CSIRO PUBLISHING

Marine and Freshwater Research, 2011, **62**, 72–82 www.publish.csiro.au/journals/mfr

The value of host and parasite identification for arripid fish

Sarah R. Catalano[A,G], *Kate S. Hutson*[A,B], *Rodney M. Ratcliff*[C,D] *and Ian D. Whittington*[A,E,F]

[A]Marine Parasitology Laboratory, DX 650 418, School of Earth and Environmental Sciences, The University of Adelaide, North Terrace, Adelaide, SA 5005, Australia.
[B]Discipline of Aquaculture, School of Marine and Tropical Biology, James Cook University, Townsville, Qld 4811, Australia.
[C]Infectious Disease Laboratories, Institute of Medical and Veterinary Science, SA Pathology, Adelaide, SA 5000, Australia.
[D]School of Biomedical Science, The University of Adelaide, Adelaide, SA 5005, Australia.
[E]Parasitology Section, The South Australian Museum, North Terrace, Adelaide, SA 5000, Australia.
[F]Australian Centre for Evolutionary Biology and Biodiversity, The University of Adelaide, North Terrace, Adelaide, SA 5005, Australia.
[G]Corresponding author. Email: sarah.catalano@adelaide.edu.au

Abstract. Accurate identification of fishes and their parasites is fundamental to the development, management and sustainability of fisheries and aquaculture worldwide. We examined three commercially and recreationally exploited Australian arripid species (Pisces: Arripidae), namely Australian herring (*Arripis georgianus*), eastern Australian salmon (*A. trutta*) and western Australian salmon (*A. truttaceus*), to determine their metazoan parasite assemblages and infection parameters. We identified 49 parasite species including 35 new parasite–host records and recognised seven ambiguous parasite–host records in the literature, largely a consequence of unsubstantiated host identifications in previous studies. Morphological and molecular methods confirmed a new western extension for the range of *A. trutta*, ~1000 km west of the previous record. Confusion about host identification and the range extension documented here has implications for the management of these economically important arripid species in southern Australian waters. Our examination of an endemic Australian fish family emphasises that accurate identification of fishes and their parasites is a fundamental prerequisite for efficient and sustainable resource management.

Additional keywords: Arripidae, Australian herring, Australian salmon, fish parasites, fisheries management, molecular techniques, taxonomy.

Introduction

Accurate species identification underpins knowledge of biodiversity, biogeography, biosecurity, biology, ecology, conservation, management and animal health. Published examples emphasise this for parasites (e.g. Peters *et al.* 1983; Siddall *et al.* 2007), commercially important fish (e.g. Dulvy and Reynolds 2009) and parasites infecting fish (e.g. Barber *et al.* 2000; MacKenzie 2002; Young *et al.* 2007). Morphological taxonomy remains a fundamental scientific tool and has immediate relevance to applied marine science. There is an increasing need to return to basics, survey fishes and their parasite fauna across broad geographic ranges and accurately identify hosts and parasites to species level. Fundamental knowledge of parasite assemblages is missing for members of the Arripidae, fishes endemic to southern Australian and New Zealand (NZ) waters. The Arripidae contains a single genus *Arripis* of four species (Paulin 1993). The following three species comprise important commercial and recreational fisheries in Australian waters: Australian herring or tommy rough (*Arripis georgianus*), eastern Australian salmon (*A. trutta*) and western Australian salmon (*A. truttaceus*). About 3000 t of 'Australian salmon' (*A. trutta* and *A. truttaceus* combined) are taken commercially in Australian waters per annum, and ~100 t of *A. georgianus* are captured commercially in South Australia (SA) (ABARE 2009).

Arripis georgianus and *A. truttaceus* school inshore and share similar distributions and reproductive strategies; however, they are distinct morphologically. They each comprise a single stock distributed from Western Australian (WA) to Victorian waters and waters around Tasmania (Malcolm 1960; Hoedt and Dimmlich 1994; Fairclough *et al.* 2000*b*). *A. georgianus* also occurs off the eastern coast of New South Wales (NSW) (Gomon *et al.* 2008). *A. georgianus* and *A. truttaceus* share the same single spawning ground off the south-western coast of WA (Fairclough *et al.* 2000*b*; Jones 2008). *A. trutta* overlaps

 10.1071/MF10193 1323-1650/11/010072

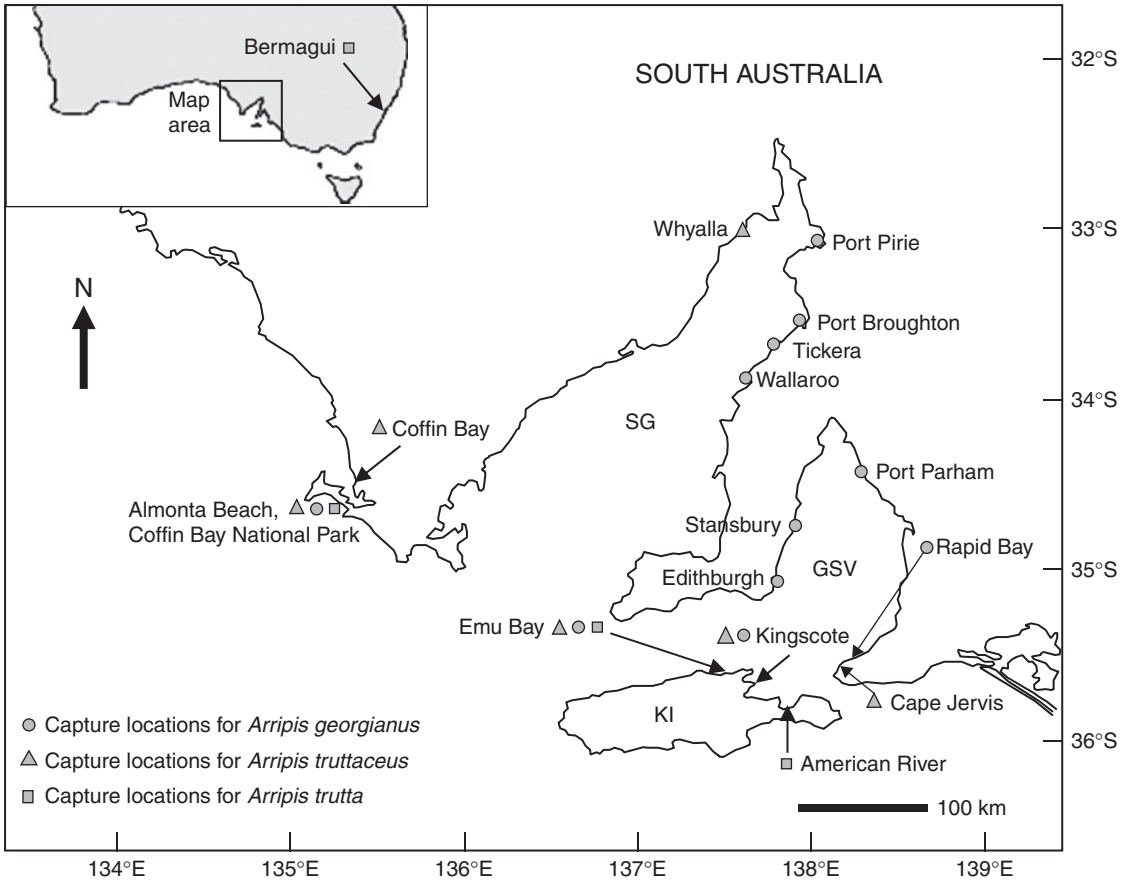

Fig. 1. Sample localities for *Arripis* spp. in southern Australian waters and one site off the coast of New South Wales (inset). GSV, Gulf St Vincent; KI, Kangaroo Island; and SG, Spencer Gulf.

