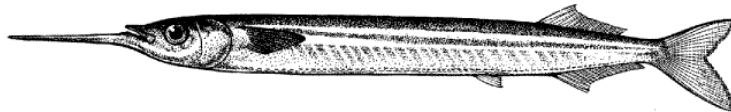


**EARLY LIFE STAGES OF THE SOUTHERN SEA GARFISH,
HYPORHAMPHUS MELANOCHIR (VALENCIENNES, 1846),
AND THEIR ASSOCIATION WITH SEAGRASS BEDS**

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Short Communication

Molecular Discrimination of Garfish *Hyporhamphus* (Beloniformes) Larvae in Southern Australian Waters

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Abstract: A multiplex polymerase chain reaction (PCR) assay developed for discrimination between garfish larvae (family Hemiramphidae, order Beloniformes) found in southern Australian waters was based on species-specific amplification of part of the mitochondrial *control region*. The species were easily discerned by the number and distinct sizes of PCR products (*Hyporhamphus melanochir*, 443 bp; *H. regularis*, 462 and 264 bp). Although based on a single gene, the method will correctly identify the species of individuals in at least 96% of tests for *H. melanochir* and 94% of tests for *H. regularis*.

Key words: garfish, *Hyporhamphus*, larva, mtDNA, PCR, species identification.

INTRODUCTION

Garfishes (order Beloniformes) are targeted in major commercial and recreational fisheries in many parts of the world, including southern Australia (Collette, 1974). In this region, here defined as including southern Western Australia (W.A.), South Australia (S.A.), Victoria, and Tasmania, the garfish fishery is a multispecies fishery, with catch effort principally focused on 2 species, the southern sea garfish *Hyporhamphus melanochir* (Valenciennes 1846) and the river garfish *H. regularis* (Günther 1866).

Recent efforts to manage the commercial and recreational garfish fishery in southern Australia have focused on developing population models for predicting the strength of recruitment. Critical for such models is the identification of spawning and recruitment locations and populations. This depends on being able to identify garfish species at all life-

history stages. While identifying adult garfish in southern Australia is not problematic (Collette, 1974), some uncertainty exists when allocating larvae to a particular species on the basis of traditionally used morphological characters such as pigmentation, meristic counts, and body measurements (C.J. Noell, unpublished data). This uncertainty is due to intraspecies variation, growth and development-related changes, and the occasional requirement for extrapolation between different-sized specimens. This is complicated by the fact that larvae of both species have been collected together in the same samples (C.J. Noell, unpublished data).

The identification of closely related species of organisms is a frequent problem in marine biology, especially in the egg or larval stages of the life cycle (Burton, 1996). The advent of DNA analysis based on polymerase chain reaction (PCR) has provided a quick, often cheap, and potentially automatable method to solve these problems (Silberman and Walsh, 1992; Banks et al., 1993; Medeiros-Bergen et al., 1995; Grutter et al., 2000; Rocha-Olivares et al., 2000). Here we present a method, based on PCR of the mitochondrial

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control region (CR), that discriminates between life stages of *H. regularis* and *H. melanochir* or the eastern sea garfish *H. australis* (Steindachner 1866) in southern Australia. Initially we partially sequenced the CR from a selection of adult garfish samples geographically representative of each species' range to phylogenetically identify nucleotide sites that distinguish between their mitochondrial lineages. We developed a multiplex PCR assay that distinguishes the species on the basis of the presence or absence of diagnostic bands and verified the assay on an extensive sample of adults from each species.

MATERIALS AND METHODS

Specimens Examined

Adult samples for DNA analysis were collected for the 2 *Hyporhamphus* species found in southern Australian waters. A sample of *H. australis* found in New South Wales (N.S.W.), was included to ensure that our test could successfully discriminate this species from *H. regularis* of eastern Victoria in the event the distribution of *H. australis* extended there. Our analysis will also provide a preliminary assessment of discrimination of *H. australis* and *H. melanochir* whose distributions overlap in southern N.S.W. A snub-nosed garfish, *Arrhamphus sclerolepis* (Günther, 1866) was used for the outgroup (Table 1). Adults were identified using the keys and descriptions in Collette (1974). A sample of larval *H. melanochir* and *H. regularis*, identified a priori by C.J. Noell, was included to establish that this life stage could be successfully genotyped.

DNA Extraction, PCR Amplification, and Nucleotide Sequencing

DNA was extracted from either larvae preserved in 70% ethanol or frozen livers of adult fish using a salt extraction method (Miller et al., 1988). A length of tissue 2 to 4 mm taken from the tail end of all larvae ($n = 39$; body length range, 5.8–26.3 mm) was sufficient to obtain enough DNA for PCR analysis. A fragment of approximately 443 to 462 bp from the mitochondrial CR was PCR amplified using primers H16498 (designed by Meyer et al., 1990) and L-M252 (Table 2). That this product was of mitochondrial origin rather than a nuclear paralogue (Zhang and Hewitt, 1996) was verified by Donnellan et al. (2001). Amplifications were carried out on a Hybaid Omn-E Thermal Cycler.

Table 1. Sample Details of Garfish Examined for Mitochondrial DNA Variation*

Location	n_s	n_{PCR}	Life stage
<i>Hyporhamphus melanochir</i>			
Cockburn Sound W.A.	1	3	Adult
Oyster Harbour W.A. (OH)	1	3	Adult
Thevenard S.A.	1	3	Adult
Tickera S.A.	1	3	Adult
Arno Bay S.A.	1	3	Adult
Port Gawler S.A. (PG)	2	6	Adult
Western Port Victoria	1	3	Adult
Corner Inlet Victoria	1	3	Adult
Marion Bay Tasmania (MB)	1	3	Adult
Flinders Island Transmania (FI)	1	3	Adult
Bay of Shoals, Kangaroo Island S.A.	1	19	Larval
<i>Hyporhamphus regularis</i>			
Port Adelaide S.A.	1	20	Larval
Angas Inlet S.A.	1	18	Adult
Onkaparinga River S.A.	2	11	Adult
Peel Inlet, Mandurah W.A. (PI)	1	8	Adult
Broken Bay N.S.W.	—	1	Adult
Gippsland Lakes Victoria	2	11	Adult
<i>Hyporhamphus australis</i>			
Broken Bay N.S.W.	1	—	Adult
<i>Arrhamphus sclerolepis</i>			
N.S.W.	1	—	Adult

* n_s indicates sample size for nucleotide sequencing; n_{PCR} , sample size for PCR assay. Locality codes are in parentheses.

Table 2. Oligonucleotide Sequences of Primers Used to Discriminate Garfish *Hyporhamphus* Species Found in Southern Australian Waters

Primer	Sequence
L-M252	5'-ACCATCAGCACCCAAAGCTAGG-3'
L-M282	5'-GTGCTTCGCCATATAATCCAAC-3'
H16498 (Meyer et al., 1990)	5'-CCTGAAGTAGGAACACAGATG-3'

Reaction volumes of 50 μ l contained 50 to 100 ng of template DNA, 0.2 μ M of each primer, 0.2 mM each of dATP, dTTP, dGTP, and dCTP, 4 mM MgCl₂, 1 \times GeneAmp PCR Buffer II (PerkinElmer) and 1 U AmpliTaq Gold DNA polymerase (PerkinElmer). PCR cyclic conditions were 95°C for 9 minutes, 50°C for 1 minute, 72°C for 1 minute for 1 cycle;

94°C for 45 seconds, 50°C for 45 seconds, 72°C for 1 minute for 34 cycles; and 72°C for 6 minutes, 30°C for 10 seconds for 1 cycle.

