DEPARTMENT OF
PRIMARY INDUSTRY AND RESOURCES

Optimising the Management of Tropical Reef Fish through the Development of Indigenous Scientific Capability

FRDC Project No. 2013/17



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Optimising the Management of Tropical Reef Fish through the Development of Indigenous Scientific Capability

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May 2017

FRDC Project No 2013/017

Fishery Report No. 117
ISBN: 978-0-7245-4769-2

FRDC Project No. 2013/17

This publication (and any information sourced from it) should be attributed to Saunders, T., Barton, D., Crook, D., Ovenden, J., Newman, S.J., Saunders, R., Taillebois, L., Taylor, J., Travers, M.J., Dudgeon, C., Maher, S. and Welch, D.J. (2016), *Optimising the management of tropical reef fish through the development of Indigenous scientific capability*. Darwin, Northern Territory, Fishery Report No. 117.

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Acknowledgements

We acknowledge the Fisheries Research and Development Corporation (FRDC) and the Northern Territory (NT) Government as the primary sources of funding for this project. Additionally, we thank the Western Australian Department of Fisheries (DoF), the Queensland Department of Agriculture, Forestry and Fisheries (QDAFF), CARDNO consulting, Charles Darwin University (CDU), North Australia Marine Research Alliance, the Australian Institute of Marine Science , the Australian National University and the University of Queensland for providing funding for the project. We would also like to thank Indigenous Marine Rangers (IMRs) from Borroloola, Maningrida, Groote Eylandt, Wadeye, Elcho Island, Larrakia and Nhulunbuy for participating in the training course and collecting a substantial number of the samples for the analyses. Thanks are also extended to the traditional owners and Indigenous ranger groups in Western Australia who assisted with the collection of samples, particularly the people of Balangarra, Wunambal Gaambera, Dambimangari and Bardi-Jawi.

Executive Summary

Report overview

This project was a collaborative undertaking between government research agencies and universities across northern Australia. The project examined the stock structure of key tropical reef fish species as well as using this research as a basis to develop a certified training course for Indigenous community members. Both of these outputs addressed key needs of filling a knowledge gap in the biology of important fish species to assist with their sustainable management as well as providing increased research capacity within Indigenous communities.

Background

This project was developed to address two key needs in northern Australia: filling a knowledge gap for three key tropical reef fish species which have suffered significant declines in this region and to develop the scientific research capability of Indigenous communities. These two needs are explicitly linked as building capability has the capacity to bring research and management costs down through local capability as well as increase employment opportunities in the form of monitoring contracts from government agencies. To help achieve these outcomes, a certified training course was developed that gave Indigenous community members skills in scientific field and laboratory work, which underpins sustainable fisheries management. The project also enabled training to be conducted in conjunction with research into the stock structure of the three key species studied.

The results of this project have the potential to provide benefits to all stakeholders involved in the harvest and management of these species. The three species studied in this project were: Golden Snapper (*Lutjanus johnii*), Black Jewfish (*Protonibea diacanthus*), and Grass Emperor (*Lethrinus laticaudis*). These species are popular targets for both the commercial and recreational fishing sectors and are increasingly becoming the focus in developing Indigenous fisheries. They are also prone to overexploitation because of their vulnerable biological characteristics, aggregative nature and susceptibility to barotrauma-related injuries upon release. These issues have resulted in substantial declines in these species around population centres in the NT and managers have been unable to apply appropriate strategies due to a lack of knowledge of the stock structure and total harvest by all sectors.

Objectives

1. Gain information on stock structure of key tropical reef fish species.
2. Develop Indigenous capability in scientific monitoring and participation in co-management through the development of a certified training program.
3. Identify appropriate spatial scale of management for tropical reef fish based on biological sustainability and sectoral aspirations.

Methodology

Sample collections of the three species were conducted across their entire range in Australian waters and concentrated in the Darwin region where recent overfishing of these species has been identified. All samples were analysed using otolith microchemistry, parasite and genetic analyses. This holistic approach provided the best opportunity to identify the scale of stock structure for each species.

The Certificate II course 'Measuring and Analysis' was developed by the Department of Primary Industry and Resources (DPIR) and Labtech Training (a registered training organisation) with input from IMR groups. While much of the material focussed on fisheries research monitoring activities, the course units provided the basis for an understanding of the key processes that need to be followed in accurate data and sample collection both in the field and the laboratory, which could then be transferred to many fields of scientific monitoring.

Findings

All three species were found to have fine-scale stock structures. Black Jewfish stocks had genetic connectivity at the scale of hundreds of kilometres, which was similar to the scale of juvenile and adult movements determined by the parasite and otolith microchemistry analyses. Golden Snapper and Grass Emperor stocks demonstrated genetic connectivity over hundreds to thousands of kilometres, which was much higher than the tens of kilometres scale stock structure indicated by the other analyses.

The training course was very successful as the students enjoyed and achieved competency in all the units. Subsequent benefits of the course included gaining employment by graduates in government research agencies and in IMR groups conducting fisheries research monitoring activities on a fee-for-service basis in this as well as in several other projects.

Implications for relevant stakeholders

The finding by this project that all three species have fine-scale stock structures needs to be taken into consideration by managing the fisheries that harvest them. Overfishing of these species in the Darwin region highlights their vulnerability to serial depletion of localised stocks. Given the success of the training conducted in this project, it is intended that this course will become a regular training component for IMRs by DPIR. However, in addition to training Indigenous Marine Rangers, it is intended to broaden the course to target school teenagers to increase employment opportunities for young Indigenous community members.

Keywords

Stock structure, Fisheries management, Indigenous development, Black Jewfish, Golden Snapper, Grass Emperor, Northern Australia, Training

1 Introduction

1.1 Background

This project was developed to address two key needs in northern Australia. The first was around filling knowledge gaps for three key coastal reef fish species which have suffered significant declines across the tropics and recent stock assessments in the NT have identified current harvest levels to be unsustainable. However, managers have been unable to apply appropriate arrangements due to a lack of knowledge on the stock structure of these species. The second need was related to Indigenous community's aspirations to develop their scientific research capability and increase their involvement in co-management of their sea country fisheries resources. Their aim is to be involved in developing sustainable Indigenous fisheries underpinned by scientific information collected by Indigenous community members.

During discussions on how to address these needs, it was realised that the two needs could be linked into one project. The need to develop the scientific capacity of Indigenous communities therefore underpinned a certified training course that gave Indigenous community members skills in scientific field and laboratory work and knowledge on how this information underpins sustainable fisheries management. The project also enabled this training to be run in direct conjunction with research into the stock structures of the three key species identified.

The results of this project have the potential to provide benefits to recreational, Indigenous and commercial stakeholders as well as to fisheries managers. To ensure these benefits had the highest likelihood of being realised, there was substantial consultation with scientific experts on the design of the stock structure component of the project, Indigenous ranger groups, peak bodies and communities on the content of the Indigenous training package and with peak body representatives of the commercial and recreational fishing sectors to ensure that the project was addressing the highest research priorities. Despite being based primarily on NT priorities, it is a direct outcome of the Northern Research Partnership and has cross jurisdictional support across northern Australia. It addresses the FRDC's strategic priority around sustainable fisheries development and is closely related to several projects that have been recently completed on identifying the stock structure of species to underpin their sustainable management. This project builds on these by using the same team of scientists and methods to conduct the analyses. The project also addresses the strategic priority around people development with the Indigenous training component and will closely align with two currently funded projects in this area.

1.2 Need

The three key species identified for this project are: Golden Snapper (*Lutjanus johnii*), Black Jewfish (*Protonibea diacanthus*) and Grass Emperor (*Lethrinus laticaudis*). These species are popular targets for both the commercial and recreational fishing sectors and are increasingly becoming the focus in developing Indigenous fisheries. These species are also prone to overexploitation because of their vulnerable biological characteristics, aggregative nature and susceptibility to barotrauma-related injuries upon release. In the NT, these issues have resulted in substantial declines in these species around population centres and managers have been unable to apply appropriate arrangements due to a lack of knowledge on the stock structure, unknown levels of recreational harvest and contested resource ownership and access rights. It is clear that the knowledge gap on stock structure needs to be filled to move towards the spatial management needed to ensure the sustainability of these fishery resources as well as their optimal allocation amongst sectors.

However, exploitation in remote areas of the NT is also increasing due to an expanding recreational fleet, driven largely by new mining and gas developments and aspirations by the Indigenous sector to develop fisheries on these species. While gaining information on stock structures of these species will greatly aid the sustainable development of fisheries in this area, there is still the requirement to ensure regular collection of biological data to monitor these stocks. One method of obtaining this information is to train

Indigenous rangers/community members by developing an appropriately certified course. By underpinning the course with the stock structure component of this project, students will also receive skills to assist with co-management and developing sustainable Indigenous fisheries. This project addresses the number one NT Research Advisory Committee research priority on reef fish biology as well as the NT and cross-jurisdictional priorities on Indigenous development.

1.3 Species Biology

1.3.1 Black Jewfish

The black jewfish (*Protonibea diacanthus)* (Lacepède, 1802) is a large sciaenid species that attains lengths in excess of 1.5 m and is an important component of commercial, recreational and subsistence fisheries in several countries, including Australia (Phelan et al., 2008; Dutta et al., 2014). They occur broadly through the tropical Indo-West Pacific in coastal waters and estuaries (Froese and Pauly, 2015). In Australia, it is distributed along the northern coast from Hervey Bay in Queensland to Shark Bay in Western Australia (Bray, 2011). The species exhibits extremely rapid growth, reaches sexual maturity at a large size and has a maximum recorded age of 13 years (Phelan, 2008). In the NT, it has been estimated that 50% of individuals are mature (L50) at ~89 cm total length (TL) at two years of age (Phelan, 2008). In the eastern Gulf of Carpentaria in Queensland, the L50 has been estimated at 98 cm TL (McPherson, 1997). Data on the spawning and early life history of Black Jewfish is limited, although histological examination of ovaries indicates multiple batch spawning (Phelan, 2008). Spawning of Black Jewfish in Australia occurs from August to December and in common with other sciaenids, they are likely to produce pelagic eggs and have a pelagic larval phase (Leis and Carson-Ewart, 2000; Nelson, 2006; Froese and Pauly, 2015). Seasonal aggregations of Black Jewfish occur throughout its distribution and it has been speculated that these are for spawning (Semmens et al., 2010), although direct evidence of the behaviour associated with aggregation is limited (Phelan et al., 2008). Black Jewfish are widely targeted by commercial, recreational and subsistence fishers across their range and are heavily overfished in some regions (Phelan et al., 2008; Mok et al., 2009; Semmens et al., 2010; Saunders et al., 2014a).

Stock assessments in the NT have determined that sequential localised depletion of Black Jewfish was occurring, particularly near major population centres (Walters et al., 1997; Grubert et al., 2013; Saunders et al., 2014a). Like many other large sciaenids, Black Jewfish are vulnerable to over-exploitation largely because of their predictable aggregating behaviour related to spawning (Phelan, 2001; Liu et al., 2008; Mok et al., 2009; Semmens et al., 2010) and several aggregation sites have been reported across northern Australia from Queensland to northern Western Australia (Newman, 1995; Bowtell, 1995). In India, overfishing during the 1980s led to the collapse of Black Jewfish fisheries (James, 1994). In Queensland, during the late 1990s, catches were found to consist almost exclusively of immature fish (Phelan, 2008). This resulted in a two-year fishing moratorium for Black Jewfish, which only resulted in a slight recovery of the adult stock (Phelan et al., 2008). In the NT, new management in the form of spatial closures and catch limits were introduced in 2015 to reduce the harvest of Black Jewfish by 20% to promote the recovery of this species (Saunders et al., 2016; Grubert et al., 2013).

