent yellowish with row of blue spots between black and translucent portions; anal fin white basally and remainder of fin bright red except row of blue spots between white and red portions and narrow blue outer margin; caudal fin red medially with 2–3 transverse rows of small blue spots, dorsal and ventral one-fourth of fin pale yellow; pelvic fins translucent whitish; pectoral fins translucent with red spot covering base; eye with red-orange iris and narrow orange ring surrounding pupil. The freshly captured male holotype is illustrated in Fig. 1. Colour of nuptial male



**Figure 4.** *Cirrhilabrus marinda*, underwater photograph at Ayau Atoll, West Papua Province Indonesia, showing mixed group of males (approximately 40–45 mm SL) and females (approximately 25–35 mm SL)(G.R. Allen).

TABLE 2

Proportional measurements of selected type specimens of *Cirrhilabrus marinda*, n. sp.  
as percentages of the standard length

	holotype				paratypes						
	MZB 22718	MZB 22719	WAM P 34338	USNM 432484	MZB 22719	WAM P 34338	BPBM 41211	WAM P 34338	BPBM 41211	MZB 22719	BPBM 41211
	males						females				
Standard length (mm)	45.9	45.3	44.6	44.1	43.5	42.1	38.3	38.4	36.4	34.3	32.0
Body depth	32.4	34.0	33.0	31.3	30.0	28.8	30.9	31.9	32.2	35.3	30.6
Body width	16.0	15.8	15.8	15.3	15.4	15.3	15.6	14.6	14.9	15.8	14.3
Head length	33.5	32.7	33.9	33.4	33.3	35.1	34.1	34.0	32.7	33.0	35.4
Snout length	9.0	8.9	8.8	8.7	7.6	9.5	8.4	8.8	7.3	8.3	7.4
Orbit diameter	8.9	8.8	8.8	9.3	7.9	9.4	8.8	10.0	10.1	10.4	9.7
Interorbital width	7.9	7.7	7.6	8.3	7.8	8.9	8.6	7.7	7.5	10.2	7.9
Upper jaw	8.3	7.8	7.4	7.5	6.3	7.8	7.1	7.0	6.7	6.8	8.2
Depth of caudal peduncle	14.0	12.4	14.4	13.5	12.9	13.6	15.8	13.6	13.4	14.9	15.1
Length of caudal peduncle	20.4	17.0	20.1	17.5	18.1	18.3	17.8	15.9	16.1	18.4	14.4
Predorsal distance	33.2	33.8	33.2	32.6	32.6	34.4	32.1	35.5	31.2	34.7	34.3
Preanal distance	58.0	56.4	60.6	58.6	57.5	60.0	56.7	64.8	64.1	63.5	62.1
Prepelvic distance	33.6	33.4	35.1	36.3	33.2	34.8	34.0	34.6	33.9	34.2	31.0
Length of dorsal-fin base	57.0	56.8	59.9	56.1	61.4	57.2	58.7	54.3	58.7	59.8	55.4
1st dorsal spine	10.8	7.2	7.1	6.2	7.1	6.0	5.8	7.2	7.3	6.2	8.0
Tallest (7th) dorsal spine	22.6	19.9	21.5	17.1	16.9	20.2	18.5	13.7	14.4	14.0	13.0
Longest (1st) soft-dorsal ray	18.2	16.9	17.3	16.5	14.2	16.0	16.8	14.9	15.7	15.0	16.2
Length of anal-fin base	25.8	27.2	27.9	23.7	24.9	25.4	28.4	23.2	24.1	23.1	25.9
1st anal spine	4.5	5.1	6.0	5.6	4.6	5.2	5.9	5.2	6.5	6.7	6.3
2nd anal spine	7.0	8.0	8.3	9.2	7.3	8.6	9.6	8.8	10.4	9.1	10.4
3rd anal spine	9.7	9.9	11.3	10.2	10.0	9.9	10.4	10.8	11.9	10.5	11.7
Longest (8th) soft-anal ray	19.0	18.1	18.4	18.5	16.2	15.6	19.8	14.6	14.5	14.7	14.9
Caudal-fin length	26.0	24.7	26.9	24.9	23.6	26.2	27.2	27.1	24.8	25.9	28.0
Pectoral-fin length	22.6	23.7	23.1	20.0	22.7	22.6	22.0	22.0	22.2	22.9	19.5
Pelvic fin-spine length	11.8	10.4	11.7	10.8	9.8	9.8	12.1	11.8	10.6	11.7	10.9
Pelvic fin length	44.6	41.2	45.0	37.6	38.8	34.5	35.4	16.6	16.5	15.9	17.4