PCR products were purified for sequencing with the UltraClean PCR Clean-Up DNA Purification Kit (Mo Bio Laboratories, Inc.). Both strands of the purified PCR product were cycle sequenced with the same primers used for PCR with the BigDye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems Inc.). Reaction volumes of 10 µl contained 50 to 100 ng of PCR product, 0.5 µM primer, and 3 µl BigDye. PCR cyclic conditions were 94°C for 30 seconds, 50°C for 15 seconds, 60°C for 4 minutes for 25 cycles, and 60°C for 4 minutes, 30°C for 10 seconds for 1 cycle. Products were run on an ABI 373A automated DNA sequencer.

Phylogenetic Analysis

The sequence alignment, done initially with CLUSTAL X (Thompson et al., 1997), was improved manually. Individual sequences of the alignment are deposited with GenBank under accession numbers AF368258 to AF368268. Phylogenetic relationships among garfish haplotypes were reconstructed with the maximum parsimony (MP) criterion of optimality with branch and bound searches. Phylogenetic trees were tested for robustness with bootstrapping (2000 pseudoreplicates done with branch and bound searches). All phylogenetic analyses were performed with PAUP* 4.0b4a (Swofford, 1999).

PCR Test for Species Identification

A species-specific primer for *H. regularis*, L-M282 (Table 2), was designed from the aligned garfish *CR* sequences once apomorphic sites had been identified from the phylogenetic analysis. This internal primer was used in conjunction with the external primers L-M252 and H16498 in a multiplex PCR with reaction volumes and cyclic conditions the same as those already described. Because of the presence of the external primer pair, unsuccessful amplifications could be detected for any of the species; i.e., the external primer pair acts as an amplification control. Amplified DNA fragments were electrophoresed for 1 hour at 100 V in a 1.5% agarose gel, stained with ethidium bromide, and visualised by UV transillumination.

A random sample of 30 individuals is sufficient to detect at least one copy of a haplotype (i.e., a gel pheno-

type) that occurs at 10% frequency with 95% confidence (Schwager et al., 1993). So, the PCR test was validated on 49 adult *H. regularis* (6 were also sequenced) and 33 *H. melanochir* samples (11 were also sequenced) (Table 1). We also visually inspected for the L-M282 primer sequence in the *CR* sequences of a further 67 *H. melanochir*, sampled from across the species range, available from Donnellan et al. (2001). We subsequently PCR tested larvae that we could unequivocally assign to species on the basis of morphology from a much larger series of samples of each species (Table 1).

RESULTS AND DISCUSSION

We initially sequenced part of the mitochondrial *CR* from 11 adult fish to survey nucleotide sequence variation in southern Australian *Hyporhamphus*. Haplotype diversity of *H. melanochir CR* was surveyed previously by Donnellan et al. (2001) with a denaturing gradient gel-nucleotide sequencing approach in which 39 haplotypes were identified among 273 fishes sampled from across the species range in southern Australia. We chose 5 haplotypes from this study to represent the haplotype lineages identified by phylogenetic analyses of these data. Donnellan et al. (2001) also tested whether the PCR primers amplified nuclear paralogues of the *CR* in *Hyporhamphus*. These tests based on titrations of enriched mitochondrial DNA did not show any evidence that the primers we used were capable of amplifying nuclear paralogues of the *CR* in either *H. melanochir* or *H. regularis*.

The final alignment of garfish *CR* haplotypes included 423 sites. For phylogenetic analyses, alignment gaps (indels), used to optimize the sequence alignment, were treated as a fifth state. Under the MP criterion of optimality, multisite gaps were treated as a single "mutation." Under these conditions, 142 nucleotide sites were variable and 100 were parsimony informative. The MP analysis recovered a single tree of 185 steps (Figure 1). Two major lineages, strongly supported by bootstrapping (100%), are apparent among the *Hyporhamphus* haplotypes, one including both *H. australis* and *H. melanochir* and the other including *H. regularis*. Each lineage is characterized by a long basal branch (40 or more characters changing along these branches) and short branches among haplotypes reflecting the substantial nucleotide divergence between the 2 major lineages (21.6% to 25.6% uncorrected sequence divergence) and the small

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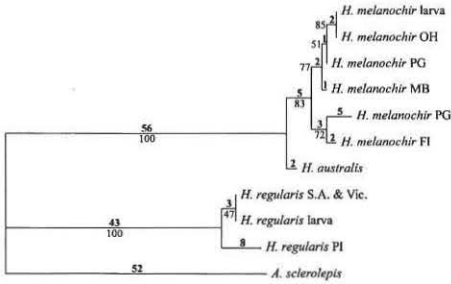


Figure 1. Phylogenetic relationships among garfish CR haplotypes recovered with maximum parsimony. Unbolded numerals represent bootstrap proportions from 2000 pseudoreplicates; numerals in boldface are the number of sites that change along that branch. Refer to Table 1 for locality codes.

genetic distances among conspecific haplotypes (0% to 3.2% uncorrected sequence divergence). For both *H. melanochir* and *H. regularis*, sequences derived from larvae were identical in each case to a haplotype found among the adults (Figure 1). Although both *H. australis* and *H. melanochir* are clearly genetically distant from *H. regularis*, the CR haplotypes of *H. australis* and *H. melanochir* are genetically much more closely related. Collette (1974) recognized the latter pair as separate species because of the lack of morphological intermediates in the region where their distributions overlap in southern N.S.W. A more thorough survey of CR haplotype diversity in these species in this region would be required before CR sequences could be used to discriminate between these taxa.

Examination of the aligned CR sequences revealed 2 multisite indels of 6 and 12 bp starting at nucleotide positions 149 and 178, respectively, of the alignment. The insertion character state for both indels is present in the 6 sequenced *H. regularis* specimens and the outgroup *A. sclerolepis*, while the deletion character state was present in both *H. melanochir* and *H. australis* (Figure 2). Primer L-M282, located in the vicinity of the 12-bp indel (Figure 2), was designed to amplify in combination with primer H16498 only the *H. regularis* CR. The final PCR test used was a multiplex of the 3 primers (L-M252/L-M282/H16498). While the predicted gel phenotypes for each species were the 443-bp product only for *H. melanochir* and both the 264-bp and 462-bp products for *H. regularis* (Figure 3), a third outcome, the 264-bp product only, was observed in a minor proportion of *H. regularis* samples. The results of the

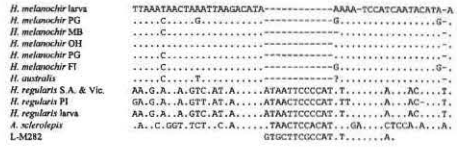


Figure 2. Part of the nucleotide sequence alignment of the mitochondrial CR haplotypes from adult and larval *H. melanochir* and *H. regularis*, *H. australis*, and the outgroup *A. sclerolepis*. This represents the section of the alignment from which the PCR primer L-M282, used to discriminate between *H. melanochir* and *H. regularis*, was designed. This section is from nucleotide sites 155 to 210 of the complete alignment. Dots (.) indicate identical nucleotides to *H. melanochir* larva; dashes (-) indicate alignment gaps; question mark (?) indicates unknown nucleotide.