These examples highlight the urgency for informed management of Black Jewfish stocks across northern Australia. The determination of the stock structure of Black Jewfish will provide the necessary spatial scale for management decision-making.

1.3.2 Golden Snapper

Golden Snapper (*Lutjanus johnii)* (Bloch, 1792) is one of 65 species of the genus *Lutjanus* from the 103 species of the family Lutjanidae (Allen and Talbot, 1985). This species is widely distributed throughout the Indo-West Pacific, inhabiting tropical inshore waters from East Africa to Fiji and northern Australia to Taiwan (Allen and Talbot, 1985). This species is also known as “Fingermark” in Queensland and has a distribution that extends from the Pilbara region in north Western Australia across northern

Australia to the mid-east coast of Queensland (Travers et al., 2006; Saunders et al., 2014b). Throughout this region, this species is a highly prized sport and food fish and is harvested in the commercial, recreational, charter and Indigenous sectors of northern Australia.

Resource pressure on inshore reef fish, particularly Golden Snapper in the NT, has increased significantly in recent years, particularly in areas close to population centres (Grubert et al., 2010). Contributing factors include escalating fishing effort by a rapidly expanding charter industry and a growing recreational sector as the NT's population climbs. The increase in effort by these sectors has been exacerbated by advances in technology (e.g. GPS, high quality sounders, web forums and accurate weather predictions) enabling fishing to be much more precise and targeted (DPIR, 2014).

The current life history paradigm for Golden Snapper is complex with distinct inshore and offshore phases. In estuaries and near-shore embayment's, Golden Snapper are predominantly juveniles and sub-adults, while most fish encountered on coastal near-shore and offshore reefs are larger adult fish (Kiso and Mahyam, 2003; Hay et al., 2005). They prefer to inhabit reefs, rocks, submerged woody debris and pinnacles in both deep and shallow habitats within these areas (Hay et al., 2005; Travers et al., 2010) and move about on the nearby sandy areas possibly to feed (Kiso and Mahyam, 2003; Cappo et al., 2013). Adult Golden Snapper grow to at least 900 mm in length and attain an age of 20+ years (Marriott and Cappo, 2000). Data collected by NT Fisheries since 2009 indicates that Golden Snapper grow relatively quickly in their first few years before slowing down and taking several years to reach maturity (NT Government, unpublished data). Growth rates of 250 mm TL by age one, 500 mm TL by age seven and 600 mm TL by age ten were recorded in this research (NT Government, unpublished data). Golden Snapper were also found to be late maturing with the size at 50% maturity for male fish to be around 47 cm full length (FL) (age ~ 5 years) and 63 cm FL for females (age ~ 8 years) (Hay et al., 2005; NT Government, unpublished data).

Observations by Hay et al. (2005) indicated that in the NT this species has a protracted spawning period from September to late April. It has been hypothesised that Golden Snapper undertake at least two major movements during their life cycle: an inshore migration as post-larvae or early juveniles from offshore spawning grounds and a subsequent offshore migration of sub-adult or mature fish (Kiso and Mahyam, 2003). While limited data exists on the movements of this species, recaptures of 39 animals from a long-term tagging program on the Queensland east coast suggests that movement is limited to local scales regardless of size (Welch et al., 2014).

1.3.3 Grass Emperor

Grass Emperor (*Lethrinus laticaudis)* (Alleyne and Macleay, 1877; Lethrinidae) is a medium sized (<600 mm) spcies that occurs in tropical waters of the western Pacific and south-eastern Indian oceans throughout southern Indonesia, Papua New Guinea, Solomon Islands, New Caledonia and Australia (Carpenter and Niem, 2001). In Australia, it occurs along the northern coastline from Shark Bay in Western Australia to south-east Queensland (Ayvazian et al., 2004; Bray and Gomon, 2011). Mature Grass Emperor occur most commonly in depths from 5 to 35 m over reef habitats with juveniles thought to utilise inshore seagrass meadows (Carpenter and Niem, 2001; Travers et al., 2010). Grass Emperor are suggested to have site fidelity to reefs, unless patches of suitable habitat are close enough to allow movement between sites (Ayvazian et al., 2004), with a study of tagged fish having most fish recaptured within 1 km of their release site, even after extended periods of time (Sumpton et al., 2008). The species is a popular food fish exploited by commercial fishers and recreational anglers across northern Australia (Coleman, 2003; Grubert et al., 2010).

The biology of Grass Emperor is not well known, with a single key study done on the population in Shark Bay, Australia (Ayvazian et al., 2004). The study determined that Grass Emperor grew to nearly 600 mm TL and that the size of 50% maturity was 230 mm TL for females and 180 mm TL for males. The maximum age estimate was 16 years and age at 50% maturity occurred between two and three years for males and females. Grass Emperor have rarely been reported as hosts for parasites in Australian waters, with only two records, both from Moreton Bay, south-east Queensland (Young, 1968; Kabata, 1979).

Previous work on otolith microchemistry has concentrated on carbon and oxygen stable isotope ration work in Shark Bay (Ayvazian et al., 2004). Johnson et al. (1993) clarified the species status of Grass Emperor in north-western Western Australian waters using electrophoretic analysis, finding them to be reproductively isolated from other lethrinid species in the same waters. Despite being increasingly targeted by recreational fishers (Ayvazian et al., 2004; Knuckey et al., 2005) the status of Grass Emperor is unknown. Given their rapidly increasing importance in recreational fishing catches, knowledge of their stock structure throughout their fishery range will inform future management.

1.4 Indigenous Fisheries Monitoring Capability

The NT has about 11 000 km of coastline, of which 84% is owned by Indigenous communities (NLC, 2011). There are hundreds of communities scattered across the NT (Gorman and Vemuri, 2012) that have a significant interest in the sustainable management of the aquatic resources associated with their land for subsistence use as well as developing Indigenous enterprise (e.g. DPIR 2011; Fleming et al. 2015). Given the synergy between Indigenous communities and the environment they live in, there have been a number of programs focussing on developing skills in natural resource management with land and sea ranger positions being the most substantial area of employment (Altman et al. 2011). There are now over 500 Indigenous people working as land and sea rangers in the NT (NLC, 2014). These groups undertake a large range of activities, including fire management, feral animal and weed control, biodiversity monitoring, threatened species protection and enforcement (Altman et al. 2011). Within this program, there are 16 Indigenous IMR groups that regularly conduct surveillance activities for illegal fishing, monitoring of protected species and a range of fisheries monitoring activities. This experience along with their intimate knowledge of remote coastal areas of the NT means that they are ideally placed to assist government agencies to monitor coastal waters and their associated aquatic resources (DPIR, 2012).

DPIR currently utilises the capability of the IMR groups by providing them funding assistance to conduct compliance and research activities in waters adjacent to their communities (DPIR, 2012). To increase the capability of IMRs, DPIR has developed a compliance training program that has been completed by over 100 Indigenous students. This training course received considerable recognition for its success in increasing the capability of Indigenous communities winning the 5th Australian Seafood Industry training award in 2010 and the NT Seafood Industry training award in 2009 and 2011. Given the success of this training, there was agreement by both DPIR and IMR groups that the research and monitoring aspect of their work should also have a training course associated with it. By providing IMRs with functional science skills this training offered an opportunity for achieving research goals in a cost-effective manner (e.g. Prescott et al., 2016) with the additional benefits of providing community capability development, potentially increased employment opportunities as well as the health and wellbeing benefits associated with working within their communities (Burgess et al. 2009). This science training can also provide the important first steps of building research partnerships to work towards co-management of these resources (e.g. Almany, 2010; Cohen and Steenbergen, 2015; Dobbs et al., 2016).

1.5 Objectives

1. Gain information on stock structure of key tropical reef fish species.
2. Develop Indigenous capability in scientific monitoring and participation in co-management through the development of a certified training program.
3. Identify appropriate spatial scale of management for tropical reef fish based on biological sustainability and sectoral aspirations.

2 Methods

2.1 Stock Structure

2.1.1 Sample collections

All fish samples were collected using a range of sources, including DPIR, WADAF, QDAFF, IMRs, fishing tour operators and various recreational and commercial fishers. Fish caught by research staff and Indigenous rangers were euthanized in ice slurry immediately after capture (CDU Animal Ethics Approval A 13014); for fish caught elsewhere, they were placed on ice or frozen and transported to the laboratory for processing.

In the laboratory, TL and sex of each specimen were recorded. Biological samples were also taken from each specimen for analyses by the respective methods for stock structure determination. For genetic analyses, samples were collected by one of three methods: a clip from the spine of the dorsal fin, a clip at the base of the pectoral fin, or a section of muscle taken near the junction of the spine and skull. Genetic samples were placed in 95% molecular grade ethanol and frozen with the exception of fin clips from fish collected at Halifax Bay that were placed in vials of 20% dimethyl sulfoxide solution in 5M NaCl. For otolith microchemistry analyses, the pair of sagittal otoliths were dissected from each fish, cleaned and rinsed thoroughly, dried and stored in paper envelopes. For parasite analyses, the gills, pharyngeal teeth plates and internal body organs were removed, placed in a labelled bag and frozen for later examination.

From 11 sampling locations across northern Australia, from Roebuck Bay (Western Australia) on the western coast to Vanderlin Islands in the Gulf of Carpentaria, 297 Black Jewfish were collected (Figure 1, Table 1).

From across 13 locations across northern Australia, from Locker Point (in the Pilbara region of Western Australia) to Moreton Bay (south-east Queensland) 342 Grass Emperor were collected (Figure 3, Table 3).

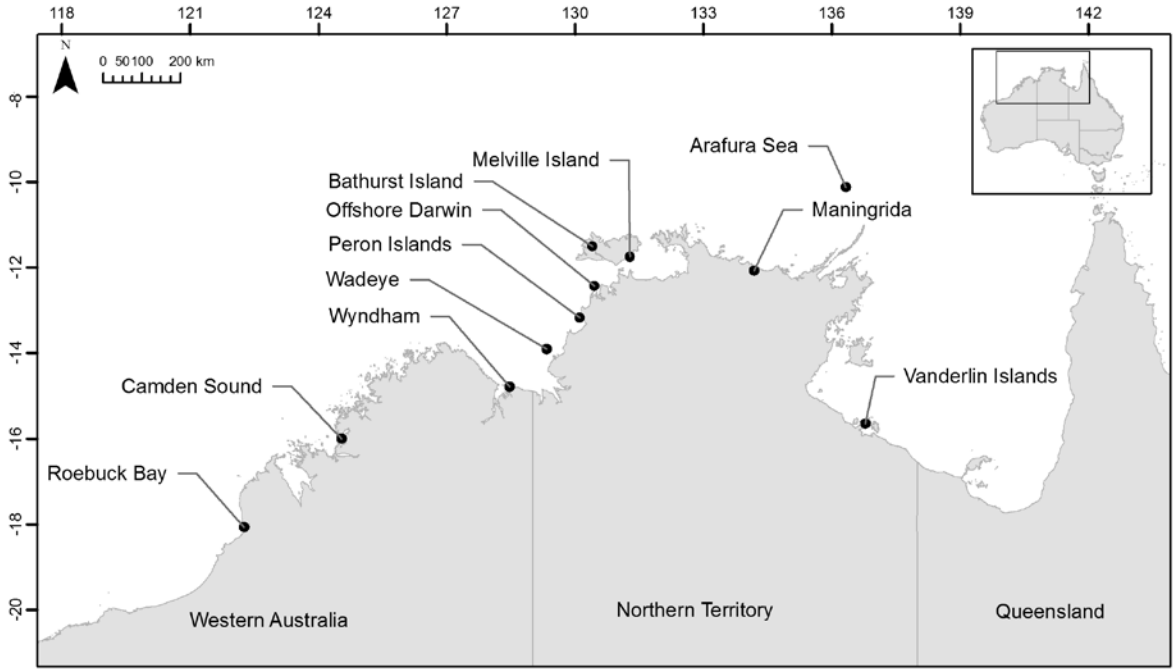

Figure 1. Location of the 11 Black Jewfish sampling sites across northern Australia showing the two jurisdictions (Western Australia and Northern Territory)

From 18 sampling locations across northern Australia, from Camden Sound (Western Australia) to Halifax Bay (north Queensland) 486 Golden Snapper were collected (Figure 2, Table 2). An additional 124 samples were collected for otolith chemistry analysis only from other four locations centred around Camden Sound.