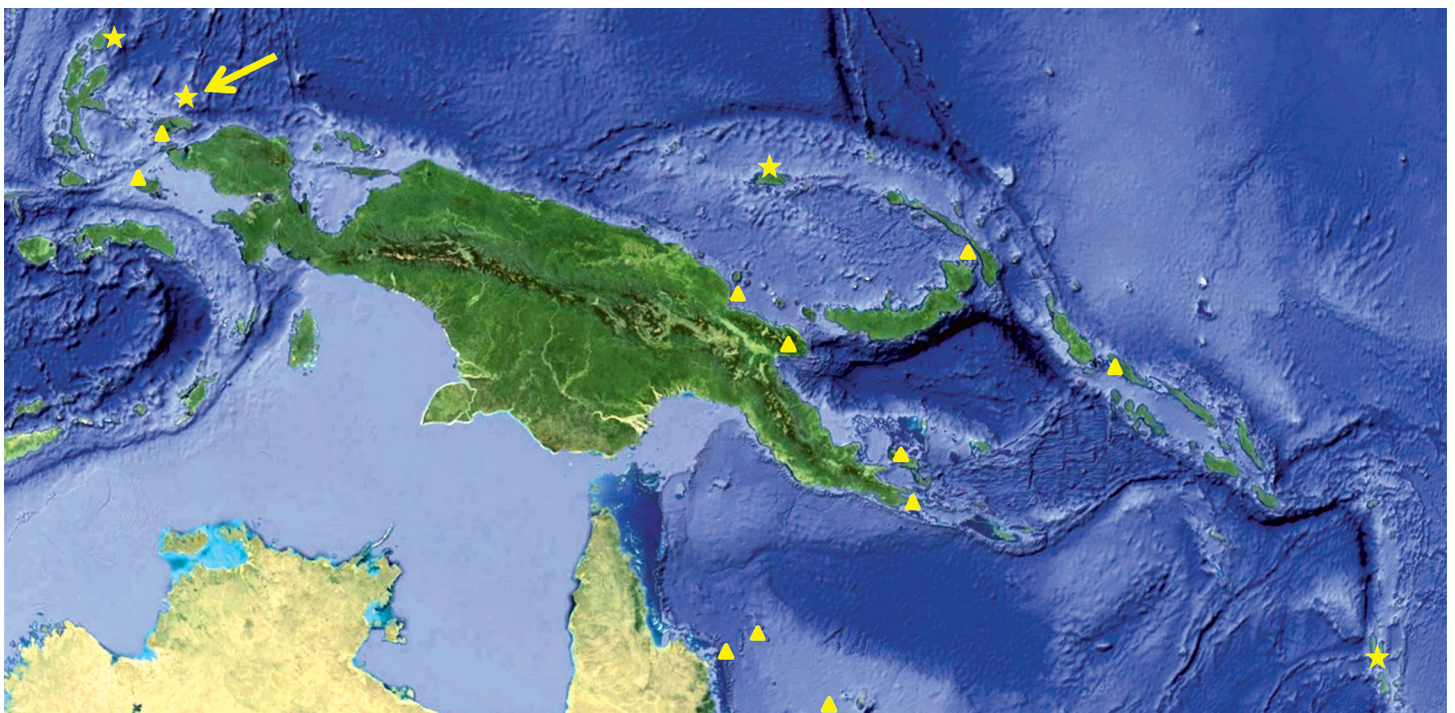
generally similar to colouration described above, but red/orange area on upper part of body with irregular patches of pink, red, and orange as shown in Fig. 3C; fins similar to above description, except middle part of caudal with broad bluish red area on outer margin and lacking pronounced yellow areas dorsally and ventrally.