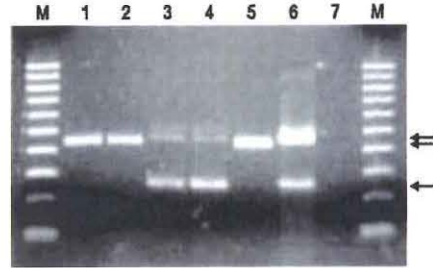


Figure 3. Electrophoretic discrimination between mtDNA CR multiplex PCR products from *H. melanochir* (443 bp) and *H. regularis* (462 and 264 bp). Lanes 1 and 2, *H. melanochir* larvae; lanes 3 and 4, *H. regularis* larvae; lane 5, *H. melanochir* adult; lane 6, *H. regularis* adult; lane 7, no template PCR control. M indicates 100-bp ladder for molecular weight marker. Arrows indicate the position of DNA products of 264, 443, and 462 bp.

PCR multiplex were 100% compatible with the a priori species identification of the 33 adult *H. melanochir* and 49 adult *H. regularis* tested. Inspection of a further 67 *H. melanochir* partial CR sequences along with the 11 that were also subjected to the multiplex PCR revealed that the 12-bp sequence required for annealing of the 5' end of L-M282 in *H. regularis* was deleted. We therefore inferred that the 264-bp product would not be amplified from the samples that had been sequenced only. These sample sizes for adults of known species identity (*H. melanochir*, $n = 100$; *H. regularis*, $n = 49$) represent the ability to detect a copy of the other species' gel phenotype if it were present at a frequency of less than 4% and 6% for *H. melanochir* and *H. regularis*,

respectively, with 95% confidence. Larvae that had been unequivocally assigned to species a priori on a morphological basis (*H. melanochir*, $n = 19$; *H. regularis*, $n = 20$) were subsequently tested, and the gel phenotypes were 100% compatible with the predicted phenotype (Figure 3).

The results of this study demonstrate the impact that PCR technology using the mitochondrial CR has on resolving the discrimination of larvae of hemiramphid species from across southern Australia. The mitochondrial CR can have high haplotype diversity but low nucleotide diversity within fish taxa, such as is the case for garfish in this study, as well as for species of perches of the family Percidae (Faber and Stepien, 1997), in contrast with high nucleotide divergence between related taxa. Divergence often includes indels, making the CR ideal for species-level discrimination tests. However, unlike some other mitochondrial genes for which "universal" PCR primers are available, e.g., *cytb* and *16S rRNA*, initial PCR amplification of the CR can be problematic because of the limitations on the taxonomic scope of the homology of available CR primers.

Morphological criteria that could be used to discriminate between southern Australian garfish species throughout their early life histories now can be independently verified by molecular techniques. The molecular method described allows partitioning of morphological variation, due to intraspecific variation and the morphologic plasticity associated with larval growth and development, among the within-species and between-species components. A possible outcome of this analysis is that the morphological characters may still be unable to adequately discriminate between the larvae of these species, in which case the molecular approach could replace the morphological one entirely. Also, regardless of whether larval identification by morphology alone is achievable, morphological identification may require more work per specimen, making it relatively more efficient to use the molecular approach.

This study demonstrates a nonsequencing method that is potentially automatable, permitting analysis of large numbers of specimens and thereby avoiding much of the labor-intensive identification work using morphological criteria. Furthermore, ecologists without detailed knowledge of taxonomy or molecular biology would require only a little technical training for species discrimination.

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APPENDIX B. Continued

<i>H. australis</i>A.....G.....A.....
<i>H. regularis</i> S.A. & Vic.	..AC...T...A.GAA.AC.TTT.TG	..T.TC.TTGC	..A..CGT.T.A..A.GCC.G
<i>H. regularis</i> PI	..AC-...T...A.GAA.AC.TTT.TG	..T.TC.TTGC	..A..CGT.T.A..A.GCC.G
<i>H. regularis</i> larva	..AC...T...A.GAA.AC.TTT.TG	..T.TC.TTGC	..A..CGT.T.A..A.GCC.G
<i>A. sclerolepis</i>	CCA.A...A.GTGA...AA	C..AGAT.GA	CA.--AGTAC
<i>H. melanochir</i> larva	ATCCCTAAA	TTTCAAATAT	TTAATGTAGT
<i>H. melanochir</i> PGC.....A.....C.....
<i>H. melanochir</i> MBW.....
<i>H. melanochir</i> OH
<i>H. melanochir</i> PG
<i>H. melanochir</i> FI
<i>H. australis</i>A.....C.....N.....
<i>H. regularis</i> S.A. & Vic.	..T.G.-GA...T...A.C.	..T...C.	..T.C.
<i>H. regularis</i> PI	..T.G.-GA...T...A.C.	..T...C.	..T.C.
<i>H. regularis</i> larva	..T.G.-GA...T...A.C.	..T...C.	..T.C.
<i>A. sclerolepis</i>	C.T..GG.TAA.....	..T...C.	..T.C.
<i>H. melanochir</i> larva	TTCACTTCTT	GAAATATTCC	TGG
<i>H. melanochir</i> PG
<i>H. melanochir</i> MB
<i>H. melanochir</i> OH
<i>H. melanochir</i> PG
<i>H. melanochir</i> FI
<i>H. australis</i>
<i>H. regularis</i> S.A. & Vic.
<i>H. regularis</i> PI
<i>H. regularis</i> larva
<i>A. sclerolepis</i>

◀H16498

Abstract—Larval development of the southern sea garfish (*Hyporhamphus melanochir*) and the river garfish (*H. regularis*) is described from specimens from South Australian waters. Larvae of *H. melanochir* and *H. regularis* have completed notochord flexion at hatching and are characterized by an elongate body with distinct rows of melanophores along the dorsal, lateral, and ventral surfaces; a small to moderate head; a heavily pigmented and long straight gut; a persistent pre-anal finfold; and an extended lower jaw. Fin formation occurs in the following sequence: caudal, dorsal and anal (almost simultaneously), pectoral, and pelvic. Despite the similarities between both species and among hemiramphid larvae in general, *H. melanochir* larvae are distinguishable from *H. regularis* by 1) having 58–61 vertebrae (vs. 51–54 for *H. regularis*); 2) having 12–15 melanophore pairs in longitudinal rows along the dorsal margin between the head and origin of the dorsal fin (vs. 19–22 for *H. regularis*); and 3) the absence of a large ventral pigment blotch anteriorly on the gut and isthmus (present in *H. regularis*). Both species can be distinguished from similar larvae of southern Australia (other hemiramphids and a scomberoscid) by differences in meristic counts and pigmentation.

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Larval development of the southern sea garfish (*Hyporhamphus melanochir*) and the river garfish (*H. regularis*) (Beloniformes: Hemiramphidae) from South Australian waters

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The beloniform family Hemiramphidae (garfishes or halfbeaks) are small to medium-size surface-dwelling marine, estuarine, and freshwater fishes. The family contains 12 genera and 101 species worldwide, and more than one-third of the species belong to the genus *Hyporhamphus* (Froese and Pauly¹). The Hemiramphidae are related to the Exocoetidae (flyingfishes) and, more distantly, to the Scomberosocidae (sauries), Belonidae (needlefishes), and Adrianichthyidae (ricefishes) (Collette et al., 1984). Six genera and 17 species of hemiramphids occur in Australian waters, where garfishes have long been considered valuable food and bait fish (Collette, 1974; Kailola et al., 1993).