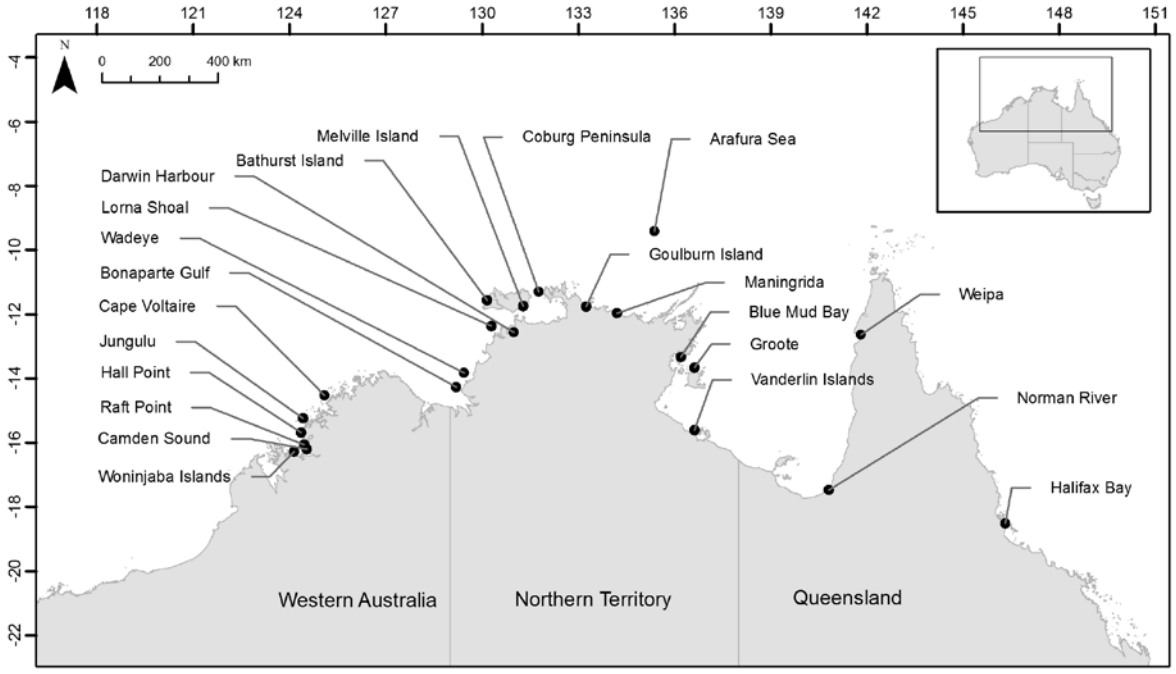

Figure 2. Location of the 22 sampling sites of Golden Snapper across northern Australia showing the three jurisdictions (Western Australia, the Northern Territory and Queensland)

Table 1. Summary of the locations sampled for Black Jewfish separated into jurisdictions, numbers of fish sampled, the date(s) when samples were collected and the mean total length (TL in mm) and age (in years) of fish from each location (see Figure 1) used in this study. Range of TL and age are indicated in bracket after the mean. Number of fish aged is indicated italicised in brackets after the range.

Jurisdiction	Sampling location	Prefix	Sample size	Collection date	Mean TL	Mean age
Western Australia						
	Roebuck Bay	RB	36	Jul, Aug, Oct, Nov 2014 - May, Jun, Jul, Aug 2015	1018 (720-1199)	6 (2-10) *(34)*
	Camden Sound	CS	19	Sep, Oct 2013	647 (520-920)	3 (3-4) *(4)*
	Wyndham	Wy	34	May, Jun 2015	1061 (804-1300)	5 (3-8) *(26)*
Northern Territory						
	Wadeye	Wa	25	Jun, Nov 2014	789 (540-1160)	3 (2-5) *(17)*
	Peron Islands	PI	29	May 2015	N/A	4 (3-5) *(13)*
	Offshore Darwin	OD	17	Oct, Dec 2012 - Jul, Sep 2013 - Mar 2014	608 (395-1150)	3 (2-4) *(8)*
	Bathurst Island	BI	28	Nov 2013 - Sep, Nov 2014 - Aug, Sep 2015	981 (387-1235)	6 (4-8) *(19)*
	Melville Island	MI	30	Aug 2012 - Sep, 2013 - Apr, Aug 2015	646 (405-1170)	2 (2-5) *(26)*
	Maningrida	Ma	30	Aug 2014 - Jun, Jul 2015	746 (420-1210)	3 (2-5) *(17)*
	Arafura Sea	AS	20	Jul 2013	N/A	2 (2-3) *(10)*
	Vanderlin Islands	VI	29	Feb 2014	592 (440-770)	2 (2-3) *(25)*
	Total		297		806 (387-1300)	*4 (2-10) (199)*

Table 2. Summary of the locations sampled for Golden Snapper separated into jurisdictions, numbers of fish sampled, the date(s) when samples were collected and the mean total length (TL in mm) and age (in years) of fish from each location (see Figure 2) used in this study. The range of TL and age are indicated in brackets after the mean. *Indicates sampling locations where only otolith data was collected.

Jurisdiction	Sampling location	Code	Sample size	Collection date	Mean TL	Mean age
Western Australia						
	Camden Sound	CS	30	Sep. 13	386 (240 – 496)	NA
	Woninjaba Islands*	CSWI	48	Sep 2012, Sep 2014	386 (200 – 826)	4.5 (2-17)
	Raft Point*	CSRP	18	Sep 2012, Sep 2013, Sep 2104	450.8 (264 – 765)	5.3 (2-15)
	Hall Point*	CSHP	38	Aug 2012, Sep 2013	404 (267– 710)	4.4 (2-12)
	Jungulu*	CSJU	20	Aug 2013, Sep 2014	630.7(296 – 783)	10.6 (2-17)
	Cape Voltaire	CV	31	Aug. 15	379.8 (260 – 689)	4.5 (2-11)
Northern Territory						
	Bonaparte Gulf	BG	23	Aug-15	518.9 (447 – 569)	9.8 (6-16)
	Wadeye	WA	30	Sept 13, May 14	455 (400 – 560)	5.2 (4-7)
	Lorna Shoal	LS	26	Mar-14	428 (290 – 660)	NA
	Darwin Harbour	DH	25	Aug 13, Mar 14	221 (150 – 315)	2.3 (2-3)
	Bathurst Island	BI	31	Nov-14	368 (247 – 513)	3.4 (2-5)
	Melville Island	MI	25	Aug 12, Sep 13	311 (240 – 410)	3.4 (3-5)
	Coburg Peninsula	CoP	35	Nov 14, Sep 15	465 (322 – 631)	5.2 (2-9)
	Goulburn Island	GI	30	Jun-15	282.8 (200 – 360)	2.6 (2-4)
	Maningrida	MA	16	Aug-14	386.4 (270 – 590)	3.5 (3-5)
	Arafura Sea	AS	31	Mar-15	540.9 (457 – 625)	11.1 (6-30)
	Blue Mud Bay	BMB	29	Mar-15	503 (370 – 765)	5.1 (3-8)
	Groote Eylandt	GE	25	Nov/Dec 13, Jan & Oct 14	541 (360 – 690)	6.2 (3-10)
	Vanderlin Islands	VI	25	Nov 14, Apr 15	408.3 (310 – 645)	4.1 (2-9)
Queensland						
	Normanton	NR	13	Aug-14	630 (396 – 710)	9.4 (3-24)
	Weipa	WE	10	May/Jun 14	430 (355 – 550)	4.3 (3-7)
	Halifax Bay	HB	51	May, Oct, Nov, Dec 14	590.6 (364 – 822)	7.2 (3-12)
	Total		610		438 (150-826	5.6 (2-30)

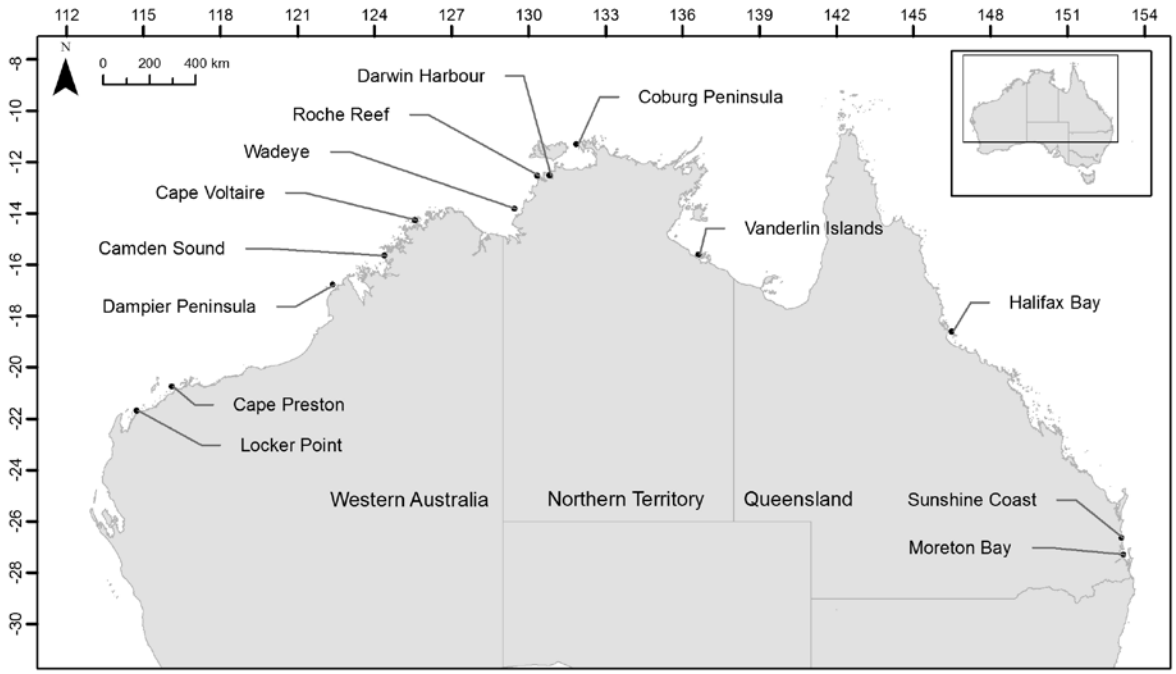

Figure 3. Location of the 13 sampling sites of Grass Emperor across northern Australia showing the three State and Territory Government jurisdictions (Western Australia, Northern Territory and Queensland)

Table 3. Summary of the locations sampled for Grass Emperor separated into jurisdictions, numbers of fish sampled, the date(s) when samples were collected and the mean total length (TL in mm) and age (in years) of fish from each location (see Figure 3) used in this study. The range of TL and age are indicated in bracket after the mean. Number of fish aged is indicated italicized in brackets after the range.