their distribution in Victorian and Tasmanian waters, and is also found off NSW and NZ. Its stock structure is currently unknown (Smith *et al.* 2008).

Morphological similarity among some *Arripis* species has led to an identity crisis (Paulin 1993). *A. trutta* and *A. truttaceus* can be distinguished only by maximum attainable size and the number of gill rakers on the first gill arch (Gomon *et al.* 2008), a character suggested to result from different prey species consumed (Malcolm 1959; Hoedt and Dimmlich 1994). The practical difficulty in distinguishing these species has ultimately confounded scientific research and fishery data (SARDI 2000; ABARE 2009). Indeed, *A. trutta* and *A. truttaceus* are not treated as separate species for current Australian fishery catch statistics (ABARE 2009). Furthermore, the distribution of these species remains unclear. Reports that indicate capture records outside the recognised distribution of these species are available only through 'grey' literature and no corresponding specimens are deposited in museum collections for verification and future study.

Ambiguity in fish identification also mars parasite–host records, with many reports failing to detail methods used to identify hosts. Knowledge of the parasite fauna of arripids is valuable because individuals may aggregate near structure, including fish farms (Dempster and Kingsford 2004; Neira 2005; Catalano and Hutson 2010), a behaviour that presents an opportunity for parasite interactions between farmed and wild fish. Several parasite species are documented from *A. trutta* but few are reported from *A. georgianus* and *A. truttaceus*. The aim of our study was to extend knowledge of the metazoan parasite fauna of the Arripidae in southern Australian waters, provide comprehensive host and parasite identifications and validate host identity via molecular genetics.

Materials and methods

Fish collection and identification

In all, 183 *A. georgianus* individuals (mean fork length (FL) = 179 mm, range = 154–220 mm) and 67 *A. truttaceus* individuals (mean FL = 350 mm, range = 185–601 mm) obtained from Spencer Gulf (SG), Gulf St Vincent (GSV), Kangaroo Island (KI) and Coffin Bay (CB) in SA waters (Fig. 1) were examined between February and July 2009 for metazoan parasites (University of Adelaide, Animal Ethics Committee Project S-098-2007). Four *A. trutta* individuals were examined from KI and Almonta Beach, and CB National Park in SA waters (Fig. 1), and 19 were examined from Bermagui in NSW (mean FL = 448 mm, range = 179–545 mm) (Fig. 1, inset). Fishes were collected either via line fishing or from market catches

(Safcol Fish Market, Mile End, Adelaide, SA, and Sydney Fish Market, Pyrmont, NSW). Most fish individuals were examined fresh; others were frozen on capture and processed later. We distinguished *A. trutta* from *A. truttaceus* by using gill raker counts on the first gill arch (Gomon *et al.* 2008) and used molecular genetics to confirm our morphological differentiation.

Fish necropsies

Fish were examined for metazoan parasites by standard parasitological methods following Hutson *et al.* (2007). Tissue samples (fin clips) were collected from each fish examined, stored in 95% undenatured ethanol and lodged with the Australian Biological Tissue Collection (ABTC 108509–108777) at the South Australian Museum (SAMA). Four partially dissected *A. trutta* individuals were deposited in the Ichthyology Collection at SAMA ($n = 2$ from KI, F12179–80; $n = 1$ from Almonta Beach, CB National Park, F12182) and Museum Victoria (MV) ($n = 1$ from KI, A 30606-001). One individual of *A. georgianus* and one of *A. truttaceus* captured from Edithburgh and Pt Broughton, respectively, were also deposited (partially dissected specimens) in the Ichthyology Collection at SAMA ($n = 1$ from Edithburgh, F12378; $n = 1$ from Pt Broughton, F12379).

Parasite preparation

Standard methods following Hutson *et al.* (2007) were used to preserve, stain, mount and examine parasites. Original descriptions, redescriptions (see Tables 1–3), keys and borrowed vouchers assisted identification. Parasite prevalence and intensity are given in whole numbers and follow Bush *et al.* (1997). Mean and maximum intensity for *Ceratomyxa* sp. (Myxozoa) from *A. truttaceus* could not be determined because of the high level of infection observed prohibiting accurate counts of individuals. Parasites are deposited in the Australian Helminthological Collection (AHC) and the Crustacean collection (C) at SAMA, the Parasitology Collection at Queensland Museum (G), the collections at the Natural History Museum, London (BMNH) and the United States National Parasite Collection (USNPC) (Tables 1–3).

Molecular methods

Total genomic DNA was extracted, amplified and sequenced from fin clips of *A. truttaceus*, *A. trutta* and *A. georgianus*, sourced from different localities in SA and NSW (Table 4, available as an Accessory Publication to this paper), using the molecular methods in Catalano *et al.* (2010). Three partial gene segments were amplified and sequenced using the following primers: Cox1 fragment – Primers Fish F2 and Fish R2 (Ward *et al.* 2005); 16S fragment – Primers L2510–16S and H3084–16S (Doiuchi and Nakabo 2006); 28S fragment – Primers 28SV and 28SJJ (Smith and Wheeler 2004). Representative sequences are deposited in GenBank (Table 4, available as an Accessory Publication to this paper). The recovered sequences were compared with reference strains (Table 4, available as an Accessory Publication to this paper). All pair-wise similarities are presented in Table 5, available as an Accessory Publication to this paper.