Two hemiramphid species inhabit the waters of South Australia (S.A.), namely the southern sea garfish *Hyporhamphus melanochir* (Valenciennes, 1846) and the river garfish *H. regularis* (Günther, 1866). Adults of both are widely distributed along southern Australia from Western Australia (W.A.) to New South Wales, although *H. regularis* have not been recorded in Tasmania (Tas.). They support important commercial and recreational fisheries, particularly in S.A. (Kailola et al., 1993). *H. melanochir* are commonly found in sheltered coastal waters, whereas *H. regularis* are confined to estuaries (Jones et al., 1996). Juveniles and adults of both species co-occur in some estuaries

of southern Australia, e.g. Port River-Barker Inlet of S.A. (34°45'S, 138°31'E) (Jones et al., 1996) and Peel-Harvey Estuary of W.A. (32°32'S, 115°43'E) (Noell, unpubl. data).

Despite their widespread distribution and economic importance, the early life history of *H. melanochir* is only partially described (i.e. reproductive biology [Ling, 1958]; egg development [Jordan et al., 1998], and there is no published information for *H. regularis*). Furthermore, although adults are easily identified with keys and descriptions provided by Collette (1974), no such information exists for the larvae. A fundamental prerequisite for any larval fish study is, undoubtedly, their accurate identification (Neira et al., 1998).

Thus far, at least some larval stages have been described for 19 hemiramphids worldwide (Sudarsan, 1966; Talwar, 1967; Hardy, 1978; Chen, 1988; Watson, 1996; Prince Jeyaseelan, 1998), eight of which belong to *Hyporhamphus*. The purposes of this paper are to describe the larval development of *H. melanochir* and *H. regularis* and to document distinguishing characters between larvae of these species.

¹ Froese, R., and D. Pauly. 2001. FishBase. World Wide Web electronic publication. Accessed 28 Nov 2001. Web site: www.fishbase.org.

Materials and methods

Most larvae were collected with a neuston net in Gulf St. Vincent (34°29'S, 138°15'E) and the Bay of Shoals (35°37'S, 137°37'E) of South Australia. The neuston net was a square-framed bongo net with a mouth area of 0.5 m² fitted with 500-µm mesh, to which a 30-cm diameter pneumatic float was attached to both sides of the frame. This attachment ensured that, while being towed, the top of the frame rode steadily above the water surface and that ~0.4 m² of the mouth area was submerged. The net was towed from the stern of the vessel inside a circular direction for 5 min at speeds of 2–4 knots. Additional larvae were collected by hand from beneath a wharf in Barker Inlet where they often school during daylight at mid-flood tide. Transforming larvae and juveniles were collected at night with a dip net and spotlight at Outer Harbor (34°46'S, 138°28'E) and Barker Inlet. The term "transforming" is used here to describe the stage between the end of the larval phase and the start of the juvenile phase, i.e. after the attainment of all fin rays and before the formation of scales. All specimens examined in this study were collected between November and March. Larvae were sorted from plankton samples immediately after collection based on reference larval specimens from the South Australian Museum fish collection that were identified to family. Larvae were fixed in 10% formalin buffered with sodium β-glycerophosphate (1 g/L) and later preserved in 70% ethanol.

A total of 47 *H. melanochir* (6.4–48.3 mm body length, BL) and 49 *H. regularis* (7.0–46.9 mm BL) larvae through juveniles were used to describe morphometrics, meristics, and pigmentation. Larvae were identified as hemiramphids based on larval and adult characters reported in the literature (Collette, 1974; Hardy, 1978; Collette et al., 1984; Chen, 1988; Watson, 1996; Trnski et al., 2000). Developmental series were assembled by using the series method (Neira et al., 1998), the accuracy of which was verified by a molecular technique (Noell et al., 2001). Terminology of early life history stages follows that of Kendall et al. (1984). Representative series for both species are deposited with the I.S.R. Munro Fish Collection (CSIRO, Hobart, Tas.). (Registration numbers: *H. melanochir* (n=13), CSIRO L 3072-01, 3073-01 to -08, 3074-01 to -02, 3075-01 to -02; *H. regularis* (n=12), CSIRO L 3076-01 to -07, 3077-01 to -02, 3078-01 to -03.)

Larvae were examined with a Wild M3Z stereomicroscope at 6.5–40× magnifications by using various combinations of incident and transmitted light. Body measurements were taken with SigmaScan Pro® 4.01 image measurement software (SPSS Inc., 1999) and are accurate to less than 0.05 mm. This method was particularly useful for measuring cumulative distances of bent larvae. Abbreviations and definitions of routinely taken body measurements follow Leis and Carson-Ewart (2000). Lower jaw length (LJ) is defined as the horizontal distance from the tip of the lower jaw to the anterior margin of the pigmented region of the eye. Lower jaw extension (LJx) is defined as the horizontal distance from the tip of the lower jaw to the tip of the snout. Eye diameter was measured along both horizontal (EDh) and vertical midlines (EDv) of its

pigmented region. Body depth was measured at two points: at the pectoral base (BDp) and at the anus (BDa). Other measurements taken were snout length (SnL), head length (HL), pre dorsal-fin length (PDL) and preanal length (PAL). All measurements are expressed as a percentage of BL. Pigment refers to melanin. Drawings were prepared with the aid of a camera lucida.

Selected specimens were cleared and stained with alcian blue and alizarin red-S, following the method of Potthoff (1984), in order to count fin rays and vertebrae. Myomeres were difficult to count reliably at either end and thus vertebral counts (which include the urostyle) of stained larvae were taken instead. For small larvae that had unformed centra, corresponding neural or haemal spines were counted to obtain the number of vertebrae.

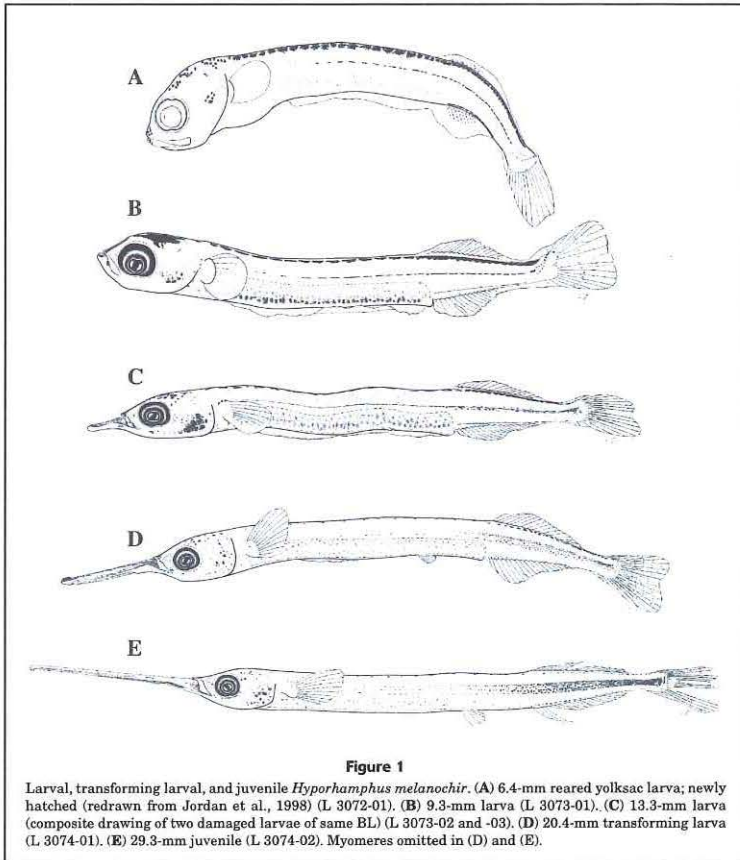
Results

Southern sea garfish (*Hyporhamphus melanochir* Valenciennes, 1846) (Fig. 1)

Description of larvae The smallest *H. melanochir* larva examined was a 6.4-mm newly hatched, laboratory-reared, postflexion-stage specimen. Some yolk remained, although yolk absorption was complete in the smallest field-collected larva (6.9 mm).