Jurisdiction	Location	Prefix	Sample size	Collection date	Mean TL	Mean age
Western Australia						
	Locker Point	LP	34	Jul-14	351.7 (285-489)	5.8 (3-14) *(30)*
	Cape Preston	CP	35	Jul-14	373 (259-489)	5.8 (2-10) *(30)*
	Dampier Peninsula	DP	28	Oct-13	338.9 (260-477)	4.4 (2-9) *(24)*
	Camden Sound	CS	29	Sep & Oct 2013	306 (220-400)	3.6 (3-5) *(18)*
	Cape Voltaire	CV	30	Aug-15	359.6 (264-427)	5.5 (3-8) *(30)*
Northern Territory						
	Wadeye	Wa	30	Jun & Jul 2015	396.2 (290-440)	7.7 (3-11) *(30)*
	Roche Reef	RR	29	Aug 2013 & Jun 2015	300 (250-395)	3.1 (2-4) *(18)*
	Darwin Harbour	DH	24	Jul & Aug 2015	209.6 (175-250)	2 *(15)*
	Coburg Peninsula	CoP	33	Aug-15	308.8 (230-370)	4 (3-8) *(29)*
	Vanderlin Islands	VI	30	Nov-14	307.9 (245-433)	4.9 (2-7) *(30)*
Queensland						
	Halifax Bay	HB	14	May-14	354.1 (239-405)	7 (4-9) *(14)*
	Sunshine Coast	SC	14	Apr 2013 – Jan 2014	440 (333-547)	8.2 (4-13) *(14)*
	Moreton Bay	MB	12	Jan 2013 – Apr 2014	305.2 (268-356)	3.4 (3-4) *(11)*
Overall						
			342		333.2 (175-547)	5.2 (2-14) *(293)*

2.2 Otolith Chemistry Analyses

2.2.1 Otolith preparation

The left sagittal otolith was selected from each individual and embedded into epoxy resin (West System 105 epoxy resin and West System 206 hardener) with the sulcus facing downwards. A Buehler IsoMet® low speed saw was used to cut transverse sections through the primordium of each otolith at approximately 350 µm thick. Sections were polished with three grades of 3M diamond lapping film (30, 9 and 3µm), rinsed thoroughly with Milli-Q water and air-dried. Otolith sections were mounted onto microscope slides using epoxy resin; once dry, the section mounts were triple-rinsed with Milli-Q water and allowed to dry in a laminar flow cabinet.

2.2.2 Analysis of trace elements

Elemental analysis was performed using the laser ablation-ICP-MS (LA-ICPMS) located at the University of Melbourne, which comprises an Agilent 7700x quadrupole inductively coupled plasma mass spectrometer coupled to a custom-built RESOlution laser ablation system with a HelEx cell. The RESOlution system is constructed around a Compex 110 ArF excimer laser which was operated using a spot size of 72 µm in diameter with laser energy at 2.7 J/cm² and a repetition rate of 5 Hz. Laser software (GeoStar v6.14) was used to digitally plot three ablation areas on each individual otolith section. The first at the primordium (referred to hereafter as "core"), the second area just outside the first opaque zone ~500 µm to ventral side of the core ablation ("near core") and the third at the ventral margin adjacent to the sulcus acusticus ("margin"). The multi elemental data collected from each ablation position is intended to represent the general locations of the larval dispersal phase (core), post-larval juvenile phase (near core), and the sub-adult/adult phase (margin). Ablations occurred inside a sealed chamber in an atmosphere of pure He with the ablated material being transported to the ICPMS in the Ar carrier gas.

A total of 11 trace elements (^{7}Li, ^{25}Mg, ^{23}Al, ^{49}Ti, ^{53}Cr, ^{55}Mn, ^{60}Ni, ^{63}Cu, ^{66}Zn, ^{88}Sr, ^{138}Ba) and the internal standard (^{43}Ca) were analysed from all three ablation zones for each otolith. The laser ablation spot sample consisted of a 20 second blank, followed by an ablation period of 50 seconds, of which the first 5 seconds and the last 1-second were excluded from data integration to allow for signal stabilisation. Data reduction and processing was completed using the trace elements data reduction scheme (Woodhead et al., 2007) of the specialised software package Iolite version 3 (Paton et al., 2011). Subtraction of background ion counts from otolith counts was followed by the normalization of each element to ^{43}Ca and the National Institute of Standards and Technology (NIST 612) glass standard was used as the external calibration standard, which was analysed after every 10 otolith samples to correct for any long-term drift in the instrument.

The limits of detection (LOD) were calculated for each sample from the ablation yield equivalent to 3 x standard deviation (SD) of the blank background measurements. Concentrations of ^{23}Al, ^{49}Ti and ^{53}Cr were <LOD and were not included in the analysis. For all elements, the ratio of element isotope intensity to ^{43}Ca intensity was used to estimate the element:^{43}Ca ratio. These ratios were converted to molar ratios and were expressed as element:Ca molar ratios in mmol mol-1 or µmol mol-1. Finally, the ablated otolith sections were digitally photographed using a Leica M80 stereo dissecting with image analysis software (Image-Pro Plus 7.0) and ablation zones checked for accuracy.

For annual age estimation, each otolith section was examined under a Leica M80 stereo dissecting microscope at 12.5X magnification with reflected light and a black background. Increments were counted along the ageing transect from the primordium to the ventral edge of the otolith adjacent to the sulcus according to the methods of Marriott and Cappo, 2000 (Golden Snapper); Ayvazian et al., 2004 (Grass Emperor); Phelan, 2008 (Black Jewfish).

2.2.3 Statistical analysis

To test the validity and relevancy of the current jurisdictional management units the data for each species was separated into regions based on jurisdictional management boundaries for analyses.

Black Jewfish were separated into three management regions: Western, Darwin and Arnhem/Gulf. The Western region includes all of the Western Australian locations (RB, CS and Wy) as well as Wadeye (Wa) from the NT; Wadeye was included due to its proximity to the nearest Western region location of Wyndham. The Darwin region includes all the NT locations from Wadeye to Melville Island (Wa, PI, OD, BI and MI). The Arnhem/Gulf region includes all the Arnhem Land and Gulf of Carpentaria populations of the NT (Ma, AS and VI) as well as Melville Island (MI) due to its proximity to the nearest Arnhem/Gulf region location of Maningrida.

For Golden Snapper, the data was separated into five management regions: Western, Darwin, Arnhem, Gulf and East Coast. The Western region includes all of the Western Australian locations (CS, CSWI,

CSRP, CSHP, CSWI, and CV) as well as Bonaparte Gulf (BG) from the NT; Bonaparte Gulf was included due to its proximity to the nearest Western region location of Cape Voltaire. The Darwin region includes all the NT locations from Bonaparte Gulf to Goulburn Island (BG, Wa, LS, DH, BI, MI, CoP and GI). The Arnhem region includes the three locations across the northern coast of the NT from Goulburn Island to the Arafura Sea (GI, Ma, and AS). The Gulf region includes the western Gulf of Carpentaria locations (BMB, GE, VI) as well as the Arafura Sea and the eastern Gulf of Carpentaria locations of Normanton (NR) and Weipa (WE). The East Coast region includes all the Queensland locations from Normanton to Halifax Bay (NR, We and HB).

For Grass Emperor, the data was separated into three management regions, which coincided with the State or Territory of collection: WA, NT, and Queensland. Due to the large distances between adjacent collection locations between the management regions, it was assumed that it would be highly unlikely for there to be exchange of individuals at this scale so overlapping collection locations were not undertaken in the analyses as for the other species.

All multi-elemental otolith data was examined and subsequently $\log_{10}$ transformed to meet assumptions of normality and homogeneity of variance (Quinn and Keough, 2002). Spatial variation in otolith core, near core and margin chemistry among regions and locations within regions were investigated using single-factor multivariate analysis of variance (MANOVA). The Pillai's trace statistic was reported as it is considered the most robust (Scheiner, 1993). Correlation between total length of fish at each of the collection sites and each of the otolith elemental ratios measured were tested using Pearson's parametric correlations. Linear discriminant function analysis (LDFA) was conducted to provide statistical and visual indication of the similarities within the multi-elemental otolith chemical signatures among samples at the regional spatial scale. Standardised coefficients for the discriminant functions were used to measure which elements contributed most to group separation. Results of the LDFA were plotted as graphs of the first and second discriminant axes, with 95% confidence interval (CI) ellipses established around the centroid. Significant statistical differences between locations occurred when there was no overlap between the 95% CI ellipses. Classification success for the LDFA was calculated by jack-knife cross-validation matrices. All the above analyses were conducted using R (R Core Team 2015).

The otolith jack-knife cross-validation matrices were analysed by means of randomisation tests to determine if the jack-knifed classification estimates were significantly different from random and were conducted using code supplied in White and Ruttenberg (2007). A script was run in Matlab (version 2013a) to calculate the classification success rates and associated P values (probability of obtaining the observed classification rate due to chance alone) using uniform prior probabilities and 10 000 randomisations of the data (White and Ruttenberg, 2007).

2.3 Parasites

2.3.1 Parasite collection

Once defrosted, gills were removed, separated into individual arches and washed in water (vigorously shaken to dislodge parasites). Gill arches were then examined individually under a dissector microscope; any parasites still attached were removed. The length of the gill arch was opened for examination and any parasites encountered were removed as gently as possible.

The mouth of the fish (i.e., pharyngeal teeth plates and the tissue behind them) was also washed before examination under a dissector microscope. Parasites found attached to the pharyngeal teeth plates (e.g., *Encotyllabe* sp.) were gently grasped with forceps and pulled. The tissue behind the pharyngeal plates was examined. Encysted parasites were easily removed; Philometrid nematodes were dissected from between tissue layers.

The gill and pharyngeal teeth wash was allowed to settle, then the supernatant was poured off, discarded and the sediment examined under a dissector microscope for parasites that had been removed in the wash.

Examination of the internal organs involved the separation of the stomach and intestinal tract from the mesenteries and associated organs. The liver, swim bladder and spleen were not examined for parasites. The stomach and intestine was each slit along its length and washed (as above) for parasite examination. Philometrid nematodes and didymozoid digeneans in the stomach wall were visible through the tissues and were dissected out as carefully as possible.

The supernatant of the intestinal washings was decanted as above. If there was a large amount of intestinal content (i.e., partly digested food), the process was repeated until the remaining sediment was clear enough to be able to find parasites. The mesenteries that connect the internal organs were removed from the organs, washed and examined under a dissector microscope. Encysted parasites were removed from the mesenteries. All encysted parasites were released from their associated cysts for identification prior to fixation. For female fish, ovaries were slit along their length and examined under a dissector microscope for the presence of philometrid nematodes.

Representative samples of parasites from each fish host and collection location were placed directly into 70% ethanol.

2.3.2 Parasite identification

As parasites were collected, they were identified as far as possible and counted within those identifications. The identifications and counts were re-checked after all dissections had been completed. Parasites were identified to the lowest possible taxonomic unit; some were able to be identified to species but many could not be identified beyond family in the time scale of the project. While we are confident in the taxonomic separation of the parasites into their various groups based on morphological examination, further study will undoubtedly find different, new or cryptic species among the larger groupings used here. For example, the *Caligus* specimens collected from Golden Snapper have subsequently been identified as two new species (Geoff Boxshall, pers. Comm.); however, this separation was not identifiable at the time of collection so they have not been subdivided for analysis.

Some groups of parasites, however, could not be differentiated into different species during the time scale of this project. For example, the opecoelid digeneans are currently under a taxonomic review, particularly for the *Allopodoctyle* and *Pseudoplagioporus* genera, which were commonly encountered in Grass Emperor (Storm Martin, pers. Comm.) and were subsequently excluded from the analyses. Similarly, other parasites, such as larval *Aniskidae* spp. were excluded from Black Jewfish analyses due to difficulties in counting of specimens, with many hundreds often found encysted within a single mass within the mesenteries of the body cavity.