**Color of female in life.** (Figs. 3A & 4) Tip of snout, upper half of head and adjacent anterior body, and upper edge of caudal peduncle yellowish red, grading to pink on remainder of body except belly and lower half of head whitish red; about 6–7 narrow white to bluish stripes on upper half of head (including snout), continuing on side of body (corresponding with lateral scale rows) to caudal-fin base; individual body scales also with intricate pattern of small pale blue to whitish spots; a small (less than pupil size) black to grey spot on upper caudal peduncle; dorsal fin with broad yellow basal stripe, dark grey to black on remainder of spinous portion, and translucent white to pale yellow posteriorly; caudal fin translucent pale grey to pink with transverse white bands; pelvic and pectoral fins translucent to white.

**Color in alcohol.** (Fig. 2) Males in alcohol are mainly white except yellowish tan lower head and belly, broad pinkish grey stripe from rear edge of eye to posterior margin of head, pinkish grey nape merging with stripe of same colour along base of dorsal fin, and diffuse pinkish grey saddle on upper half of caudal peduncle; thin grey stripes on side of body corresponding with lateral scale rows (including most conspicuous one corresponding with lateral line); spinous dorsal fin and basal portion of soft dorsal mainly blackish, remainder of soft dorsal translucent with longitudinal row of black-edged white spots across middle of fin; caudal fin mainly translucent with narrow black posterior margin and large dusky blackish patch encompassing outer portion of middle rays; anal fin mainly translucent white base and narrow black basal stripe and narrow black outer margin; pectoral and pelvic fins translucent to whitish. Females in alcohol are uniformly yellowish tan with small greyish spot on upper caudal peduncle; fins translucent except diffuse blackish band along margin of spinous dorsal.

**Distribution and habitat.** The new species is currently known from eastern Indonesia at Halmahera (Morotai Island) and West Papua (Ayau Atoll) and also from Vanuatu (Fig. 5). We also have photographic evidence of its occurrence at Manus Island, Papua New Guinea. Kuitert (2010, p. 131 E) illustrated a nuptial male from Fiji, but according to the photographer (H. Tanaka), the fish actually originated from Vanuatu.

The new species was collected and observed in depths between about 25–40 m. The habitat consists of flat or gently sloping, mixed *Halimeda* sand and rubble bottoms with scattered, low outcrops of rock or coral, usually on exposed outer reefs with periodic strong currents. The species appears to be common at Ayau Atoll and typically occurs in groups of about 10–20 individuals, the majority of which are initial phase fish (Fig. 4).



**Figure 5.** Distribution map showing locality records for *Cirrhilabrus marinda* (stars) and *C. condei* (triangles). The type locality at Ayau Atoll is indicated by an arrow.



**Etymology.** The species is named *marinda* in honour of the Bupati and Vice Bupati of Raja Ampat, Drs. Marcus Wanma and Drs. Inda Arfan, who have ably led the world's most marine biodiverse regency since 2003. Under their wise and forward-thinking leadership, Raja Ampat's coral reefs are now amongst the best managed in the Coral Triangle, with nearly 1.5 million hectares of the archipelago contained within Indonesia's largest marine protected area network. It is a pleasure to honour their globally significant marine conservation efforts in naming this striking fairy wrasse in their honour. The name is based on a combination of the first part of their respective names (Marcus and Inda, resulting in *marinda*) and is treated as a noun in apposition.

**Comparisons.** The new species is closely related to *Cirrhilabrus condei* (Figs. 3D–F & 6–8), which ranges from West Papua to the Solomon Islands and northern Great Barrier Reef. Although the two species have broadly sympatric distributions, they do not appear to inhabit the same reef locations. For example, at the Raja Ampat Islands off the extreme western end of New Guinea, *C. marinda* is known only from Ayau Atoll, which is truly oceanic, situated about 45 km offshore from the main island group. Although *C. condei* is rare at the Raja Ampat Islands (only two sightings over a 12-year period near Waigeo and Misool), it was invariably encountered on more sheltered high-island reefs proximal to the New Guinea mainland or at least part of a dense network of islands linked to the mainland. This same pattern is evident throughout the New Guinea range of these species, with *C. marinda* generally occurring in more exposed oceanic situations (e.g. Manus and Vanuatu) at depths of 25–40 m, often in the vicinity of white *Halimeda* sand, in contrast to *C. condei*, which is usually encountered on reefs close to the mainland at depths of 6–20 m. However, records of *C. condei* from the Solomon Islands and Osprey



**Figure 6.** *Cirrhilabrus condei*, underwater photographs: A) approximately 65 mm SL, Samarai Island, Milne Bay Province, Papua New Guinea, and B) approximately 45 mm SL, Raja Ampat Islands, West Papua Province, Indonesia (G.R. Allen).