Larvae are elongate to very elongate (BDp=7–13% BL), and have a body depth slightly tapered towards the anus (BDa= 7–9% BL). Relative body depth at the pectoral base decreases slightly during larval development (Table 1). Larvae have 58–61 vertebrae (Table 2). The gut is relatively thick, long, straight, and nonstriated. PDL and PAL remain in the ranges of 70–75% and 71–76% BL, respectively (except for the 17.0-mm larva, which had a PDL and PAL of 62% BL). The first dorsal-fin ray is slightly anterior to or directly above the corresponding anal-fin ray. There is no gap between the anus and the anal fin. A long preanal finfold, initially the same length as the gut, persists through to the transformation stage before it disappears. There is no head spination. The small to moderate head (HL=16–24% BL) decreases in size in relation to BL with larval growth (Table 1). The longer lower jaw protrudes beyond the snout (LJx) by 4% BL at 11.0–11.5 mm, increasing to a maximum of 34% BL in the 29.3-mm juvenile. The mouth is oblique and reaches to the level of the center of the eye in newly hatched larvae. The maxilla subsequently moves forward in relation to the eye and by 12.1–14.4 mm it does not reach the eye. Very small villiform teeth are present on both the premaxilla and dentary in newly hatched larvae. The moderate to large eye (EDh=6–10% BL or 33–42% HL) is elongate (EDv=78–88% EDh) and decreases in size in relation to BL. A single rudimentary nasal papilla first appears as a small fleshy lump in the olfactory pit by 17.0 mm. Scales first appear between 20.4 and 29.3 mm laterally on the tail, anterior to the caudal peduncle.

Development of fins Completion of fin development in *H. melanochir* occurs in the following sequence: C → D → A → P₁, P₂ (Table 2). All principal rays of the caudal fin (7+8)



and several incipient dorsal- and anal-fin rays are present in newly hatched larvae. A full complement of 15–18 dorsal-fin and 17–20 anal-fin rays is attained at 11.4 and 12.1 mm, respectively. The pectoral base and finfold form prior to hatching, and incipient rays appear shortly after (by 7.2 mm); all 11–13 rays are formed by 19.6 mm. The pelvic fin buds appear by 13.3 mm, and all six pelvic-fin rays are formed by 19.6 mm.

Pigmentation *Hyporhamphus melanochir* larvae are moderately to heavily pigmented. Head pigmentation consists of melanophores on the tip of the lower jaw, snout, olfactory pit, and opercula, and a patch of several large

melanophores on the midbrain. The extended lower jaw is heavily pigmented throughout development and melanophores extend laterally along the dentary. The eye is partially pigmented in the newly hatched larva, but fully pigmented by 6.9 mm. The gut is heavily and uniformly pigmented dorsally and laterally along the entire length, and melanophores are often coalesced, but pigmentation becomes obscured as the overlying musculature develops. Dorsal pigmentation initially consists of 12–15 large melanophore pairs in longitudinal rows between the head and origin of the dorsal fin (Fig. 2A), and a continuous band along either side of the dorsal-fin base. Dorsal pigmentation gradually decreases in intensity thereafter. Three

APPENDIX C. *Continued*

Table 1

Morphometrics of larval, transforming larval, and juvenile *Hyporhamphus melanochir* (expressed as % of BL). Mean \pm SD is given when sample size $n > 1$. Dashed lines differentiate larvae, transforming larvae, and juveniles in descending order.

BL (mm)	<i>n</i>	SnL	LJ	LJx	EDh	EDv	HL	PDL	PAL	BDp	BDa
6.4 ¹	1	2.1	2.7	0.6	9.9	8.7	24.4	74.6	75.5	16.3 ²	8.0
6.9	1	3.0	4.0	1.0	9.2	7.5	23.5	69.7	71.9	12.7	8.6
7.0-7.5	9	2.8 \pm 0.8	3.9 \pm 1.1	1.1 \pm 0.4	9.1 \pm 0.3	7.3 \pm 0.3	22.0 \pm 0.8	70.8 \pm 0.9	72.6 \pm 1.0	11.9 \pm 0.3	8.9 \pm 0.3
7.5-8.0	7	3.6 \pm 0.9	4.6 \pm 1.2	1.0 \pm 0.4	9.1 \pm 0.5	7.1 \pm 0.3	22.8 \pm 1.6	71.3 \pm 1.3	73.0 \pm 0.9	11.8 \pm 0.6	8.9 \pm 0.7
8.0-8.5	9	3.6 \pm 0.5	4.9 \pm 0.8	1.3 \pm 0.4	8.8 \pm 0.3	7.1 \pm 0.3	21.9 \pm 1.0	70.9 \pm 0.7	72.7 \pm 0.9	11.7 \pm 0.7	8.9 \pm 0.7
8.5-9.0	3	3.5 \pm 0.8	5.0 \pm 1.1	1.5 \pm 0.3	8.6 \pm 0.2	7.0 \pm 0.3	21.1 \pm 0.2	71.5 \pm 0.2	72.5 \pm 0.4	11.3 \pm 0.5	9.1 \pm 0.5
9.0-9.5	4	3.4 \pm 0.5	5.0 \pm 0.7	1.6 \pm 0.3	8.0 \pm 0.3	6.5 \pm 0.2	20.9 \pm 0.8	71.7 \pm 0.7	72.8 \pm 0.6	11.4 \pm 0.7	8.4 \pm 0.3
11.0-11.5	4	3.7 \pm 0.7	7.2 \pm 1.5	3.5 \pm 1.2	7.5 \pm 0.4	6.3 \pm 0.2	20.3 \pm 1.3	71.6 \pm 0.6	72.3 \pm 0.5	10.6 \pm 0.7	8.5 \pm 0.6
12.1	1	4.1	9.0	4.9	7.6	6.4	19.7	72.6	72.6	10.2	8.6
14.4	1	3.7	12.3	8.6	6.9	5.8	19.2	70.2	71.4	9.4	7.8
17.0	1	2.9	10.3	7.4	5.6	4.7	15.9	61.7	61.7	7.3	6.6
19.6	1	4.9	28.7	23.8	6.0	4.9	18.6	70.4	71.2	8.2	7.4
20.4	1	4.0	24.2	20.2	5.7	5.0	17.5	72.5	71.6	8.9	7.6
29.3	1	4.4	38.4	34.0	5.3	4.8	17.0	69.9	71.0	8.2	7.2
33.3	1	4.9	38.3	33.4	5.3	4.6	17.9	71.7	72.7	8.5	7.6
41.3	1	5.2	36.2	31.1	5.5	5.1	18.6	74.1	74.1	9.2	7.8
48.3	1	5.6	36.9	31.3	5.2	4.8	17.8	74.0	74.0	9.7	8.1

¹ Yolksac larva.
² Includes yolk sac.