Where a relevant expert in a particular parasite group had been identified and was able to assist with identifications, parasite specimens were sent for examination. The relevant experts who provided assistance with identifications of parasites in this study are listed in Appendix 4. For parasites not sent elsewhere, identification was completed as far as possible by Dr D. Barton. The following techniques were used for examination of these particular parasitic groups:

Monogeneans, digeneans and cestodes: specimens were stained in Aceto-Carmine, dehydrated in a graded ethanol series, cleared in xylene and mounted in Canada balsam as permanent slides. Some specimens were mounted unstained. Some specimens of monogeneans were mounted in lactophenol which dissolves the soft tissues of the organism, leaving the sclerotised haptoral armature. Coverslips of specimens mounted in lactophenol were ringed with nail varnish to seal the slide and make a permanent mount.

Nematodes: specimens were mounted as temporary wet mounts in lactophenol or glycerol. Upon completion of the required examination and measurements, specimens were returned to 70% ethanol.

Pentastomes: specimens were mounted as temporary wet mounts in lactophenol. Some specimens were mounted whole, while other specimens were partly dissected for the removal of the anterior hooks required for identification. Upon completion of the required examination and measurements, whole specimens were returned to 70% ethanol. Coverslips of dissected specimens were ringed with nail varnish to seal the slide and make a permanent mount.

Parasites were identified by morphological examination of whole mounted material. Published records and keys in scientific papers assisted in identification, with distinctive characters being used to classify parasites to family, genus or species. In addition, voucher and type material was borrowed from collections within Australia for comparison with material collected in this study. Drawings of specimens were made with the aid of a camera lucida and measurements were made using an ocular micrometre. Photos were taken using a 9MP Microscope Digital Camera (AmScope Model MU900).

Small sections of relevant parasites were collected and placed in 100% ethanol for future DNA analysis. Initial genetic analyses have been undertaken for some parasites (conducted by Dr Jess Morgan, Queensland Alliance for Agriculture and Food Innovation, University of Queensland, Brisbane). Voucher specimens of parasites will be deposited within the collections of the Museum and Art Gallery of the NT , the Australian Helminthological Collection and Marine Invertebrates section of the South Australian Museum, the Parasitology Collection of the Queensland Museum, the Helminthological Collection of the Czech Republic Institute for Parasitology and the Natural History Museum, London.

2.3.3 Parasite descriptions

A number of new species of parasites were identified during this study. Descriptions have already been published for a number of philometrid nematodes collected from both Black Jewfish and Golden Snapper (Moravec and Barton, 2015; Moravec and Barton, 2016). Barton and Morgan (2016) also described the first report of nymphal sebekid pentastomes from fish in Australian waters. Details of other species are at different levels of the publication process.

2.3.4 Statistical analysis

For each species, data was analysed overall (all locations, independent of State) and by region (determined by current jurisdictional management boundaries) as for the otolith chemistry analyses.

Summary statistics were compiled for each location and included mean abundance (total number of individuals of a particular parasite per sample divided by the total number of hosts examined, including uninfected hosts) and prevalence (number of hosts infected with a particular parasite divided by the number of hosts examined, expressed as a per cent) for each of the parasite species, following the terminology of Bush et al. (1997). Parasites were identified as potential biological markers if they exhibited a prevalence ≥ 10% in at least one sample location component species (Bush et al., 1990), were relatively easy to find, identify and count. The natural logarithm of the parasite +1 [ln(x+1)] was used to minimise the variance of the abundance data. These transformed data were used throughout the analyses. Parasites that were collected but subsequently omitted from the analyses are listed in Supplementary Data 1.

Pearson's correlations were used to explore the relationships between the total lengths of fish with individual parasite species. For parasites that showed a significant correlation, parasite abundances were corrected to the mean host TL as described in Moore et al., (2003). No correction was made if the parasite abundance was zero. This was not performed for Black Jewfish as at least two locations did not have TL data for fish collected and it was determined best to leave all data uncorrected.

Spatial variation in parasite assemblages among regions and locations within regions were investigated using single-factor MANOVA. As for the otolith chemistry analyses, the Pillai's trace statistic was reported as it is considered the most robust (Scheiner, 1993).

LDFA (R Core Team, 2015) was conducted to provide a visual indication of the similarities of the parasite assemblages among samples. Results of the LDFA were plotted as graphs of the first and second discriminant axes, with 95% CI ellipses established around the centroid. Significant statistical differences occurred when there was no overlap between the 95% CI ellipses. A jack-knife reclassification success matrix, indicating overall per cent correct for fish classified to each location, as well as the number of fish classified across the locations examined, is presented.

In accordance with Poulin and Kamiya (2015), comparison of the calculated per cent correct classification (by LDFA) was compared against the "proportional chance criterion", which is the expected proportion of fish classified correctly based on chance alone. This allows a benchmarking of the performance of the classification.

2.4 Genetic Analyses

2.4.1 Microsatellites

Genomic DNA from samples from all species for genotyping was extracted using ISOLATE II Genomic DNA Kit (Bioline) following the manufacturer's instructions. This resulted in 100 µL of eluted DNA for each sample. All the DNA extracts were quantified using the Qubit v3 (ThermoFisher) fluorometric machine.

The potential for null alleles, large allele dropout and stuttering to interfere with scoring accuracy was evaluated for each microsatellite locus in each sample using Microchecker 2.2.3 (Van Oosterhout et al., 2004). Summary statistics for microsatellite loci, including the number of alleles, allelic richness, expected and observed heterozygosity and fixation indexes were obtained for each sampling locality using GenAlEx 6.5 02 (Peakall and Smouse, 2006). Tests of conformance of genotypic proportions to Hardy-Weinberg equilibrium expectations and tests of genotypic equilibrium between pairs of microsatellites (linkage disequilibrium) were carried out for each sample locality, using an exact probability test as implemented in Genepop 4.5 (Rousset, 2008). The exact test was estimated using a Markov Chain that employed 1000 dememorisations, 500 batches and 1000 iterations per batch. Fixation indices (FST) between pairs of sample localities were estimated as implemented in Arlequin 3.5.2.2 (Excoffier and Lischer, 2010) to identify possible spatial boundaries to genetically cohesive populations among sample locations.

In order to assess whether localities could be treated as independent genetic units and see if we had mixed genotypes between close locations, we performed population assignment using the Bayesian model-based clustering program Structure (Pritchard et al., 2003). Structure determines the posterior probability that an individual's genotype originates from its capture location and estimates the proportion of its genotype that is derived from any of the included locations. We tested for the likely number of clusters within the dataset from two to the number of sampling locations (k=2-11). The analysis was run 10 times for each k tested with 100 000 generations after 100 000 of burn-in. We performed the analysis using the no admixture model, correlated allele frequencies (Falush et al., 2003) and the sampling location as a prior to improve the program performance and ability to find the clusters (Hubisz et al., 2009). The results were visualised in Pophelper (Francis, 2016) and the optimal number of clusters was estimated using the second order rate of change between runs of different k (ΔK) as described by Evanno et al., (2005). However, given the large degree of uncertainty around the statistical estimation of k (Meirmans, 2015) we looked at all the clustering patterns that warranted a biological interpretation. A further traditional population assignment was performed on a reduced subset of the data to assign individuals between adjacent or geographically close locations using Genepop. We assessed the per cent of genetic variance explained by the groupings from Structure and the pairwise FST results using an analysis of molecular variance (AMOVA) as implemented in Arlequin. The significance of differentiation was

determined by permutation of 22000 replicates. To test whether spatial patterns for each species is constrained by a pattern of isolation by distance (IBD), we performed using a Mantel test (Mantel, 1967) of FST/ (1-FST) (G) versus geographic (D) distances among locations using Arlequin.

2.5 Integration

This study used multiple methods for three species in a holistic approach to determine stock structure (see Table 4). To integrate the potentially contrasting results of the different techniques for each species we used the stock differentiation matrix (SDM) described by Welch et al., (2015). This enabled clear and simple visualisation of the complex spatial comparisons made across the different techniques, thereby facilitating interpretation and conclusions about appropriate spatial management units through pooling adjacent non-significantly different sampling locations within the management regions identified in 2.2.3. If at least one technique showed differences between sampling locations, they were considered separate stocks. If sampling locations showed no differences in any technique they were considered a joint stock. This also provided a parsimonious explanation of the spatial structure of the respective species in a way that is potentially more meaningful to fisheries managers and other stakeholders by taking into account the different spatial and temporal scale that each method informs (Welch et al., 2015). To further facilitate the description of each species stock structure for fisheries managers, we also developed conceptual diagrams for each species based on the integration of results.

Table 4. Numbers of specimens of each fish species that were used across the three methods in this study

Fish species	Total number collected	Number used for otolith analyses	Number used for parasite analyses	Number used for genetic analyses
Black Jewfish	297	286 (96.3%)	289 (97.3%)	284 (95.6%
Golden Snapper	486*	462 (95.1%)	480 (98.8%)	444 (91.4%)
Grass Emperor	342	329 (96.2%)	341 (99.7%)	279 (81.6%)

*Only the fish collected from locations where all three techniques were used are included in this total

2.6 Indigenous Training

2.6.1 Background engagement with communities

The DPIR's Indigenous Development Unit (IDU) is responsible for engaging with Indigenous communities to support their development of sustainable and culturally appropriate business and employment opportunities in fisheries management, research, development, training, industry participation and resource protection (DPIR, 2014). The IDU primarily consults with IMR groups in the larger Indigenous communities but also liaises with Indigenous enterprise groups and land councils on broader issues (e.g. allocation of marine resources and access by other fishery sectors to Indigenous waters). Dating back to the establishment of IDU, one of the primary areas of interest by these groups was to be involved in the management of the aquatic resources in waters adjacent to their communities (e.g. Muller, 2008). Initially, this led to a focus on developing the compliance capacity of IMRs. However, since 2010 these discussions have focussed more on the development of Indigenous fishing licences for communities. Given that some of the intended target species are reef fish species that have been identified as being vulnerable (e.g. Saunders et al., 2014), a preliminary data collection program was developed whereby IMRs collected biological samples from a suite of reef species either during routine patrols or from frames collected from recreational or commercial fishers. This training was conducted with IMRs from Groote Eylandt, Nhulunbuy, Elcho Island, Maningrida, Borroloola and Port Keats. One of the key components of this project was that the IMRs were trained to measure length, determine sex and maturity as well as

extracting otoliths for ageing by DPIR. This information was then provided back to researchers for use in stock assessment of these species. While this program was relatively successful with the collection of information for the inclusion in stock assessments (e.g. Grubert et al., 2013), there was minimal engagement of the IMRs on the purpose of the collection and how this information was used in the management of these species. Additionally, this initial approach provided a very specific set of skills for the community members to learn which did not have broader application outside of the collection of fish biology specific data.

2.6.2 Course development

The development of a specific training course in data and sample collection methodology both in the field and the laboratory was initiated through discussions between DPIR and seven IMR groups during 2012. The course content development was initiated in 2013 and was finalised in early 2014. The content was initially developed by IDU and DPIR scientists. The content was then discussed with IMR groups to ensure that it contained information on the areas of research and monitoring that they wanted to be trained in. IDU then worked with Labtech Training, which is the registered training organisation engaged to deliver the course. Labtech Training ensured that the course content met the Certificate II level under the Australian Vocational Education and Training scheme. While the course was based on the Certificate II in Sampling and Measurement (MSL20109), the content was customised to suit the training needs. The course that was developed contained seven units that were to be completed by students within a two-week period in two five- day blocks. The course development was able to occur fairly rapidly given that IDU had developed a compliance course described above, so many elements of the approach for the successful delivery of the current course had already been established. This approach is to ensure that the course has relevant content with presentations that are largely pictorial in nature and include examples that the participants can relate to during both theoretical and practical components and to provide a numeracy and literacy mentor to accommodate participants where English is not their first language. Another critically important element that has led to the successful training of Indigenous students in the previous compliance training by IDU is providing Indigenous students appropriate accommodation. Because all participants comprised a broad age range (20-50+ with a ratio of 10 males to seven females) of Indigenous rangers who flew or drove in from remote communities they could have easily felt out of place and disconnected from their communities. To ensure that students were supported through their studies, they were accommodated in a specific training facility (Nungalinya College in Darwin) for Indigenous students that provided them with all of their food and accommodation needs in an environment that was much more similar to their communities compared with typical hotel style accommodation.