Results and discussion

Range extension for Arripis trutta *and distribution of arripid species*

Our morphological (different gill raker counts) and molecular analyses (0% variance in Cox1 sequences between SA and NSW *A. trutta*) confirmed the presence of *A. trutta* in SA waters and extended its western range by ~1000 km from Port Philip Bay, Victoria (38°19′11″S, 144°42′48″E) to Almonta Beach, CB National Park, SA (Fig. 1). On the basis of the molecular analyses, we have confirmed that gill raker counts morphologically discriminate the species and also noted a consistent difference in the appearance of the gill rakers; those of *A. trutta* are relatively long, thin and closely spaced compared with those of *A. truttaceus.* Primers specific to *A. georgianus* 28S rRNA failed to amplify product from *A. trutta* and *A. truttaceus*, prohibiting sequence comparison for this gene. Furthermore, the 16S rRNA sequence fragment (545–563 bp) from *A. trutta* was identical to that from *A. truttaceus*, also prohibiting the discrimination of these species by using this gene fragment. Given the morphological similarity of these two arripid species, except maximum attainable size and gill raker number on the first gill arch (Gomon *et al.* 2008), it is easy to understand why their coexistence in SA waters has gone undetected. Our results indicated a considerable overlap in the distribution of three *Arripis* spp. in SA waters (Fig. 1). It is likely that *A. trutta* schools with *A. truttaceus* in SA waters because they were always captured together in our study.

Fairclough *et al.* (2000*a*) indicated that *A. trutta* spawns in south-eastern Australia in summer, when the southward-moving Eastern Australian Current (EAC) and subsequent residual current moving westward are strong (Richardson and Poloczanska 2009). In recent years, the strength of the EAC has intensified, with a predicted increase of >20% by 2100, resulting in changes in the range of several marine species (Ridgway and Hill 2009). This suggests that the occurrence of *A. trutta* in SA waters may increase in the future. We believe our discovery is significant for the Australian salmon fishery in SA waters. However, before any action is taken to modify fishery management, it is crucial to determine whether or not *A. trutta* is common in SA waters and also whether the species contributes significantly to the catch limit. This will require subsampling over an extended time period.

A single fish species that exhibits divergent migration behaviours may exhibit subtle, but demonstrable morphological differences (Secor 1999). It is plausible that *A. truttaceus* and *A. trutta* may represent a single *Arripis* species and that differences in gill raker number and morphology and the maximum body size attained may correlate with different feeding habits along separate migration paths (Malcolm 1959). Fish tissue accessioned for all arripid individuals examined by us may be valuable for future investigation of this hypothesis. Irrespective of the outcome, the distinct life-history differences between *A. truttaceus* and *A. trutta* should be acknowledged by fishery managers and it is recommended that the relative proportions of these species in commercial catches should be assessed.

Table 1. Metazoan parasite fauna from *Arripis georgianus* collected in the present study and from published literature

Under infection parameters, prevalence is expressed as a percentage (%); mean intensity is followed in parentheses by maximum intensity. SA, South Australia; and WA, Western Australia

Parasite	Habitat	Reference	Location	Infection parameters	Accession number
Cestoda					
Lacistorhynchidae					
Callitetrarhynchus gracilis Rudolphi, 1819	Viscera	[A]	SA[B]	13; 4 (13)	AHC 45416
Order: Tetraphyllidea Carus, 1863					
Type 1	Intestine	[A]	SA[B]	1; 1 (1)	AHC 29765
Type 2	Intestine	[A]	SA[B]	1; 1 (1)	AHC 29766
Tentaculariidae					
Nybelinia thyrsites Korotaeva, 1971	Intestine	[A]	SA[B]	1; 1 (1)	AHC 29788
Digenea					
Acanthocolpidae					
Monostephanostomum georgianum Kruse, 1979	Digestive tract	Bray and Cribb (2002)	SA, SA[B]	11; 2 (7)	AHC 29759–60
Monostephanostomum manteri Kruse, 1979	Digestive tract	Braicovich and Timi (2008)	SA, SA[B]	10; 3 (11)	AHC 29761
Bucephalidae					
Telorhynchus arripidis Crowcroft, 1947	Digestive tract	[A]	SA[B]	42; 32 (653)	AHC 29764
Hemiuridae					
Elytrophalloides humerus Bray, 1990	Stomach, intestine	[A]	SA[B]	11; 1 (4)	AHC 29755–58
Erilepturus tiegsi Woolcock, 1935	Digestive tract	Bray (1990)	WA, SA[B]	6; 2 (3)	AHC 29754 AHC 29789
Opecoelidae					
Pseudopecoeloides arripi Aken'Ova *et al.*, 2009	Intestine, caeca	Aken'Ova *et al.* (2009)	WA, SA, SA[B]	30; 3 (21)	AHC 29762–3
Monogenea					
Microcotylidae					
Microcotyle arripis Sandars, 1945	Gills	Sandars (1945)	WA, SA, SA[B]	72; 5 (21)	AHC 29751–53 AHC 29883–84 BMNH 2009.12.28.1–2 USNPC 102673.00–102675.00
Nematoda					
Anisakidae					
Hysterothylacium sp.	Digestive tract	[A]	SA[B]	3; 11 (51)	AHC 45417–18
Camallanidae					
Procamallanus sp.	Digestive tract	[A]	SA[B]	1; 40 (40)	AHC 45421
Philometridae					
Philometra sp.	Gonad	[A]	SA[B]	2; 2 (3)	AHC 45422–23
Trichinellidae					
Capillaria sp.	Digestive tract	[A]	SA[B]	2; 1 (2)	AHC 45419–20
Branchiura					
Argulidae					
Argulus diversicolor Byrnes, 1985	Skin	Catalano and Hutson (2010)	SA[B]	2; 2 (3)	BMNH 2009.261
Copepoda					
Caligidae					
Caligus punctatus Shiino, 1955	Gills	Catalano and Hutson (2010)	SA[B]	1; 1 (1)	C6814

[A]New host record; [B]from the current study.

Table 2. Metazoan parasite fauna from *Arripis truttaceus* collected in the present study and from published literature

Under infection parameters, prevalence is expressed as a percentage (%); mean intensity is followed in parentheses by maximum intensity. NR, not recorded; SA, South Australia; Tas., Tasmania; and Vic., Victoria