Table 2

Meristic counts of larval, transforming larval, and juvenile *Hyporhamphus melanochir*. Numbers in bold indicate the BL at which a full complement of rays is first attained. Dashed lines differentiate larvae, transforming larvae, and juveniles in descending order. D = dorsal; A = anal; P₁ = pectoral; P₂ = pelvic; C = caudal.

BL (mm)	Fin rays					Branchiostegal rays	Vertebrae
	D	A	P ₁	P ₂	C		
6.4 ¹	8	9	base		0+7+8+0	3	38+21
7.2	8	8	1		0+7+8+0	3	39+20
7.3	9	10	1		0+7+8+0	3	39+19
7.6	11	11	1		0+7+8+0	3	38+20
7.9	10	11	1		0+7+8+0	3	40+20
8.3	11	11	2		0+7+8+0	4	39+20
8.4	13	14	2		1+7+8+1	5	39+21
9.4	14	16	4		1+7+8+1	5	40+21
11.4	15	16	6		2+7+8+1	7	38+20
12.1	16	17	7		2+7+8+2	7	39+20
14.4	16	19	9	bud	2+7+8+2	9	39+20
19.6	17	19	11	6	4+7+8+4	12	38+20
20.4	16	17	12	6	4+7+8+4	12	39+19
29.3	17	18	11	6	4+7+8+4	13	38+20
33.3	17	18	12	6	5+7+8+5	12	38+20
41.3	16	19	11	6	4+7+8+5	12	40+19
48.3	16	19	11	6	4+7+8+5	12	39+19

¹ Yolksac larva.

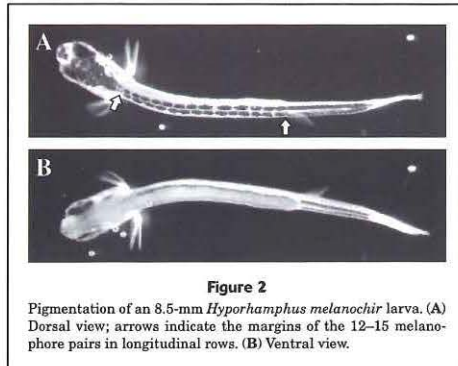


Figure 2
Pigmentation of an 8.5-mm *Hyporhamphus melanochir* larva. (A) Dorsal view; arrows indicate the margins of the 12–15 melano-phore pairs in longitudinal rows. (B) Ventral view.

Table 3
Morphometrics of larval, transforming larval, and juvenile *Hyporhamphus regularis* (expressed as % of BL). Mean \pm SD is given when sample size $n > 1$. Dashed lines differentiate larvae, a transforming larva, and juveniles in descending order.

BL (mm)	n	SnL	LJ	LJx	EDh	EDv	HL	PDL	PAL	BDp	BDa
7.0 ¹	1	3.2	4.4	1.2	8.2	6.5	20.4	73.2	71.6	11.6 ²	7.4
7.5–8.0	9	2.8 \pm 0.3	4.4 \pm 0.4	1.7 \pm 0.3	7.6 \pm 0.1	6.3 \pm 0.1	19.9 \pm 0.6	73.1 \pm 0.6	71.8 \pm 0.4	11.2 \pm 0.2	8.2 \pm 1.2
8.0–8.5	12	2.8 \pm 0.4	4.3 \pm 0.5	1.5 \pm 0.3	7.5 \pm 0.3	6.2 \pm 0.2	19.6 \pm 0.9	72.8 \pm 0.7	71.6 \pm 0.6	11.0 \pm 0.5	7.7 \pm 0.3
8.5–9.0	10	2.8 \pm 0.2	4.2 \pm 0.2	1.5 \pm 0.2	7.2 \pm 0.2	5.9 \pm 0.1	19.2 \pm 0.3	72.9 \pm 0.9	71.8 \pm 0.9	10.6 \pm 0.2	7.4 \pm 0.3
9.0–9.5	5	2.8 \pm 0.1	4.4 \pm 0.4	1.6 \pm 0.4	7.0 \pm 0.1	6.0 \pm 0.2	19.1 \pm 0.4	72.3 \pm 0.7	71.5 \pm 0.6	10.6 \pm 0.2	7.6 \pm 0.3
9.5–10.0	3	2.8 \pm 0.1	4.4 \pm 0.3	1.7 \pm 0.2	6.9 \pm 0.4	5.8 \pm 0.2	18.7 \pm 0.5	72.1 \pm 1.6	71.2 \pm 1.7	10.6 \pm 0.4	7.3 \pm 0.2
10.0–10.5	3	3.0 \pm 0.3	4.8 \pm 0.9	1.8 \pm 0.6	6.8 \pm 0.2	5.8 \pm 0.2	18.9 \pm 0.6	72.2 \pm 0.6	71.3 \pm 0.6	10.2 \pm 0.3	7.6 \pm 0.3
13.1	1	4.0	7.6	3.7	6.9	5.4	19.6	73.2	71.9	9.1	7.8
18.1	1	4.5	18.6	14.1	6.3	5.4	19.9	73.8	72.6	9.5	8.1
24.7	1	5.6	27.7	22.1	6.3	5.5	20.8	72.9	73.6	9.7	8.1
31.5	1	6.2	30.0	23.9	6.0	5.5	21.0	74.4	75.5	10.7	8.5
33.8	1	6.4	27.7	21.3	6.1	5.6	21.6	74.3	74.3	10.9	8.9
46.9	1	7.3	damaged	damaged	5.6	4.7	21.8	75.4	75.4	11.2	9.8

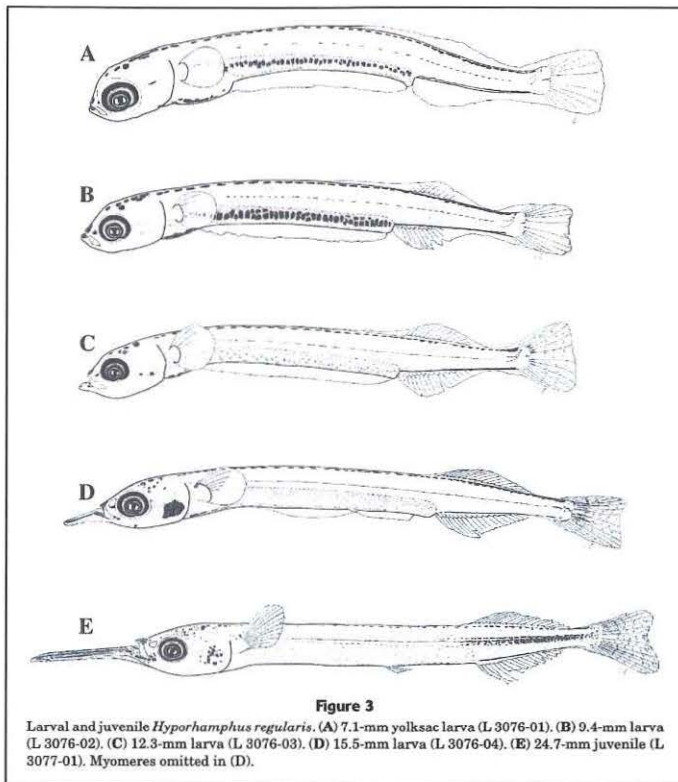
¹ Yolk sac larva.
² Includes yolk sac.

distinct lines of pigment appear along the dorsal margin in juveniles (by 29.3 mm) and remain to adult stage. A series of melanophores form a dashed, sometimes continuous, midlateral line. Melanophores appear laterally on the caudal peduncle by 14.4 mm and then proliferate anteriorly to form a broad medial stripe that remains, forming a silver stripe from the caudal peduncle to the operculum of adults. Ventral pigmentation consists of continuous bands of melanophores either side of the anal-fin base (Fig. 2B). Fins are unpigmented, except the caudal fin, which has small melanophores on the ray bases.