Reef, Coral Sea are anomalous in this respect with specimens having been collected from outer reefs in about 30 m depth.

The two species are very similar with regards to general meristic and morphometric features, the one exception relating to the height and profile of the dorsal fin of mature males (Figs. 3B & E and 7). The spinous dorsal fin of *C. marinda* is noticeably taller than the soft portion in comparison with *C. condei*, which has a more uniform fin profile. This difference is reflected in the mean maximum dorsal spine height which is 15.2% of the SL (range 13.0–16.7, n = 11) for *C. condei* and 19.5% of the SL (range 16.9–22.7, n = 13) for *C. marinda*.

Dorsal fin colouration of mature males is also useful for separating the two species. The shape and extent of black colouration is particularly diagnostic. *C. marinda* has a black area that is most extensive anteriorly, almost completely engulfing the spinous portion of the fin, which gradually tapers in width posteriorly on the soft portion of the fin. In contrast, the spinous dorsal of *C. condei* is mostly red with the black area confined to the outer margin and generally about equal width or narrower than the posterior extension of black on the soft dorsal fin.

There also appears to be differences in the male nuptial displays of the two species (Fig. 1C & F) including a more fully erect dorsal in *C. marinda* and more white ornamentation in *C. condei*, including a patch behind the eye, a broad zone above the pectoral fin, a broader stripe at the base of the dorsal fin, and a more strongly contrasted



**Figure 7.** Comparison of *Cirrhilabrus condei* above, WAM P.32539-022, 44.0 mm SL, Choiseul, Solomon Islands and paratype of *C. marinda* below, WAM P.34338-001, 45.7 mm SL, Ayau Atoll, West Papua Province, Indonesia (G.R. Allen).





**Figure 8.** Comparison of adult male paratypes of *Cirrhilabrus marinda* above, BPBM 40774, 36.4-38.3 mm SL and adult male of *C. condei* below, WAM P.34321-001, 64.6 mm SL, Samari Island, Papua New Guinea Indonesia (G.R. Allen).

stripe on the posterior body and caudal peduncle. The latter species also has more bluish-white colouration on the caudal fin and smaller orange and pink areas on the body compared to *C. marinda*.

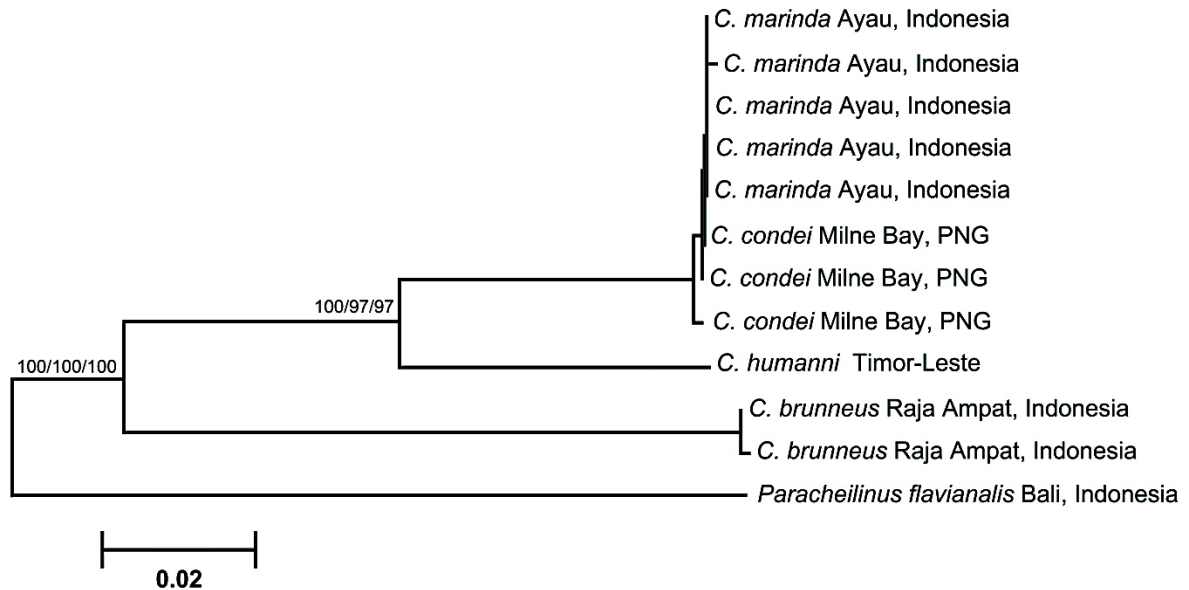
The population of *C. marinda* at Ayau Atoll also exhibits a considerable difference in maximum size compared to *C. condei* (Fig. 8). The largest individuals are invariably terminal males and the maximum standard length for Ayau fish is 45.9 mm SL compared with 76.5 mm SL for *C. condei*. Our smallest mature male of *C. marinda* from Ayau Atoll is 36.4 mm SL and the smallest female (indicated by presence of ripe eggs) is only 30.4 mm SL. However, this unusually small size is perhaps a local anomaly, as our collections of this species include a 59.3 mm SL male from Morotai Island, Halmahera, which lies 326 km northwest of Ayau. We have also examined a non-type, 67.0 mm SL male specimen of *C. marinda* from Vanuatu (BPBM 40774).