Parasite	Habitat	Reference	Location	Infection parameters	Accession number
Myxozoa					
Ceratomyxidae					
Ceratomyxa sp.	Gall bladder	[A]	SA[B]	33; NR	G465430–31
Cestoda					
Lacistorhynchidae					
Callitetrarhynchus gracilis Rudolphi, 1819	Viscera	Beveridge and Campbell (1996)	Vic., SA[B]	16; 5 (25)	AHC 45424
Order: Tetraphyllidea Carus, 1863					
Type 1	Intestine, caeca	[A]	SA[B]	3; 1 (1)	AHC 29777–78
Type 3	Caeca	[A]	SA[B]	12; 3 (12)	AHC 29779
Tentaculariidae					
Nybelinia thyrsites Korotaeva, 1971	Stomach	Beveridge and Campbell (1996)	SA, SA[B]	6; 1 (1)	AHC 29780 AHC 45425
Digenea					
Acanthocolpidae					
Monostephanostomum georgianum Kruse, 1979	Digestive tract	[A]	SA[B]	16; 6 (21)	AHC 29773–74
Monostephanostomum manteri Kruse, 1979	Digestive tract	[A]	SA[B]	4; 1 (2)	AHC 29912–14
Bucephalidae					
Telorhynchus arripidis Crowcroft, 1947	Digestive tract	[A]	SA[B]	40; 169 (2351)	AHC 29775 AHC 29791
Hemiuridae					
Erilepturus tiegsi Woolcock, 1935	Digestive tract	[A]	SA[B]	25; 2 (5)	AHC 29770–72 AHC 29790
Elytrophalloides humerus Bray, 1990	Stomach	[A]	SA[B]	1; 1 (1)	AHC 29792
Elytrophallus sp. Manter, 1940	Gills – artefact	[A]	SA[B]	1; 1 (1)	AHC 29793
Lepocreadiidae					
Opechona kahawai Bray & Cribb, 2003	Intestine, caeca	Bray and Cribb (2003)	Tas., SA[B]	12; 4 (12)	AHC 29776
Monogenea					
Microcotylidae					
Kahawaia truttae Lebedev, 1969	Gills	[A]	SA[B]	39; 3 (14)	AHC 29767–69, 29882, 29885–86 BMNH 2009.12.28.3–4 USNPC 102676.00–102677.00
Nematoda					
Anisakidae					
Contracaecum sp.	Stomach, caeca	[A]	SA[B]	6; 1 (1)	AHC 45428–29
Hysterothylacium sp.	Digestive tract	[A]	SA[B]	33; 2 (14)	AHC 45426–27
Philometridae					
Philometra sp.	Stomach	[A]	SA[B]	3; 1 (1)	AHC 45430
Branchiura					
Argulidae					
Argulus diversicolor Byrnes, 1985	Skin	Catalano and Hutson (2010)	SA[B]	1; 1 (1)	C6823
Copepoda					
Caligidae					
Caligus bonito Wilson, 1905	Gills	Catalano and Hutson (2010)	SA[B]	13; 2 (3)	C6819
Caligus longipedis Bassett-Smith, 1898	Gills	Catalano and Hutson (2010)	SA[B]	3; 3 (4)	C6815–6
Caligus punctatus Shiino, 1955	Skin	Catalano and Hutson (2010)	SA[B]	3; 7 (9)	C6817–8

[A]New host record; [B]from the current study.

Table 3. Metazoan parasite fauna from *Arripis trutta* collected in the present study and from published literature

Under infection parameters, prevalence is expressed as a percentage (%); mean intensity is followed in parentheses by maximum intensity. GAB, Great Australian Bight; NA, not applicable; NR, not recorded; NSW, New South Wales; NZ, New Zealand; PR, previously recorded from the literature but not found in the current study; SA, South Australia; Tas., Tasmania; TS, Tasman Sea; and Vic., Victoria

Parasite	Habitat	Reference	Location	Infection parameters	Accession number
Myxozoa					
Ceratomyxidae					
Ceratomyxa arripica Su & White, 1994	Gall bladder	Su and White (1994)	Tas.	NA	PR
Leptotheca annulata Meglitsch, 1960	Gall bladder	Meglitsch (1960)	NZ	NA	PR
Leptotheca minima Meglitsch, 1960	Gall bladder	Meglitsch (1960)	NZ	NA	PR
Cestoda					
Lacistorhynchidae					
Callitetrarhynchus gracilis Rudolphi, 1819	NR	Beveridge and Campbell (1996)	Vic.	NA	PR
Order: Tetraphyllidea Carus, 1863					
Type 3	Intestine	[A]	NSW[B]	11; 19(19)	AHC 29803
Tentaculariidae					
Nybelinia sp. larva Baker, 1971	Stomach	Baker (1971)	NZ	NA	PR
Digenea					
Acanthocolpidae					
Monostephanostomum georgianum Kruse, 1979	Digestive tract	[A]	SA[B]	22; 3(4)	AHC 29796–97
Monostephanostomum manteri Kruse, 1979	Intestine, caeca	Kruse (1979)[C]; Bray and Cribb (2002)	SA[C], Tas., SA[B]	22; 3(3)	AHC 29798
Bucephalidae					
Prosorhynchus sp. Manter, 1954	NR	Manter (1954)	NZ	NA	PR
Telorhynchoides longicollis Lebedev, 1968	NR	Lebedev (1968)[C]	GAB[C]	NA	PR
Telorhynchus arripidis Crowcroft, 1947	Digestive tract	Crowcroft (1948); Manter (1954); Lebedev (1968)[C]	Tas., NZ, GAB[C], TS, NSW[B]	33; 4(6)	AHC 29800–01
Telorhynchus kahawai Lebedev, 1968	NR	Lebedev (1968)[C]	GAB[C]	NA	PR
Telorhynchus peacheyi Lebedev, 1968	NR	Lebedev (1968)[C]	GAB[C], TS	NA	PR
Hemiuridae					
Erilepturus tiegsi Woolcock, 1935	Stomach, caeca	Yamaguti (1958)	Vic., SA[B]	33; 1(2)	AHC 29794–95
Hemiurus (*Anahemiurus*) sp. Manter, 1947	Digestive tract	Baker (1971)	NZ	NA	PR
Parahemiurus arripidis Lebedev, 1971	NR	Bray and Cribb (2002)	NZ	NA	PR
Parahemiurus sp. Lebedev, 1971	NR	Lebedev (1971)	NZ	NA	PR
Lepocreadiidae					
Opechona kahawai Bray & Cribb, 2003	Caeca	Bray and Cribb (2003)	Tas., NSW[B]	11; 1(1)	AHC 29802

(*Continued*)

Table 3. (Continued)