2.6.3 Certificate II in sampling and measurement

The course was conducted during May 2014 and involved 17 IMRs from seven Indigenous communities located throughout the NT that were chosen by their respective community ranger coordinators. While the course was designed to be delivered to any Indigenous community member, IMRs were chosen for the first course as they were the first point of contact that were likely to put the skills to use to assist with the collection of research information from their communities.

The seven units of the course included three administrative units: 'Work within a laboratory/field workplace' (MSL912001A), 'Participate in laboratory/field workplace safety' (MSL943002A) and 'Maintain the lab/field workplace fit for purpose' (MSL933001A). The course taught how to work in a safe and responsible manner in the field or in the laboratory (Table 5). While they were important for ensuring safe working practices, obtaining the qualification and being able to assimilate into research agency style employment, they were not the most critical part of the course in terms of teaching participants about rigorous collection of scientific data and so will not be discussed further.

The unit titled 'Participate in environmentally sustainable work practices' (MSAENV272B) detailed how the collection of scientific information led to inform managers what level of restriction on harvest was

required to ensure that populations remained sustainable. This was a critical unit for participants understanding the link between information collection and sustainable management of resources. To provide this context, the example of the unsustainable fishing of coastal reef fish species around population centres (e.g. Saunders et al., 2014) was used as it is currently one of the highest priority fishery management issues in the NT. However, there were also presentations on data collection leading to sustainable management of turtles, dolphins, dugongs and whales throughout the course. The concept of populations responding to harvest and collecting information to better understand the health of a population were familiar concepts to all the participants as their communities still participated in traditional harvest of aquatic resources that incorporated knowledge of the biology of these species that was used to limit their harvest (e.g. only taking male turtles during the spawning season). Consequently, while the scientific monitoring and data techniques they were about to be taught were far less familiar, the link to their own understanding of species biology and how populations operated meant that the participants could see the relevance of collecting scientific information.

The other two units that were important in teaching the participants to understand scientific data collection were 'Conduct routine site measurements' (MSL972001A) and 'Collect routine site samples' (MSL952001A). These two units had the most time spent on them and the largest practical component as gaining skills in these areas was seen as the most important part of the course to ensure that any data collected by participants in the future was as accurate as possible. The practical components involved the full chain of data collection including data sheet design, recording data accurately and legibly on data sheets, accurately reading and recording of measurements when using such equipment as callipers or scales and accurate transcription of data sheets to computers or tablets. For the measuring component a variety of fish species were provided to get accurate length measurements in centimetres and weight measurements in grams. Additionally, students were required to accurately measure volumetric samples as an example of collecting such information as water samples. The sample collection component involved learning how to dissect a variety of fish species and extract biological samples such as otoliths, tissue for genetic samples, sex, maturity and gonad stage information. The overarching message for this component was the importance of ensuring that samples were not contaminated, were marked clearly with information that linked each sample back to the original data sheets and that the appropriate preservation/storage methods were used to ensure that samples could be later analysed in the laboratory.

While the course content was heavily biased towards collecting biological samples and measuring fish, it was highlighted that the basic principles for these collections were exactly the same for any scientific data collection and only the specific techniques, such as dissection and knowledge of fish anatomy, would differ amongst the different disciplines. The assessments for the course were all either practical or verbal in nature (Table 5) and literacy and numeracy mentors were present, which is essential to appropriately assess students who mainly have a language other than English as their first language.

Table 5. Unit description of Certificate II Sampling and Measurement (MSL20109)

Unit Description	Content	Method of delivery	Method of assessment
MSL943002A Participate in laboratory workplace safety	-Workplace induction -Duty of care (employer and employee safety responsibilities) -Risk identification and mitigation -Legislation and reporting	Verbal/visual MS PowerPoint® presentation -Practical (Hazard ID and Incident report forms)	-Verbal
MSL912001A Work within a laboratory/field workplace	-Expansion of risk identification and mitigation from first unit -Identification of specific workplace risks (manual handling, weather, sharps) -Risk mitigation methods (training, Personnel Protective Equipment	Verbal/visual MS Powerpoint® presentation -Practical (Using PPE, ergonomic lifting)	-Verbal
MSL933001A - Maintain the laboratory/field workplace fit for purpose	-Hazardous substances -Material Safety Data Sheets -Hazchem system of chemical identification -Safe use of chemicals and chemical storage	- Verbal/visual MS Powerpoint® presentation	-Verbal
MSL913001A Communicate with other people	-Methods of communication -Identifying situations for using different methods -Issues arising from poor communication	-Verbal/visual MS PowerPoint® presentation	-Verbal
MSAENV272B Participate in environmentally sustainable work practices	-Ensuring optimal use of workplace consumables (e.g. paper data sheets) -Background of resource management -Examples of fisheries management and data that underpins management systems	-Verbal/visual MS Powerpoint® presentation -Visual video of fisheries research and marine ranger monitoring	-Verbal
MSL972001A Conduct routine site measurements	-Measurement types -Linear measurement methods (e.g. rulers, callipers) -Weight measurement -Measurement accuracy (e.g. parallax error) -Recording measurements on data sheets -Basic data interpretation (e.g. taking an average)	-Verbal MS PowerPoint® presentation -Practical measuring mud crab carapace width and weight	-Verbal -Practical accurate measuring and weighing
MSL952001A Collect routine site samples	-Why samples are collected -Sampling equipment -Reducing risk of cross contamination -Correct labelling of samples	-Verbal MS PowerPoint® presentation -Practical fish dissection to collect otoliths and tissue samples	-Verbal -Practical fish dissection for sample collection and labelling

3 Results

3.1 Black Jewfish

3.1.1 Otolith chemistry

A total of 286 otoliths were examined for multi-elemental chemistry signatures. The concentrations of most trace elements varied among and within region, location and life history stage. Concentrations of ^{23}Al, ^{49}Ti and ^{53}Cr were <LOD and were not included in the analysis. Mean concentrations for each trace element analysed are presented in Supplementary Data 2. Six trace elements showed elevated concentrations in the core, which gradually decreased towards the margin. The only element to have increased concentration at the near core was ^{138}Ba, and ^{88}Sr was the only element that displayed a slight increase in levels towards the margin.

The multi-elemental fingerprint of the core, near core and margins differed significantly among the three broad-scale regions (Western, Darwin, Arnhem/Gulf) and among locations within each of the three regions (MANOVA, p<0.001, Table 6). This suggested population structuring of Black Jewfish among locations within each region across all life history stages.

Table 6. Results of the multivariate analysis of variance (MANOVA) investigating the spatial variability in otolith core, near core and margin microchemistry of Black Jewfish at two spatial scales: among and within each region df = degrees of freedom; *** = a p<0.001

		Pillai's trace			F		
Source	**Source, error df**	Margin	Near core	Core	Margin	Near core	Core
Region	80, 2200	1.80	1.04	0.79	7.973***	4.101***	2.999***
Locations (Western)	24, 291	1.11	0.88	0.55	7.120***	5.006***	2.710***
Locations (Darwin)	32, 468	1.08	0.72	0.56	5.392***	3.203***	2.388***
Locations (Arnhem/Gulf)	24, 294	1.27	0.59	0.81	8.992***	2.997***	4.545***

Linear DFA was used to predict collection location based on otolith multi-elemental composition. Average classification success among all locations was 54% in the margin, 31% in the near core and 26% in the core (Table 7). Classification success increased significantly when using the regional clustering. Average accuracy of classification was greatest for the margin with 71% in the Western region, 57% in the Darwin region and 74% in the Arnhem/Gulf region. The margin classification rate was the highest for the offshore Arafura Sea location (95%) and the lowest for the offshore Darwin location (12%). Average accuracy of classification for the near core was 57% in the Western region, 44% in the Darwin region and 38% in the Arnhem/Gulf region. The near core classification rate was the highest for Wyndham location (73%) and the lowest for the offshore Darwin location (18%). The average accuracy of classification for core was 46% in the Western region, 42% in the Darwin region and 47% in the Arnhem/Gulf region. The core classification rate was the highest for the Roebuck Bay location (65%) and the lowest for the Camden Sound location (17%).

The scores of the first two discriminant functions of the multi-elemental signatures of otolith near core and margin variations were plotted to visually represent the spatial distribution of the variation within each region (Figure 4). The absence of overlapping between the 95% CIs in the multi-elemental signatures of fish from different locations within each region was used as a statistical tool to evaluate the discriminant power of the otolith multi-elemental signatures (Table 7). The otolith multi-elemental signatures of the margins could discriminate more locations than the near core signatures. All the locations from the Western region could be discriminated by the margin; locations of Camden Sound and Wyndham could be discriminated in the near core signature leaving undifferentiated the pair Roebuck

Bay-Wadeye. In the Darwin region, the margin could discriminate Peron Island and Bathurst Island, whereas the near core only Peron Island was discriminated by the near core. The location pairs of Melville Island-Darwin offshore and Wadeye-Darwin offshore were overlapping in the margin; Wadeye-Darwin offshore, Melville Island-Darwin offshore and Melville Island-Bathurst Island were overlapping in the near core. All locations from the Arnhem/Gulf region could be discriminated by the margin; the offshore location of the Arafura Sea could be discriminated in the near core leaving undifferentiated the pairs Vanderlin Islands-Melville Island and Maningrida-Melville Island (Figure 4, Table 7).

Table 7. Jack-knife reclassification success of the linear discriminant function analysis (DFA) for the overall otolith core, near core and margin chemistry of Black Jewfish sampled from (a) all locations (b) four locations in the Western region (c) five locations in the Darwin region and (d) four locations in the Arnhem/Gulf region. Data is presented as the % of individuals that reclassify to their collection location; *** indicates that classification success rates are significantly different from random with a $p<0.001$.

		Otolith margin	**Otolith near core**	**Otolith core**
	n	% correct	% correct	% correct
(a) Among regions				
All Locations	286	54	31	26
(b) Within the Western region				
Roebuck Bay	34	76	50	65
Camden Sound	18	67	61	17
Wyndham	30	77	73	53
Wadeye	24	58	42	33
Total	*106*	*71****	*57****	*46****
(c) Within the Darwin region				
Wadeye	24	33	38	33
Peron Islands	29	93	62	59
Offshore Darwin	17	12	18	18
Bathurst Island	27	63	48	52
Melville Island	29	62	41	38
Total	*126*	*57****	*44****	*42****
(d) Within the Arnhem/Gulf region				
Melville Island	29	79	41	41
Maningrida	30	47	40	40
Arafura Sea	20	95	25	55
Vanderlin Islands	28	82	43	54
Total	*107*	*74****	*38****	*47****