River garfish (*Hyporhamphus regularis* Günther, 1886) (Fig. 3)

Description of larvae The smallest *H. regularis* larva examined (7.0 mm) had completed notochord flexion and had a yolk sac. Yolk absorption was complete by 7.6 mm.

Larval *H. regularis* closely resemble larval *H. melanochir* morphologically (see Tables 1 and 3), but differ somewhat in relative length of the lower jaw, relative positions of the dorsal- and anal-fin origins, and in number of vertebrae. The longer lower jaw protrudes beyond the snout (LJx) by



4% BL at 13.1 mm and increases to a maximum of 24% BL in the 31.5 mm juvenile. The first dorsal-fin ray is slightly posterior to or directly above the corresponding anal-fin ray. Larvae have 51–54 vertebrae. Scales first appear between 18.1 and 24.7 mm laterally on the tail, anterior to the caudal peduncle.

Development of fins Completion of fin development in *H. regularis* occurs in the following sequence: C → D → A → P₁, P₂ (Table 4). Development of the caudal fin is incomplete at birth; 6 + 7 principal rays are present in the 7.0-mm yolk sac larva, and the full complement (7+8) shortly after, by 7.7 mm. Distinct anal-fin bases are visible at 7.0 mm. A full complement of 14–17 dorsal and 15–19 anal-fin rays is attained at 10.1 and 10.5 mm, respectively. The pectoral base and finfold are present at birth, and incipient rays first appear by 8.1 mm; all 11–12 rays are formed by 18.1 mm.

The pelvic fin buds appear by 13.1 mm, and all six pelvic-fin rays are formed by 18.1 mm.

Pigmentation Pigmentation of *H. regularis* larvae is similar to that of *H. melanochir* larvae except along the dorsal and ventral margins. Dorsal pigmentation consists of 19–22 melanophore pairs in longitudinal rows between the head and dorsal fin origin (Fig. 4A). A large pigment blotch is present ventrally on the isthmus and anteriorly on the gut.

Discussion

This study provides the first descriptions of larval development of hemiramphids endemic to marine (*H. melanochir*) and estuarine (*H. regularis*) waters of Australia.

Table 4

Meristic counts of larval, transforming larval, and juvenile *Hyporhamphus regularis*. Numbers in bold indicate the BL at which a full complement of rays is first attained. Dashed lines differentiate larvae, a transforming larva, and juveniles in descending order. D = dorsal; A = anal; P₁ = pectoral; P₂ = pelvic; C = caudal.

BL (mm)	Fin rays					Branchiostegal rays	Vertebrae
	D	A	P ₁	P ₂	C		
7.0 ¹	anlage	bases	base			2	35+19
7.7	4	6	base			3	34+19
7.8	6	7	base			4	34+18
8.1	5	7	1			4	34+19
8.3	8	9	2			4	33+20
8.6	9	11	2			5	34+19
8.9	11	11	2			5	34+20
9.3	11	12	3			5	33+18
9.6	10	11	3			5	35+19
10.1	14	14	4			6	33+20
10.5	13	15	5			6	35+19
13.1	14	16	7	bud		8	35+19
18.1	14	17	11	6	4+7+8+4	12	35+18
24.7	16	17	12	6	4+7+8+4	11	34+19
31.5	15	17	12	6	4+7+8+4	11	34+18
33.8	15	18	11	6	4+7+8+4	11	33+19
46.9	16	17	11	6	4+7+8+4	11	35+18

¹ Yolksac larva.

Both *H. melanochir* and *H. regularis* share characters common to other described hemiramphid larvae. They are generally characterized by their lack of head or fin spines; elongate body; long straight gut; extended lower jaw; a main pigmentation pattern consisting of rows of melanophores on the dorsal, lateral, and ventral surfaces of the body; and advanced state of development at hatching (Collette et al., 1984; Watson, 1996; Trnski et al., 2000). Although the size at which fins develop varies slightly between *H. melanochir* and *H. regularis*, the sequence of development for both species is the same as that for most hemiramphids, i.e. C → D, A → P₁ → P₂ (Collette et al., 1984).

Hyporhamphus melanochir larvae are distinguishable from *H. regularis* by 1) having 58–61 vertebrae (vs. 51–54 for *H. regularis*); 2) having 12–15 melanophore pairs in longitudinal rows along the dorsal margin between the head and origin of the dorsal fin (vs. 19–22 for *H. regularis*); and 3) the absence of a large ventral pigment blotch anteriorly on the gut and isthmus which is present in *H. regularis*. Despite the difficulty in counting myomeres, either the number of vertebrae in cleared and stained specimens or the number of myomeres between the pectoral-fin base and anus (usually three less than the number of precaudal vertebrae; see Tables 2 and 4) revealed a consistent difference between both species.

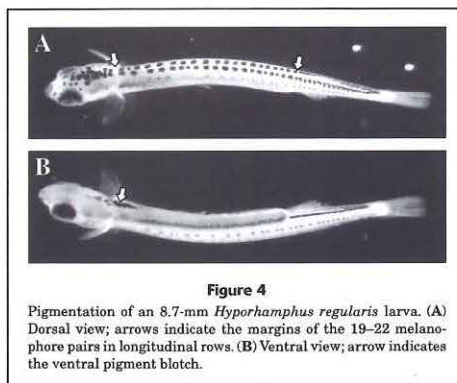


Figure 4

Pigmentation of an 8.7-mm *Hyporhamphus regularis* larva. (A) Dorsal view; arrows indicate the margins of the 19–22 melanophore pairs in longitudinal rows. (B) Ventral view; arrow indicates the ventral pigment blotch.

The geographic distributions of larval *H. melanochir* and *H. regularis* were separate in most samples; only three *H. melanochir* were found among *H. regularis* from Barker Inlet, whereas no *H. regularis* were among *H. melanochir* from the Bay of Shoals or Gulf St. Vincent. Larvae of other

hemiramphid species may overlap in distribution with those of *H. melanochir* and *H. regularis* outside South Australian waters. Meristic characters (summarized in Table 5) can often distinguish *H. melanochir* and *H. regularis* from the other species, except the eastern sea garfish (*H. australis*), which has overlapping meristic counts and currently undescribed larvae. The storm garfish (*Hemiramphus robustus*) has fewer anal-fin rays (11–14) and develops both a dark blotch below the dorsal fin and a pigmented pelvic fin in the juvenile stage (Collette, 1974; Collette et al., 1984). The long-finned garfish (*Euleptorhamphus viridis*), an oceanic species that rarely frequents nearshore waters, is strikingly different from other hemiramphids, being much more elongate and slender, and having divergent meristic counts, including more dorsal- and anal-fin rays (21–25 and 20–24, respectively), more vertebrae (69–73), fewer pectoral-fin rays (7–9), and fewer gill rakers (25–33) (Collette, 1974; Hardy, 1978; Chen, 1988; Trnski et al., 2000).