Parasite	Habitat	Reference	Location	Infection parameters	Accession number
Opecoelidae					
Pseudopecoeloides arripi Aken'Ova *et al*., 2009	Stomach	[A]	NSW[B]	11; 1(1)	AHC 29799
Syncoliidae					
Syncoelium filiferum Sars, 1885	Gills	Rohde *et al*. (1980)	NZ	NA	PR
Monogenea					
Microcotylidae					
Kahawaia truttae Lebedev, 1969	Gills	Dillon and Hargis (1965); Lebedev (1969)[C]	NZ, GAB[C], SA[B], NSW[B]	48; 2(5)	AHC 29781–82
Nematoda					
Anisakidae					
Anisakis sp. larva	Viscera	Hewitt and Hine (1972)	NZ	NA	PR
Contracaecum aduncum Rudolphi, 1802	Digestive tract	Baker (1971)	NZ	NA	PR
Contracaecum sp.	Stomach, intestine, body cavity	Hewitt and Hine (1972)	NZ	NA	PR
Hysterothylacium sp.	Digestive tract	[A]	NSW[B]	11; 2(2)	AHC 45431
Annelida					
Pisciolidae					
Austrobdella translucens Badham, 1916	Tail fin	Bolton *et al*. (2005)[C]	SA[C]	NA	PR
Copepoda					
Caligidae					
Caligus bonito Wilson, 1905	Gills	Catalano and Hutson (2010)	NSW[B]	9; 2(2)	C6821
Caligus kahawai Jones, 1988	Body surface	Jones (1988)	NZ	NA	PR
Caligus pelamydis Hewitt, 1963	Gills	Jones (1988)	NZ, NSW[B]	4; 1(1)	C6822
Caligus punctatus Shiino, 1955	Gills	Catalano and Hutson (2010)	NSW[B]	4; 1(1)	C6820
Chondracanthidae					
Chondracanthus australis Ho, 1991	Gills	Ho (1991)	NZ	NA	PR
Ergasilidae					
Abergasilus amplexus Hewitt, 1978	Gills	Hewitt (1978)	NZ	NA	PR
Isopoda					
Cymothoidae					PR
Codonophilus imbricatus Fabricius, 1787	Tongue	Baker (1971)	NZ	NA	
Nerocila orbignyi Guérin-Méneville, 1832	Body	Hewitt and Hine (1972)	NZ	NA	PR

[A]New host record; [B]from current study; [C]ambiguous parasite-host record (see Results and discussion).

Metazoan parasite fauna of the Arripidae

We recovered a total of 8455 parasites, 4959 from *A. truttaceus*, 3417 from *A. georgianus* and 79 from *A. trutta*. A diverse community of metazoan parasites infects arripids, with representation across a wide spectrum of parasite taxa in five phyla (Tables 1–3). In all, 17 parasite species were recorded and identified from *A. georgianus*, 20 from *A. truttaceus* and 12 from *A. trutta* (Tables 1–3). Including previous accounts of parasite species from *A. trutta*, together with those recorded here, a total of 34 species is now documented from this species (Table 3). Of the parasites recorded in our study from all three arripids, 71% represent new host records. Poulin and Morand (2000) stated that a central limitation in the current parasite-diversity estimates is that not all living host species are identified and/or described. The three arripid species examined here were described in the early 1800s, so discovery of such a high percentage of new host records is surprising. Host species that are well known but not *examined* carefully in sufficient numbers also contribute significantly to underestimates of parasite diversity.

We also recorded four parasitic crustacean species that have been associated with mass mortality of cultured fishes overseas. The importance of this discovery for southern Australian finfish sea-cage aquaculture is reviewed elsewhere (Catalano and Hutson 2010). Larval tetraphyllidean metacestodes, which are difficult to classify using basic morphology (e.g. Chambers *et al.* 2000), were the only parasites not identified to genus or below. They were designated as Types 1–3 on the basis of differences in length, width and position of the four triloculate bothridia and apical sucker.

Similarities and differences in parasites among Arripis spp.

Our results showed similarities as well as clear differences in the parasite assemblages and parasite species richness among *A. georgianus*, *A. truttaceus* and *A. trutta* (Tables 1–3, respectively), which can be explained by a range of host attributes. Similarities and differences in parasite assemblages could be due to host phylogeny because shared parasite species may be inherited from a common ancestor (Poulin and Rohde 1997), whereas distinct parasite species may reflect host speciation over time (Guegan *et al.* 1992). *A. trutta* is more closely related to *A. truttaceus* than to *A. georgianus* (see Ward and Holmes 2007), a fact mirrored by *A. trutta* and *A. truttaceus* having greater similarities in parasite fauna than *A. trutta* and *A. georgianus* (compare Tables 1–3). For example, *Kahawaia truttae* (Monogenea), *Contracaecum* sp. (Nematoda) and Tetraphyllidea Type 3 (Cestoda) are shared by *A. truttaceus* and *A. trutta* (Tables 2, 3) whereas *A. georgianus* has its own monogenean species (*Microcotyle arripis*) and different nematode and cestode species (Table 1).

Nonetheless, differences observed may simply be attributed to spatial scale restrictions. For instance, Marcogliese (2002) and Poulin (2007) stated that parasite distributions are superimposed on distributional patterns of free-living animals that participate as hosts in the parasite's lifecycle. Price and Clancy (1983) asserted that the geographical range of a host comprises multiple habitats, with each contributing additional parasite species to the overall fauna. Our study, together with published literature, sampled *A. georgianus*, *A. truttaceus* and *A. trutta* from only a small part of their total geographical and size range. Therefore, there is no information on the contribution of additional geographical habitats and fish ontogeny to the overall parasite fauna of each arripid species.

Parasite species richness was greatest for *A. trutta* (Table 3). This may be because *A. trutta* is the most widely distributed arripid species compared with *A. georgianus* and *A. truttaceus* and, therefore, has the potential to encounter greater numbers of parasite species across its broad range (e.g. Guegan *et al.* 1992). Nonetheless, numerous studies have also shown that larger fish hosts have greater parasite abundance and parasite species richness than do small hosts (e.g. Kearn 1967; Ho 1991; Guegan *et al.* 1992; Poulin 1997). Larger host bodies provide more space and a greater diversity of niches for parasites to colonise (Guegan *et al.* 1992; Lo *et al.* 1998). *A. trutta* and *A. truttaceus* reach a larger maximum size than *A. georgianus* (see Gomon *et al.* 2008), possibly explaining the observed result that the first two host species have a greater parasite species richness compared with the latter. Nevertheless, *A. trutta* is historically the more studied arripid species for parasites and therefore sampling bias may also explain this observation.

Food web structure is hypothesised to affect transmission of parasite species (Marcogliese and Cone 1997; Marcogliese 2002). Therefore, diet may influence the parasite assemblage associated with an individual (Braicovich and Timi 2008). Diet and feeding studies for all three arripid species are limited. Information focuses on the different prey items consumed by *A. truttaceus* and *A. trutta* corresponding to differences in gill raker anatomy, with little information on the diet for *A. georgianus* (K. Jones, pers. comm.). In our study, the highest maximum infection intensities were for the endoparasitic digenean *Telorhynchus arripidis* from *A. georgianus* and *A. truttaceus* (Tables 1, 2). Infection by *T. arripidis* occurs by ingesting intermediate hosts harbouring encysted metacercariae (Lo *et al.* 1998), suggesting prey containing these infective stages comprise a major part of the diet of *A. georgianus* and *A. truttaceus*.