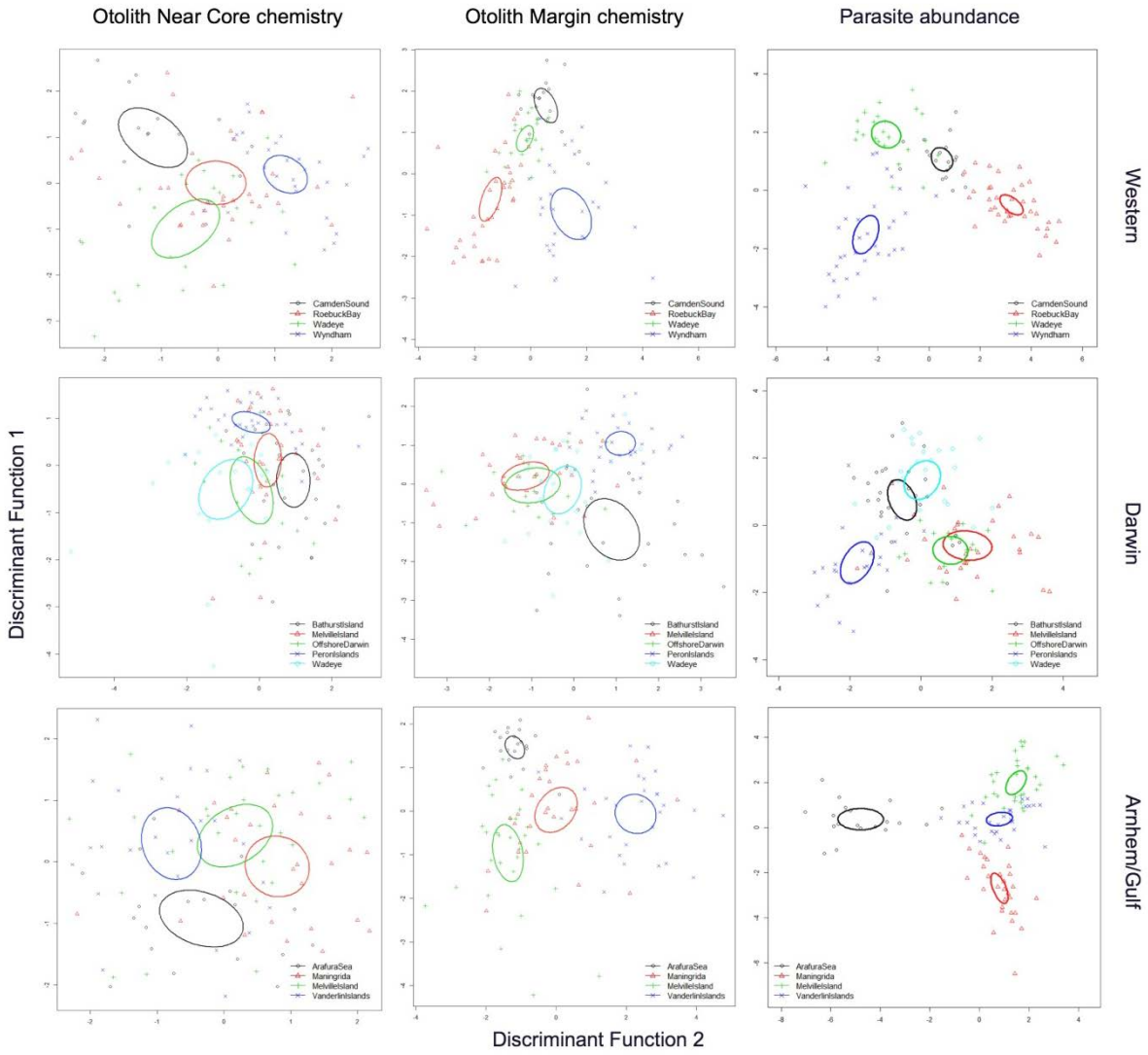

Figure 4. Plots of the first two discriminant function scores showing spatial variation in the parasite assemblage and the multi-elemental otolith near core and margin signatures of Black Jewfish collected from 11 locations within three regions: Western region, Darwin region and Arnhem/Gulf region. Ellipses are 95% CI around the group centroid for each location within each region and data points represent individual fish.

3.1.2 Parasites

A total of 289 Black Jewfish were examined for the parasitology component of this study. Overall, all fish were infected with at least one parasite individual: 44 different parasites were identified. Of these, 11 were excluded from the analyses based on prevalence and a further four groups were excluded based on issues with identification and/or enumeration (Supplementary Data 1). The remaining parasites used in subsequent analyses are presented in Supplementary Data 5. Mean parasite species richness was 5.8 (range 1-12) and mean abundance 57.3 (1-653) parasite individuals per host. The parasite assemblage differed significantly among the three broad-scale regions (Western, Darwin, Arnhem/Gulf) and among locations within each of the three regions (MANOVA, $p<0.001$, Table 8).

Table 8. Results of the multivariate analysis of variance (MANOVA) investigating the spatial variability in parasite assemblage of Black Jewfish at two spatial scales: among and within each region

Source	Source, error df	Pillai's trace	F
Region	10, 278	4.24	6.580***
Locations (Western)	3, 111	2.07	8.748***
Locations (Darwin)	4, 117	1.61	3.030***
Locations (Arnhem/Gulf)	3, 103	2.28	12.807***

df = degrees of freedom; *** = p<0.001.

As for the otoliths, a linear DFA was used to predict collection location based on the parasites assemblage. The overall parasite assemblage successfully reclassified 67% of fish back to their collection location. Prior probabilities based on random chance were calculated following Poulin and Kamiya (2015) and predicted that 10% of the fish would be correctly classified. Compared with random, a classification average of 67% is a great improvement (Table 9). Separation of the analyses into regions gave higher resolution with 81% for the Western region, 56% for the Darwin region and 89% for the Arnhem/Gulf region (Table 9). The reclassification success was the highest for Vanderlin Islands (97%) and the lowest for Bathurst Island (43%). For each of the regions examined, the reclassification success, based on the first two discriminant functions and the parasites that contributed the most to these weightings, are presented in Supplementary Data 7. Nine parasite species were the most heavily weighted across the regions: *Stephanostomum* sp., *Dasyrhynchus* sp. and *Pterobothrium* sp. 1 were the most common parasites to affect the weightings.

The scores of the first two discriminant functions of the parasite assemblage data were plotted to visually represent the spatial distribution of the parasites variation within each region (Figure 4 – see above). The absence of overlap between the 95% CIs in the parasite assemblages of fish from different locations within each region was used as a statistical tool to evaluate the discriminant power of the parasite assemblage data. The parasite assemblages could discriminate fish from all the locations within the Western and Arnhem/Gulf regions. Within the Darwin region, the pairs Wadeye-Bathurst Island and offshore Darwin-Melville Island were overlapping and therefore could not be discriminated using parasite assemblages (Figure 4, Table 9).

3.1.3 Genetics

Genotypes from 11 microsatellites were obtained for 284 individuals of Black Jewfish with 2.15% missing data (Prd012, Prd023, Prd044, Prd042, Prd018, Prd045, Prd046, Prd020, Prd036, Prd049 and Prd024 (Taillebois et al., *In Press*). The number of alleles per locus ranged from 5 (Prd046) to 21 (Prd012) (Supplementary Data 8). Microchecker indicated the possible occurrence of null alleles at location Ma and RB for locus Prd012, at OD for locus Prd020 and at CS for locus Prd018 with possible stuttering or scoring errors for the latter. As there was no evidence of null-alleles at other locations for these loci, all the raw data was checked and we proceeded without removing loci or locations from the dataset. There was only one significant result out of 55 tests for linkage disequilibrium between pairs loci (Prd049 x Prd020 for population CS, Ma and MI only) and overall deviation from the Hardy-Weinberg equilibrium (HWE) was detected at a single locus Prd012 (p-value<0.05) that was surprising given the small difference between H_O and H_E (0.866 vs 0.876). Looking at the deviation from HWE by locus for each population, only seven out of 121 were found to be significant. Heterozygosity was moderate to high for all loci across all locations (0.659 +/- 0.179) and generally similar to expectations (around 0.7 for marine fish) (DeWoody and Avise, 2000) (Supplementary Data 8).

A pattern of genetic differentiation with low but significant population-pairwise FST (range 0.009-0.054) was observed (Table 10). The pattern revealed that three locations in the western part of the sampling area (RB, CS and Wy) and two locations in the eastern part of the sampling area (AS and VI) were genetically distinct from almost all other locations surveyed in the study. By contrast, the five locations

(Wa, PI, OD, BI MI and Ma) in between formed an undifferentiated group that presented only 1/25 significant pairwise FST within the group. The pairwise FSTs were re-calculated after each step of an iterative approach consisting of pooling adjacent locations that showed no significant differentiation with the nearest location and all the others included in the group. The first round that showed an unambiguous pattern of genetic structuring consisted of the five following groups: RB (Group A), CS-Wy-Wa (Group B), PI-OD-BI-MI-Ma (Group C) AS (Group D) and VI (Group E). The comparisons between Groups B and C and Groups D and E were significant but had higher p-values than all the other comparisons between groups (Table 11).

Table 9. Jack-knife reclassification success of the linear discriminant function analysis (DFA) for the overall parasite assemblage of Black Jewfish sampled from (a) all locations (b) four locations in the Western region (c) five locations in the Darwin region and (d) four locations in the Arnhem/Gulf region.

	n	% correct
(a) Among regions		
All Locations	286	67 (10)
(b) Within the Western region		
Roebuck Bay	34	86
Camden Sound	18	95
Wyndham	30	68
Wadeye	24	80
Total	*106*	*81(26)*
(c) Within the Darwin region		
Wadeye	24	56
Peron Islands	29	73
Offshore Darwin	17	65
Bathurst Island	27	43
Melville Island	29	50
Total	*126*	*56 (21)*
(d) Within the Arnhem/Gulf region		
Melville Island	29	80
Maningrida	30	90
Arafura Sea	20	90
Vanderlin Islands	28	97
Total	*107*	*89 (26)*

Poulin and Kamiya's (2015) proportional chance criterion is shown in brackets.

Table 10. Pairwise FST estimates for comparisons among 11 locations based on 11 microsatellite data from 284 individuals of Black Jewfish. Lower diagonal, FST estimates; upper diagonal, p-values of the FST estimates. The comparisons that differed significantly from zero (p<0.05) are shaded in grey.

	RB	CS	Wy	Wa	PI	OD	BI	MI	Ma	AS	VI
RB	*	0.000	0.000	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000
CS	0.033	*	0.096	0.089	0.000	0.064	0.014	0.006	0.008	0.001	0.012
Wy	0.029	0.006	*	0.542	0.008	0.974	0.008	0.817	0.532	0.000	0.000
Wa	0.033	0.009	-0.001	*	0.385	0.991	0.743	0.984	0.806	0.002	0.069
PI	0.035	0.029	0.009	0.000	*	0.544	0.009	0.229	0.265	0.000	0.000
OD	0.030	0.014	-0.009	-0.012	-0.002	*	0.822	0.984	0.975	0.138	0.515
BI	0.035	0.016	0.010	-0.003	0.011	-0.005	*	0.574	0.091	0.000	0.007
MI	0.033	0.014	-0.004	-0.009	0.001	-0.012	-0.002	*	0.695	0.001	0.095
Ma	0.034	0.019	-0.001	-0.004	0.002	-0.011	0.007	-0.004	*	0.039	0.044
AS	0.054	0.021	0.022	0.018	0.030	0.007	0.031	0.017	0.011	*	0.020
VI	0.048	0.014	0.015	0.007	0.016	-0.001	0.013	0.004	0.009	0.011	*

Table 11. Pairwise FST estimates based on 11 microsatellite data from 284 individuals of Black Jewfish among the five groups of locations pooled based on strictly adjacent populations that showed no significant pairwise FST until all adjacent groups had significant pairwise FST. Lower diagonal, FST estimates; upper diagonal, p-values of the FST estimates, the comparisons that differed significantly from zero are shaded in grey. Group A = RB, Group B = CS-Wy-Wa, Group C = PI-OD-BI-MI-Ma, Group D = AS, Group E = VI.