**Genetic Analysis.** We resolved relationships between *C. marinda* and other *Cirrhilabrus* species using the mtDNA COI gene from 11 collected *Cirrhilabrus* individuals and a single outgroup individual of *Paracheilinus flavianalis*. The sequences obtained ranged from 594 to 683 bp. In the total *Cirrhilabrus* alignment there were 95 parsimony-informative characters. Nucleotide frequencies for the combined *Cirrhilabrus* samples were as

TABLE 3  
Average interspecific pairwise genetic distance matrix for mtDNA COI sequences

No.	Species	1	2	3	4
1	<i>C. brunneus</i>				
2	<i>C. marinda</i>	0.161			
3	<i>C. condei</i>	0.158	0.001		
4	<i>C. humanni</i>	0.154	0.081	0.081	
5	<i>P. flavianalis</i>	0.194	0.187	0.188	0.195





**Figure 9.** Neighbor-joining (NJ) tree of the mitochondrial COI sequences for four species of *Cirrhilabrus* with *Paracheilinus flavianalis* as an outgroup. Numbers above the major nodes indicate bootstrap support for 1000 replicates using neighbor joining, maximum likelihood, and bayesian posterior probability, respectively. The slight branching observed between *C. marinda* and *C. condei* is the result of different sequence lengths not the sequence itself; the sequences for 3 *C. marinda* and 2 *C. condei* specimens are the same, with no substitutions.

follows: A = 22.9, C = 25.1, G = 18.1, T = 33.9. The neighbor-joining tree for our sequences (Fig. 9) formed 4 clades including the outgroup, with average pairwise genetic distances ranging from 0.081–0.195 (Table 4). *Cirrhilabrus marinda* and *C. condei* shared a clade with mostly identical sequences and an average genetic distance of only 0.001 within the clade (Table 3). GenBank accession numbers of all COI sequences and associated collection details are provided in Table 4.

**Discussion.** Despite the striking and consistent colour differences between adult males of *C. marinda* and *C. condei*, our comparative analysis of the mitochondrial COI gene reveals no mitochondrial sequence divergence between the two species. Cryptic species with phenotypic differences, but little to no genetic divergence, have been termed “phenovariants” by Victor (2015). This result is not completely unexpected for recently evolved,

TABLE 4  
Data on tissue samples utilized in genetic analysis:  
specimen voucher number from Indonesian Biodiversity Research Center (IBRC),  
sampling location, and Genbank accession number