Ambiguous parasite–host records

Several ambiguous parasite–host records for *A. trutta* in SA waters were noted (Table 3). These may have resulted from confusion surrounding discrimination and identification of *A. trutta* and *A. truttaceus* in previous literature (see Paulin 1993 for a review), but are also a result of authors failing to acknowledge methods used to identify hosts (e.g. Lebedev 1968, 1969; Kruse 1979; Bolton *et al.* 2005; Table 3). Before our study, the known western limit for *A. trutta* was Port Phillip Bay (Hutson *et al.* 2004), rendering previous parasite–host identifications for *A. trutta* in SA ambiguous. It is clear from our study and from previous reports (e.g. Hoedt and Dimmlich 1994; Jones and Westlake 2003) that *A. truttaceus* is the common Australian salmon species in SA waters and that most previous ambiguous records are likely to be *A. truttaceus* misidentified as *A. trutta*. These doubtful reports plainly demonstrate the critical importance of stating the methods used to identify hosts (e.g. keys and/or literature consulted, authorities asked for advice) as

well as the value of lodging host specimens and/or host-tissue samples in established permanent collections for verification and future study.

Conclusions

The present study has provided new information on the distribution of *A. trutta*, with validation of morphological identification (based on gill raker number and morphology on gill arch one) via molecular genetics. The extension of the western range by ~1000 km, from Port Philip Bay, Victoria, to Almonta Beach, CB National Park, SA, has implications for the management of arripids in southern Australian waters. We have here reported 35 new metazoan parasite–host records from three arripid species in southern Australian waters. Our thorough documentation of parasite assemblages for *A. georgianus*, *A. truttaceus* and *A. trutta* provides valuable baseline data that will permit the detection of changes in parasite fauna over time.

Acknowledgements

We are grateful to Professor Geoff Boxshall (GB) and Dr Rod Bray (RB) (Natural History Museum, London), Dr Shokoofeh Shamsi (Charles Sturt University, Wagga Wagga) and Professor Ian Beveridge (University of Melbourne) for assistance with parasite identifications. Thanks also go to Leonie Barnett, Tim Benson, Kieran Brazell, Dr Mieke Burger, Angelo, Domenico, Margaret and Pepperoni Catalano, Bruce Jackson, Dr Matt Padula, Dr Richard and Brian Saunders, Pep Severino and Dr Mike Steer for assistance in the field. Dr Terry Bertozzi, Dr Leslie Chisholm, Thierry Laperousaz and Ralph Foster (South Australian Museum, Adelaide), Dr Stephen Keable (Australian Museum), Miranda Lowe (Natural History Museum, London) and Dr Martin Gomon (Museum Victoria) kindly loaned or curated accessioned material. The constructive comments of two referees improved our manuscript. Scholarship support for S.R.C. was provided from Unibooks (University of Adelaide) and Playford Memorial Trust. This research was funded by an Australian Biological Resources Study grant (207-44) and Fisheries Research and Development Corporation grant (207/225) awarded to K.S.H. and I.D.W. Travel funds were awarded by the Australian Research Council and the National Health and Medical Research Council (ARC/NHMRC) Research Network for Parasitology to K.S.H. for travel to London to work with GB and RB.

References

ABARE (2009). Australian fisheries statistics 2008. Australian Bureau of Agricultural and Resource Economics (ABARE), Canberra.

Aken'Ova, T. O., Cribb, T. H., and Bray, R. A. (2009). Seven species of *Pseudopecoeloides* Yamaguti, 1940 (Digenea, Opecoelidae) from temperate marine fishes of Australia, including five new species. *ZooKeys* **5**, 1–32.

Baker, A. N. (1971). Food and feeding of kahawai (Teleostei: Arripididae). *New Zealand Journal of Marine and Freshwater Research* **5**, 291–299. doi:10.1080/00288330.1971.9515382

Barber, I., Hoare, D., and Krause, J. (2000). Effects of parasites on fish behaviour: a review and evolutionary perspective. *Reviews in Fish Biology and Fisheries* **10**, 131–165. doi:10.1023/A:1016658224470

Beveridge, I., and Campbell, R. A. (1996). New records and descriptions of trypanorhynch cestodes from Australian fishes. *Records of the South Australian Museum* **29**, 1–22.

Bolton, T. F., Hayward, C. J., and Turner, A. J. (2005). The piscicolid leech *Austrobdella translucens*, Badham 1916: a new host record from Australian salmon, *Arripis trutta* (Forster, 1801), and a new locality record for yellowfin whiting, *Sillago schomburgkii*, Peters 1864, in South Australia. *Australian Zoologist* **33**, 385–387.

Braicovich, P. E., and Timi, J. T. (2008). Parasites as biological tags for stock discrimination of the Brazilian flathead *Percophis brasiliensis* in the south-west Atlantic. *Journal of Fish Biology* **73**, 557–571. doi:10.1111/J.1095-8649.2008.01948.X

Bray, R. A. (1990). Hemiuridae (Digenea) from marine fishes of the southern Indian Ocean: Dinurinae, Elytrophallinae, Glomericirrinae and Plerurinae. *Systematic Parasitology* **17**, 183–217. doi:10.1007/BF00009553

Bray, R. A., and Cribb, T. H. (2002). *Monostephanostomum georgianum* n. sp. (Digenea: Acanthocolpidae) from *Arripis georgianus* (Valenciennes) (Perciformes: Arripidae) off Kangaroo Island, South Australia, with comments on *Monostephanostomum* Kruse, 1979 and *Stephanostomum* Looss, 1899. *Systematic Parasitology* **53**, 61–68. doi:10.1023/A:1019902106122

Bray, R. A., and Cribb, T. H. (2003). New species of *Opechona* Looss, 1907 and *Cephalolepidapedon* Yamaguti, 1970 (Digenea: Lepocreadiidae) from fishes off northern Tasmania. *Papers and Proceedings of the Royal Society of Tasmania* **137**, 1–5.

Bush, A. O., Lafferty, K. D., Lotz, J. M., and Shostak, A. W. (1997). Parasitology meets ecology on its own terms: Margolis *et al.* revisited. *The Journal of Parasitology* **83**, 575–583. doi:10.2307/3284227

Catalano, S. R., and Hutson, K. S. (2010). Harmful parasitic crustaceans infecting wild arripids: a potential threat to southern Australian finfish aquaculture. *Aquaculture* **303**, 101–104. doi:10.1016/J.AQUACULTURE.2010.03.005

Catalano, S. R., Hutson, K. S., Ratcliff, R. M., and Whittington, I. D. (2010). Redescriptions of two species of microcotylid monogeneans from three arripid hosts in southern Australian waters. *Systematic Parasitology* **76**, 211–222. doi:10.1007/S11230-010-9247-X

Chambers, C., Cribb, T. H., and Jones, M. K. (2000). Tetraphyllidean metacestodes of teleosts of the Great Barrier Reef, and the use of *in vitro* cultivation to identify them. *Folia Parasitologica* **47**, 285–292.