Larvae of the saury (*Scomberosax saurus*) (family Scomberosocidae) also occur in southern Australia and are the only other species that could be confused with hemiramphids. These are distinguishable from hemiramphid larvae by their higher myomere count (62–70), greater number of principal caudal-fin rays (16–17), presence of dorsal and anal finlets, and much heavier pigmentation (Bruce and Sutton, 1998; Trnski et al., 2000).

Acknowledgments

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Table 5

Meristic counts of adult hemiramphids found in southern Australia. Data collated from Collette (1974) except where footnoted. A second range from another source is given if not in total agreement with Collette (1974). The distinguishing vertebral counts for *H. melanochir* and *H. regularis* in this study are also included. Vertebrae are given as precaudal + caudal; gill rakers are given as upper + lower. ? = no information available. D = dorsal; A = anal; P₁ = pectoral; P₂ = pelvic; C = caudal.

Species	Fin rays					Branchiostegal rays	Vertebrae	Gill rakers
	D	A	P ₁	P ₂	C			
<i>Euleptorhamphus viridis</i>	21–25 20–24 ²	21–24 20–24 ²	8–9 7–9 ²	6 ²	?+7+8+7 ²	?	69–73 (44–46) + (26–29) = 70–75 ⁴	(5–9) + (18–23) = 25–33
<i>Hemiramphus robustus</i>	13–15	11–14	12–13	6 ⁵	4+7+8+5 ⁵	13 ⁵	(35–37) + (17–19) = 52–55 (33–34) + (16–17) = 49–50 ¹	(27–33) + (20–25) = ?
<i>Hyporhamphus australis</i>	15–17	17–20	11–13 10–13 ¹	6 ⁵	4+7+8+4 ⁵	12–13 ⁵	(37–39) + (18–20) = 56–58 (38–40) + ?	(31–39) + (23–33) = ?
<i>Hyporhamphus melanochir</i>	15–18	17–20	11–13	6 ³	4–5+7+8+4–5 ⁵	12–13 ^{5,6}	(36–41) + (18–21) = 55–61 (38–40) + (19–21) = 58–61 ⁶	(27–35) + (21–29) = ?
<i>Hyporhamphus regularis</i>	14–17	15–19	11–12	6 ³	4+7+8+4 ^{5,6}	10–12 ^{5,6}	(33–38) + (18–20) = 51–58 (33–35) + (18–20) = 51–54 ⁶	(30–36) + (21–27) = 52–61

¹ Paris et al. (1980).
² Chen (1988).
³ Chen et al. (1994).
⁴ Trnski et al. (2000).
⁵ Noell (unpubl. data).
⁶ This study.

APPENDIX C. *Continued*

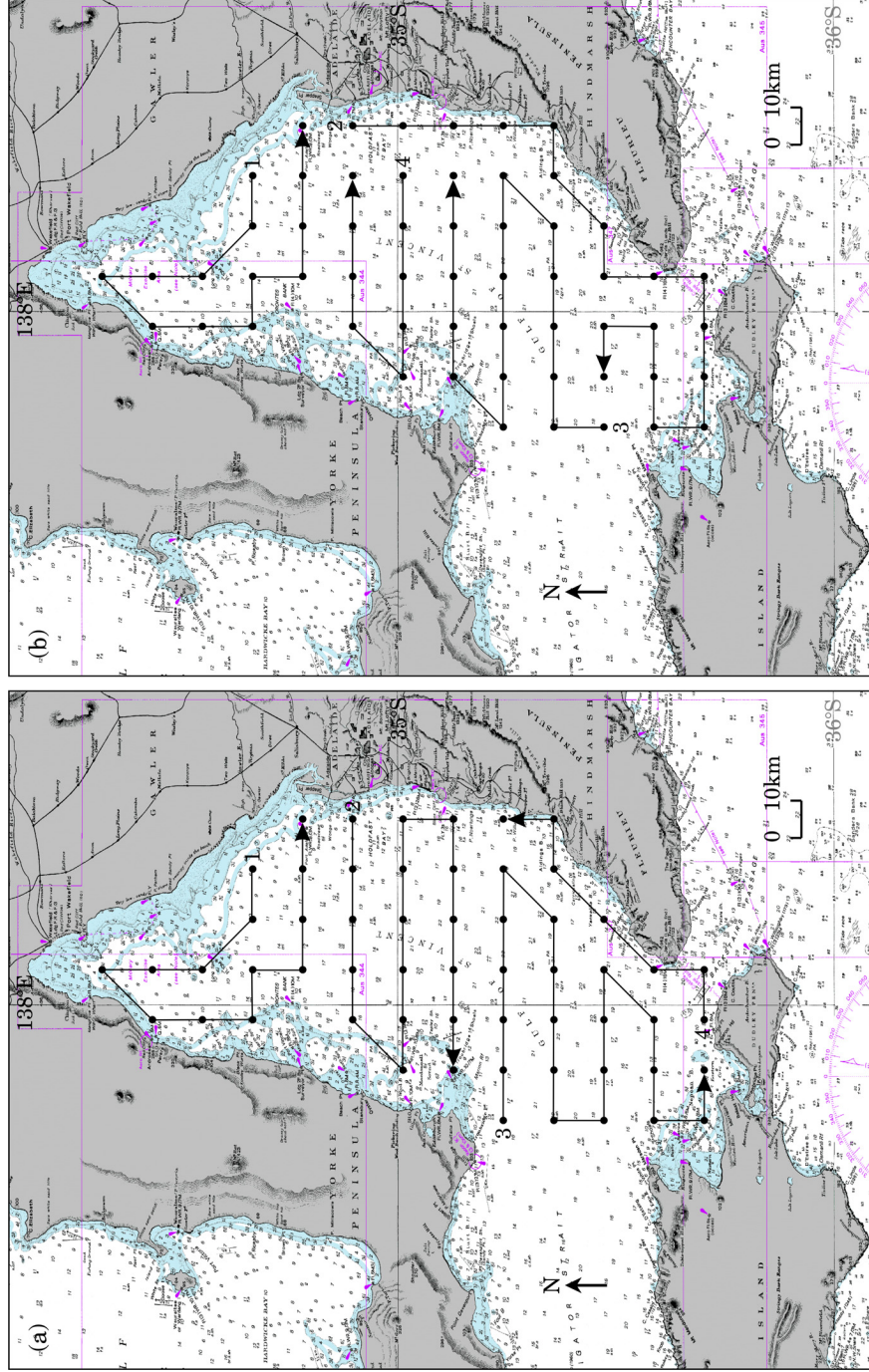
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APPENDIX D. Cruise paths for RV *Ngerin* in Gulf St Vincent during (a) Dec 14-17, 1998 (cruise 1) and (b) Dec 4-7, 2000 (cruise 3), and for RV *Pagrus* in the Bay of Shoals during (c) March 3-5, 2000 for determining the distribution and abundance of *Hyporhamphus melanochir* larvae.



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