Species	IBRC ID	Sampling Location	GenBank #
<i>C. brunneus</i>	MB0612901	Miosging, Raja Ampat, Indonesia	KR052199
<i>C. brunneus</i>	MB0612902	Miosging, Raja Ampat, Indonesia	KR052200
<i>C. condei</i>	MB0617102	Samarai, Milne Bay, PNG	KR052202
<i>C. condei</i>	MB0617103	Samarai, Milne Bay, PNG	KR052203
<i>C. condei</i>	MB0617201	Samarai, Milne Bay, PNG	KR052204
<i>C. humanni</i>	MB065501	Com, Timor-Leste	KR052205
<i>C. marinda</i>	MB0615701	Ayau, Raja Ampat, Indonesia	KR052201
<i>C. marinda</i>	MB0618401	Ayau, Raja Ampat, Indonesia	KR052206
<i>C. marinda</i>	MB0618402	Ayau, Raja Ampat, Indonesia	KR052206
<i>C. marinda</i>	MB0618403	Ayau, Raja Ampat, Indonesia	KR052206
<i>C. marinda</i>	MB0618404	Ayau, Raja Ampat, Indonesia	KR052207
<i>P. flavianalis</i>	MB040801	Bali, Indonesia	KF709103

closely related taxa, particularly among wrasses with striking male nuptial displays such as observed in the genera *Pseudojuloides*, *Paracheilinus*, and *Cirrhilabrus*. Victor & Randall (2014) report a similar case for *Pseudojuloides edwardi*, an East African labrid. As noted in that study, there is frequently strong selection pressure to evolve different colourful patterns in breeding males as incipient species diverge and it is plausible for the evolution of secondary sexual features to outpace genetic mitochondrial sequence changes as new species emerge. Most recent studies show that the majority of marine fish species are characterized by monophyletic mitochondrial lineages that are well separated (usually by more than 2%) from related species (Steinke *et al.* 2009, Ward *et al.* 2009). However, there are exceptions among reef fishes that can challenge the standard species definition (Victor 2015). It is likely that the rate of evolutionary change in reproductive displays between *C. marinda* and *C. condei* has outpaced the accumulation of neutral mutations in the mitochondrial genome, with colour pattern and dorsal-fin morphological divergence likely occurring very recently. Tornabene *et al.* (2015) provided evidence for similar rapid evolution during the Pleistocene in the gobiid genus *Eviota*.

Several recent studies (Bowen 2006, Rocha & Bowen 2008, Victor & Randall 2010 & 2014) have shown that divergence of species pairs and complexes of reef fishes is frequently characterized by the development of different colour patterns, especially among breeding males. The mating system of *Cirrhilabrus*, in which relatively few males compete for the attention of numerous females, is highly conducive to the development of enhanced male secondary sexual characters, particularly bright nuptial colours and exaggerated dorsal fins (which are fully erected during courtship), not unlike the well-documented behaviour found in terrestrial birds-of-paradise (Laman & Scholes 2012). In *Cirrhilabrus*, there appears to be fierce competition among males for the attention of gravid females during daily spawning events, which generally occur about 1–2 hours prior to sunset. The same situation is found in the closely related genus *Paracheilinus*, which is also known for its spectacular male nuptial displays and exaggerated dorsal fins (Allen & Erdmann 2012), and several sibling species pairs of *Paracheilinus* also show little or no mitochondrial sequence divergence (Allen *et al.* 2013, Yusmalinda, unpublished). As the cost of whole genome sequencing (Ng & Kirkness 2010) continues to decrease, in-depth genomic studies of these sibling species pairs may provide valuable new insights into the initiation of genetic differentiation under strong sexual selection regimes.

**Other material examined.** *Cirrhilabrus condei*: BPBM 15817 (holotype), 59.9 mm SL, Madang, Papua New Guinea; BPBM 36960 (paratypes), 3 specimens, 39.3–52.0 mm SL, Normanby Island, Milne Bay Province, Papua New Guinea; BPBM 37005 (paratypes), 4 specimens, 43.3–76.5 mm SL, Samarai Island, Milne Bay Province, Papua New Guinea; USNM 342048 (paratypes), 2 specimens, 49.7–71.5 mm SL, same data as previous specimens; WAM P.28179-002, 51.8 mm SL, Rabaul, New Britain, Papua New Guinea; WAM P.32247-006, 41.0 mm SL, Kanari Island, Misool, Raja Ampat Islands, West Papua Province, Indonesia; WAM P.32539-001, 3 specimens, 34.9–43.0 mm SL, Choiseul Island, Solomon Islands; WAM P.34321-001, 3 specimens, 64.6–71.2 mm SL, Samarai Island, Milne Bay Province, Papua New Guinea.