Crowcroft, P. W. (1948). The anatomy of two new digenetic trematodes from Tasmanian food fishes. *Proceedings of the Linnean Society of New South Wales* **71**, 108–118.

Deagle, B. E., Kirkwood, R., and Jarman, S. N. (2009). Analysis of Australian fur seal diet by pyrosequencing prey DNA in faeces. *Molecular Ecology* **18**, 2022–2038.

Dempster, T., and Kingsford, M. (2004). Drifting objects as habitats for pelagic juvenile fish off New South Wales, Australia. *Marine and Freshwater Research* **55**, 675–687. doi:10.1071/MF04071

Dillon, W. A., and Hargis, W. J. (1965). Monogenean trematodes from the southern Pacific Ocean. 2. Polyopisthocotyleids from New Zealand fishes: the families Discocotylidae, Microcotylidae, Axinidae, and Gastrocotylidae. In 'Biology of the Antarctic Seas II. Antarctic Research Series: Vol. 5'. (Ed. G. A. Llano.) pp. 251–280. (American Geophysical Union: Washington, DC.)

Doiuchi, R., and Nakabo, T. (2006). Molecular phylogeny of the stromateoid fishes (Teleostei: Perciformes) inferred from mitochondrial DNA sequences and compared with morphology-based hypotheses. *Molecular Phylogenetics and Evolution* **39**, 111–123. doi:10.1016/J.YMPEV.2005.10.007

Dulvy, N. K., and Reynolds, J. D. (2009). Skates on thin ice. *Nature* **462**, 417. doi:10.1038/462417A

Fairclough, D. V., Dimmlich, W. F., and Potter, I. C. (2000*a*). Length and age compositions and growth rates of the Australian herring *Arripis georgiana* in different regions. *Marine and Freshwater Research* **51**, 631–640. doi:10.1071/MF99118

Fairclough, D. V., Dimmlich, W. F., and Potter, I. C. (2000*b*). Reproductive biology of the Australian herring *Arripis georgiana*. *Marine and Freshwater Research* **51**, 619–630. doi:10.1071/MF99119

Gomon, M., Bray, D., and Kuiter, R. (2008). 'Fishes of Australia's Southern Coast.' (Reed New Holland: Sydney.)

Guegan, J. F., Lambert, A., Leveque, C., Combes, C., and Euzet, L. (1992). Can host body size explain the parasite species richness in tropical freshwater fishes? *Oecologia* **90**, 197–204.

Hewitt, G. C. (1978). *Abergasilus amplexus* gen. et sp. nov. (Ergasilidae; parasitic Copepoda) from fishes in Lake Ellesmere, New Zealand. *New Zealand Journal of Marine and Freshwater Research* **12**, 173–177. doi:10.1080/00288330.1978.9515738

Hewitt, G. C., and Hine, P. M. (1972). Checklist of parasites of New Zealand fishes and of their hosts. *New Zealand Journal of Marine and Freshwater Research* **6**, 69–114. doi:10.1080/00288330.1977.9515410

Ho, J. S. (1991). Two species of chondracanthid copepods parasitic on commercial fishes in the Pacific. *Publications of the Seto Marine Biological Laboratory* **31**, 1–10.

Hoedt, F. E., and Dimmlich, W. F. (1994). Diet of subadult Australian salmon, *Arripis truttaceus*, in Western Port, Victoria. *Australian Journal of Marine and Freshwater Research* **45**, 617–623. doi:10.1071/MF9940617

Hutson, K. S., Styan, C. A., Beveridge, I., Keough, M. J., Zhu, X., *et al.* (2004). Elucidating the ecology of bucephalid parasites using a mutation scanning approach. *Molecular and Cellular Probes* **18**, 139–146. doi:10.1016/J.MCP.2003.11.004

Hutson, K. S., Ernst, I., Mooney, A. J., and Whittington, I. D. (2007). Metazoan parasite assemblages of wild *Seriola lalandi* (Carangidae) from eastern and southern Australia. *Parasitology International* **56**, 95–105. doi:10.1016/J.PARINT.2006.12.003

Jones, J. B. (1988). New Zealand parasitic Copepoda; genus *Caligus* Muller, 1785 (Siphonostomatoida: Caligidae). *New Zealand Journal of Zoology* **15**, 397–413.

Jones, K. (2008). Australian salmon and herring. In 'The Natural History of Gulf of Saint Vincent'. (Eds S. Shepherd, S. Byres, I. Kirkegaard, P. Harbison and J. Jennings.) pp. 415–428. (Royal Society of South Australia: Adelaide.)

Jones, K., and Westlake, M. (2003). Marine scalefish and miscellaneous fisheries. Australian salmon (*Arripis truttacea* and *A. georgiana*), sand crabs (*Ovalipes australiensis*), tube worms (*Diopatra cacículata*) and blood worms (*Glycera* sp.). Fishery Assessment Report to PIRSA for the MSF Fishery Management Committee, No. 184. South Australian Fisheries Assessment Series 01/18, Adelaide.

Kearn, G. C. (1967). Experiments on host-finding and host-specificity in the monogenean skin parasite *Entobdella soleae. Parasitology* **57**, 585–605. doi:10.1017/S0031182000072450

Kruse, G. O. W. (1979). Trematodes of marine fishes from South Australia. 6. *Monostephanostomum manteri* gen. et sp. n. (Acanthocolpidae). *Journal of Parasitology* **65**, 921–923. doi:10.2307/3280250

Lebedev, B. I. (1968). Trematodes of the family Bucephalidae from commercially important marine fish of New Zealand and Australia. *Parasites of Animals and Plants*, **4**, 156–167. [In Russian]

Lebedev, B. I. (1969). The substantiation of a new genus *Kahawaia* gen. n. for *Gonoplasius truttae* Dillon and Hargis, 1965 (Monogenoidea: Microcotylidae). *Parasitology* **3**, 69–73. [In Russian]

Lebedev, B. I. (1971). Helminths of fishes from the Tasman Sea. In 'Parasites of Animals and Plants of the Soviet Far East'. (Ed. Y. L. Mamaev.) pp. 96–97. (Dal'nevostochnoe Knizhnoe Izdatel'stvo: Vladivostok, Russia.) [In Russian]

Lo, C. M., Morand, S., and Galzin, R. (1998). Parasite diversity/host age and size relationship in three coral-reef fishes from French Polynesia. *International Journal for Parasitology* **28**, 1695–1708. doi:10.1016/S0020-7519(98)00140-4

MacKenzie, K. (2002). Parasites as biological tags in population studies of marine organisms: an update. *Parasitology* **124**, 153–163. doi:10.1017/S0031182002001518

Malcolm, W. B. (1959). The populations of Australian 'salmon', *Arripis trutta* (Bloch & Schneider) in Australian waters. *Australian Journal of Marine and Freshwater Research* **4**, 95–104.