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## References

- Allen, G.R. & Erdmann, M.V. (2012) *Reef fishes of the East Indies. Vol. II*. Tropical Reef Research, Perth, Australia, pp. 425–856.
- Allen, G.R., Erdmann, M.V. & Yusmalinda, N.L.A. (2013) *Paracheilinus rennyae*, a new species of flasher-wrasse (Perciformes: Labridae) from southern Indonesia. *Aqua, International Journal of Ichthyology*, 19(4), 193–206.
- Allen, G. R. & Randall, J.E. (1996) Three new species of wrasses (Labridae: *Cirrhilabrus*) from Papua New Guinea and the Solomon Islands. *Revue française d'aquariologie: herpétologie*, 23 (3–4), 101–112.
- Edgar, R.C. (2004) MUSCLE: Multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Research*, 32, 1792–1797. doi:10.1093/nar/gkh340
- Geller, J., Meyer, C., Parker, M. & Hawk, H. (2013) Redesign of PCR primers for mitochondrial cytochrome c oxidase subunit I for marine invertebrates and application in all-taxa biotic surveys. *Molecular Ecology Resources*, 13, 851–61. doi:10.1111/1755-0998.12138
- Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S., Buxton, S., Cooper, A., Markowitz, S., Duran, C., Thierer, T., Ashton, B., Meintjes, P. & Drummond, A. (2012) Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. *Bioinformatics*, 28, 1647–1649. doi:10.1093/bioinformatics/bts199
- Kuiter, R.H. (2010). *Labrid Fishes: Wrasses*. Aquatic Photographics, Seaford, Australia, 398 pp.
- Laman, T. & Scholes, E. (2012) *The birds of paradise: revealing the world's most extraordinary birds*. National Geographic Society, Washington DC, 228 pp.
- Ng, P.C. & Kirkness, E.F. (2010) Whole Genome Sequencing. Chapter 12. In: Barnes, M.R. & Breen, G. (Eds.) *Genetic Variation: Methods and Protocols*. Methods in Molecular Biology, Vol. 628. Humana Press, New Delhi, India, pp. 215–226.
- Rambaut, A. & Drummond, A.J. (2009) Tracer v1.5. Available from <http://beast.bio.ed.ac.uk/Tracer>.
- Rocha, L.A. & Bowen, B.W. (2008) Speciation in coral reef fishes. *Journal of Fish Biology*, 72, 1101–1121.
- Ronquist, F. & Huelsenbeck, J.P. (2003) MRBAYES 3: Bayesian phylogenetic inference under mixed models. *Bioinformatics*, 19, 1572–1574.
- Steinke, D., Zemlak, T.S. & Hebert, P.D.N. (2009) Barcoding Nemo: DNA-Based Identifications for the Ornamental Fish Trade. *PLoS ONE*, 4(7): e6300. doi:10.1371/journal.pone.0006300
- Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M. & Kumar, S. (2011) MEGA5 : Molecular Evolutionary Genetics Analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. *Molecular Biology & Evolution*, 28, 2731–2739. doi:10.1093/molbev/msr121
- Tornabene, L., Valdez, S., Erdmann, M.V. & Pezold, F. (2015) Support for a “center of origin” in the Coral Triangle: cryptic diversity, recent speciation and local endemism in a diverse lineage of reef fishes (Gobiidae: *Eviota*). *Molecular Phylogenetics and Evolution*, 82, 200–210.
- Victor, B.C. & Randall, J.E. (2010) *Gramma dejongi*, a new basslet (Perciformes: Grammatidae) from Cuba, a sympatric sibling species of *G. loreto*. *Zoological Studies*, 49, 865–871.
- Victor, B.C. & Randall, J.E. (2014) *Pseudojuloides edwardi*, n. sp. (Perciformes: Labridae): an example of evolution of male-display phenotype outpacing divergence in mitochondrial genotype. *Journal of the Ocean Science Foundation*, 11, 1–12.
- Victor, B.C. (2015) How many coral reef fish species are there? Cryptic diversity and the new molecular taxonomy. In: Mora, C. (Ed.), *Ecology of Fishes on Coral Reefs: The Functioning of an Ecosystem in a Changing World*. Cambridge University Press, Cambridge, United Kingdom, pp. 76–87.
- Ward, R.D., Hanner, R. & Hebert, P.D.N. (2009) The campaign to DNA barcode all fishes, FISH-BOL. *Journal of Fish Biology*, 74, 329–356.