Malcolm, W. B. (1960). Area of distribution, and movement of the western subspecies of the Australian 'salmon', *Arripis trutta esper* Whitley. *Australian Journal of Marine and Freshwater Research* **11**, 282–325. doi:10.1071/MF9600282

Manter, H. W. (1954). Some digenetic trematodes from fishes of New Zealand. *Transactions of the Royal Society of New Zealand* **82**, 475–568.

Marcogliese, D. J. (2002). Food webs and the transmission of parasites to marine fish. *Parasitology* **124**, S83–S99. doi:10.1017/S003118200200149X

Marcogliese, D. J., and Cone, D. K. (1997). Food webs: a plea for parasites. *Trends in Ecology & Evolution* **12**, 320–325. doi:10.1016/S0169-5347(97)01080-X

Meglitsch, P. A. (1960). Some coelozoic myxosporidia from New Zealand fishes I. General, and family Ceratomyxidae. *Transactions of the Royal Society of New Zealand* **88**, 265–356.

Neira, F. J. (2005). Summer and winter plankton fish assemblages around offshore oil and gas platforms in south-eastern Australia. *Estuarine, Coastal and Shelf Science* **63**, 589–604. doi:10.1016/J.ECSS.2005.01.003

Paulin, C. (1993). Review of the Australasian fish family Arripididae (Percomorpha), with the description of a new species. *Australian Journal of Marine and Freshwater Research* **44**, 459–471. doi:10.1071/MF9930459

Peters, W., Evans, D. A., and Lanham, S. M. (1983). Importance of parasite identification in cases of leishmaniasis. *Journal of the Royal Society of Medicine* **76**, 540–542.

Poulin, R. (1997). Species richness of parasite assemblages: evolution and patterns. *Annual Review of Ecology and Systematics* **28**, 341–358. doi:10.1146/ANNUREV.ECOLSYS.28.1.341

Poulin, R. (2007). 'Evolutionary Ecology of Parasites.' 2nd edn. (Princeton University Press: Princeton, NJ.)

Poulin, R., and Morand, S. (2000). The diversity of parasites. *Quarterly Review of Biology* **75**, 277–293. doi:10.1086/393500

Poulin, R., and Rohde, K. (1997). Comparing the richness of metazoan ectoparasite communities of marine fishes: controlling for host phylogeny. *Oecologia* **110**, 278–283. doi:10.1007/S004420050160

Price, P. W., and Clancy, K. M. (1983). Patterns in number of helminth parasite species in freshwater fishes. *Journal of Parasitology* **69**, 449–454. doi:10.2307/3281352

Richardson, A. J., and Poloczanska, E. S. (2009). Australia's oceans. In 'A Marine Climate Change Impacts and Adaptation Report Card for Australia 2009'. (Eds E. S. Poloczanska, A. J. Hobday and A. J. Richardson.) pp. 1–6. (National Climate Change Adaptation Research Facility: Gold Coast, Qld.)

Ridgway, K., and Hill, K. (2009). The East Australian Current. In 'A Marine Climate Change Impacts and Adaptation Report Card for Australia 2009'. (Eds E. S. Poloczanska, A. J. Hobday and A. J. Richardson.) pp. 1–16. (National Climate Change Adaptation Research Facility: Gold Coast, Qld.)

Rohde, K., Roubal, F., and Hewitt, G. C. (1980). Ectoparasitic Monogenea, Digenea, and Copepoda from the gills of some marine fishes of New Caledonia and New Zealand. *New Zealand Journal of Marine and Freshwater Research* **14**, 1–13. doi:10.1080/00288330.1980.9515837

Sandars, D. F. (1945). Five new microcotylids from fish from Western Australian waters. *Journal of the Royal Society of Western Australia* **29**, 107–135.

SARDI (2000). Australian salmon (*Arripis truttacea*). South Australian Research and Development Institute (SARDI), Fisheries Assessment Series 2000/15, Adelaide.

Secor, D. H. (1999). Specifying divergent migrations in the concept of stock: the contingent hypothesis. *Fisheries Research* **43**, 13–34. doi:10.1016/S0165-7836(99)00064-8

Siddall, M. E., Trontelj, P., Utevsky, S. Y., Nkamany, M., and Macdonald, K. S. I. (2007). Diverse molecular data demonstrate that commercially

available medicinal leeches are not *Hirudo medicinalis. Proceedings. Biological Sciences* **274**, 1481–1487. doi:10.1098/RSPB.2007.0248

Smith, W. L., and Wheeler, W. C. (2004). Polyphyly of the mail-cheeked fishes (Teleostei: Scorpaeniformes): evidence from mitochondrial and nuclear sequence data. *Molecular Phylogenetics and Evolution* **32**, 627–646. doi:10.1016/J.YMPEV.2004.02.006

Smith, W. L., and Wheeler, W. C. (2006). Venom evolution widespread in fishes: a phylogenetic road map for the bioprospecting of piscine venoms. *Journal of Heredity* **97**, 206–217. doi:10.1093/JHERED/ESJ034

Smith, P. J., Hartill, B., Hamer, P., and McKenzie, A. (2008). Stock structure of kahawai, *Arripis trutta*. New Zealand Fisheries Assessment Report 2008/20, Ministry of Fisheries, Wellington, New Zealand.

Su, X., and White, R. W. G. (1994). New myxosporeans (Myxozoa: Myxosporea) from marine fishes of Tasmania, Australia. *Acta Parasitologica* **33**, 251–259.

Ward, R. D., and Holmes, B. H. (2007). An analysis of nucleotide and amino acid variability in the barcode region of cytochrome *c* oxidase I (*cox1*) in fishes. *Molecular Ecology Notes* **7**, 899–907. doi:10.1111/J.1471-8286.2007.01886.X

Ward, R. D., Zemlak, T. S., Innes, B. H., Last, P. R., and Hebert, P. D. N. (2005). DNA barcoding Australia's fish species. *Philosophical Transactions of the Royal Society of Biological Sciences* **360**, 1847–1857. doi:10.1098/RSTB.2005.1716

Yamaguti, S. (1958). 'Systema Helminthum. Vol I. Digenetic Trematodes of Vertebrates.' (Interscience Publishers Inc.: New York.)

Young, N. D., Crosbie, P. B. B., Adams, M. D., Nowak, B. F., and Morrison, R. N. (2007). *Neoparamoeba perurans* n. sp., an agent of amoebic gill disease of Atlantic salmon (*Salmo salar*). *International Journal for Parasitology* **37**, 1469–1481. doi:10.1016/J.IJPARA.2007.04.018

Manuscript received 6 August 2010, accepted 6 November 2010