	Group A	Group B	Group C	Group D	Group E
Group A	*	0.00000	0.00000	0.00000	0.00000
Group B	0.02938	*	0.02702	0.00000	0.00040
Group C	0.03251	0.00251	*	0.00000	0.00120
Group D	0.05406	0.02091	0.02247	*	0.01913
Group E	0.04829	0.01143	0.00957	0.01075	*

Bayesian analyses confirmed almost all the results from the F-statistics. Although the optimum number of clusters returned by ΔK was 3, the different k tested (k=2-11) in STRUCTURE were informative of the population genetics of Black Jewfish and showed different levels of population genetic structure (Supplementary Data 9). From the smaller k=2 the distinctiveness of RB from all of the other populations was clear (Figure 5). For k=3, the western populations RB and CS were distinct from each other and a group of central northern populations Wy-Wa-PI-OD-BI-MI-Ma appeared to be similar. There was also an eastern group with locations AS and VI appearing similar to each other, but distinct from the remainder. However, when k=4, there was a distinction between AS and VI. When k=5, the results confirmed the previous results (k=4) and revealed a couple of individuals in the Ma location with very different genetic assignment to all of the other samples. Wyndham (Wy) location stands out from the other central northern locations Wa-PI-OD-BI-MI-Ma when k=6. Above k=6, as each new k was added, did not bring more substantial information. The results from STRUCTURE also showed that RB may be a mixed population with some individuals presenting the same genotype proportions to CS location. Traditional assignment tests run in GenAlex between RB and CS showed that while 100% of individuals sampled in CS were self-assigned, only 84% of individuals sampled in RB were self-assigned and 16% of the RB samples were assigned to CS showing a possible directional gene flow from CS to RB.

AMOVA was used to compare the six-group scenario supported by STRUCTURE and the five-group scenario supported by the pairwise FST. The six-group and five-group scenarios explained 2.02% and 1.59% of the genetic variation, respectively and were statistically significant (p-value = 0.0063 and 0.0019 for respectively 6- and 5-groups). To evaluate the spatial processes that drive population structure and test if there is any isolation by distance effect, we did a Mantel test in Arlequin. The mantel correlation between the genetic and geographic distance matrices was equal to 0.655. The scatterplot between FST/ (1-FST) and geographic distances showed a linear relationship (Figure 6). Out of the 1000 randomisations performed, 999 were smaller than the observed value meaning that the chance to obtain a larger value than the observed is 1/999, indicating a p-value of 0.001. Nearby locations tend to be more similar than expected by chance and genetic differences increased linearly with distance.

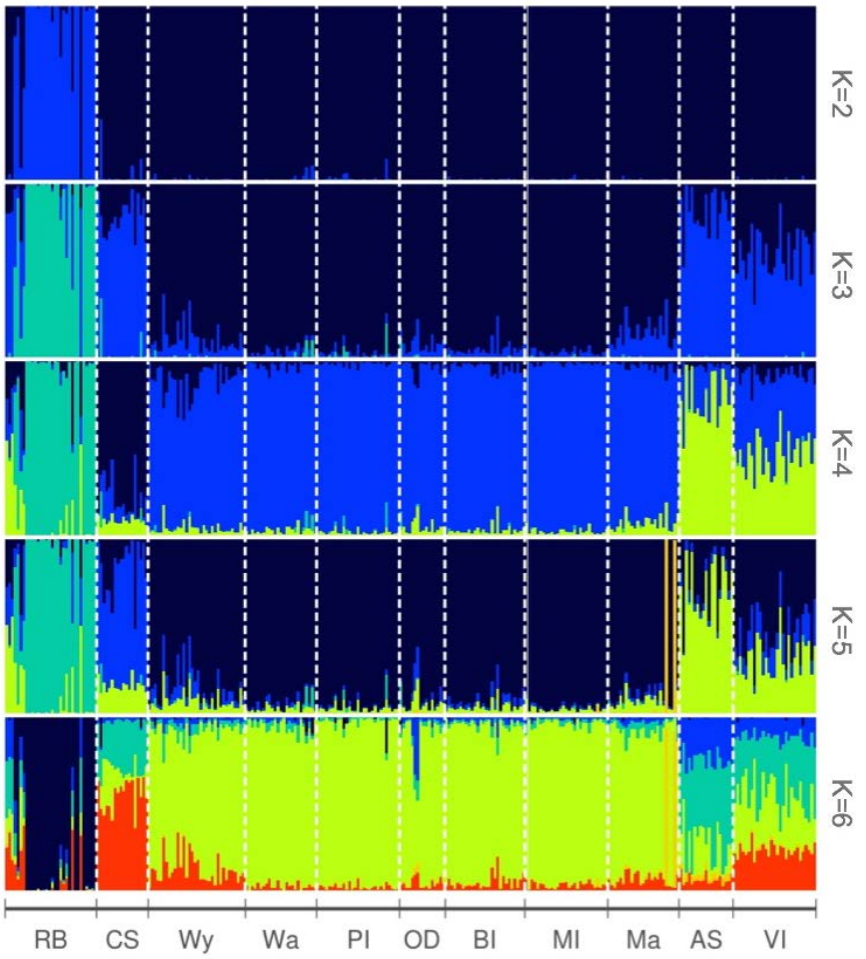

Figure 5. Results from the Bayesian population assignment of microsatellite data from Black Jewfish using the software Structure. Location prefixes follow Table 1. Each vertical line represents an individual and the posterior probability proportions of its genotype assigned to the different genetic clusters. The number of genetic clusters shown ranges from k=2 to k=6; each plot represents one tested k. Population information was used as a prior in the analysis.

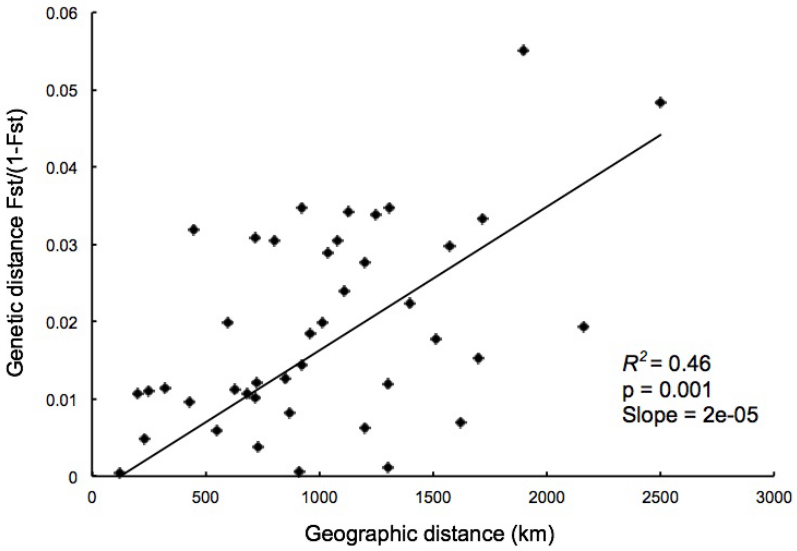

Figure 6. Isolation-by-distance analysis generated from 1000 Mantel randomisations for Black Jewfish Genetic distance FST/ (1-FST) against geographic distance (km) and corresponding values.

3.2 Golden Snapper

3.2.1 Otolith chemistry

A total of 462 otoliths were examined for multi-elemental chemistry signatures. The concentrations of most trace elements varied among and within region, location and life history stage. Concentrations of 23Al and 53Cr were <LOD at all ablation zones and were not included in the analyses. Concentrations of 55Mn and 66Zn were consistently <LOD at the margin and were also excluded from the analysis. Mean concentrations for each trace element analysed at all three ablation zones are presented in Supplementary Data 10.

The multi-elemental fingerprint of the core, near core and margins differed significantly among the five broad-scale regions (Western, Darwin, Gulf, Arnhem, Gulf and East Coast) and among locations within each of the regions (MANOVA, p<0.001 (Table 12). This suggested population structuring of Golden Snapper among locations within each region across all life history stages.

Table 12. Results of the multivariate analysis (MANOVA) investigating spatial variability in otolith core, near core and margin chemistry of Golden Snapper at two spatial scales: between states or territories and within each cluster.

		Pillai's trace			F		
Source	**df**	Margin	Near core	Core	Margin	Near core	Core
All States	21, 557	2.0853	2.0082	1.5896	11.254***	7.6184***	5.6896***
Locations (Western)	6, 190	1.4223	1.2711	0.8889	8.3893***	5.5849***	3.6136***
Locations (Darwin)	7, 203	2.1607	2.0137	1.2691	12.948***	9.0191***	4.9457***
Locations (Arnhem)	2, 73	1.4566	1.4689	0.91164	26.039***	20.282***	6.1427***
Locations (Gulf)	5, 123	1.477	1.4606	1.277	7.2473***	5.4564***	4.5351***
Locations (East Coast)	2, 68	1.1994	0.99343	1.1405	13.483***	6.6893***	8.9933***

df = degrees of freedom; *** = p<0.001.

Linear DFA was used to predict collection location based on otolith multi-elemental composition. Average classification success among all locations was 38% in the margin, 31% in the near core and 27% in the core (Table 13). Classification success increased significantly when using the regional clustering. Average accuracy of classification was greatest for the margin in the Arnhem and East Coast regions (91% and 89%, respectively); classification success was lower in the Western, Darwin and Gulf regions (54%, 58% and 56%, respectively). Classification success for the near core and core followed a similar pattern, although overall classification success levels were lower than that reported for the margin.

The scores of the first two discriminant functions of the multi-elemental signatures of otolith near core and margin variations were plotted to visually represent the spatial distribution of the variation within each region (Figure 7). The absence of overlap between the 95% CI in the multi-elemental signatures of fish from different locations within each region was used as a determination of statistical significance. The otolith multi-elemental signatures of the margins could discriminate more locations than the near core signatures. Within the Western region, Camden Sound, Jungulu and Bonaparte Gulf were discriminated as separate locations with levels of overlap between the remaining locations. The separation of Bonaparte Gulf was reinforced in the Darwin region analysis where it was also discriminated as a separate location, indicating that it is a unique stock. Additionally, Coburg Peninsula was discriminated as a separate stock; however, there was overlap between Darwin Harbour and Goulburn Island and between Wadeye, Lorna Shoal, Bathurst Island and Melville Island based on the margin multi-elemental signatures. All three locations within the Arnhem region were discriminated. All locations within the Gulf were discriminated with the exception of Blue Mud Bay and Vanderlin Islands which overlapped. As for the Arnhem region, all three locations within the East Coast region were discriminated.

Table 13. Jack-knife classification success for Golden Snapper to their sample collection location based on multi elemental signatures from the otolith core, near core and margin (a) among states and within (b) the Western region, (c) the Darwin region, the (d) Arnhem region, (e) the Gulf region and (f) the East Coast region.

		Otolith margin	Otolith near core	Otolith core
	n	% correct	% correct	% correct
(a) Among States				
All Locations	584	38	31	27
(b) Within Western region				
Camden Sound	27	67	70	26
Woninjaba Is	46	63	59	59
Raft Point	18	0	17	39
Hall Point	38	34	37	26
Jungulu	20	45	50	20
Cape Voltaire	29	72	52	38
Bonaparte Gulf	22	77	41	18
Total	197	54***	44***	36***
(c) Within the Darwin region				
Bonaparte Gulf	22	86	50	14
Wadeye	23	30	43	13
Lorna Shoal	26	38	50	35
Darwin Harbour	25	44	64	40
Bathurst Island	29	59	72	52
Melville Island	25	60	60	60
Coburg Peninsula	32	75	47	34
Goulburn Island	29	69	66	52
Total	211	58***	57***	32***
(d) Within the Arnhem region				
Goulburn Island	29	100	97	86
Maningrida	18	67	72	39
Arafura Sea	29	97	93	72
Total	76	91***	89***	70***
(e) Within the Gulf region				
Arafura Sea	29	90	76	55
Blue Mud Bay	29	69	38	41
Groote	25	68	72	64
Vanderlin Islands	23	0	26	17
Normanton	13	38	31	46
Weipa	10	40	80	100
Total	129	56***	53***	50***
(f) Within the East Coast region				
Normanton	13	62	46	69
Weipa	10	80	100	100
Halifax Bay	48	98	83	94
Total	71	89***	79***	90***

*** = p<0.001.

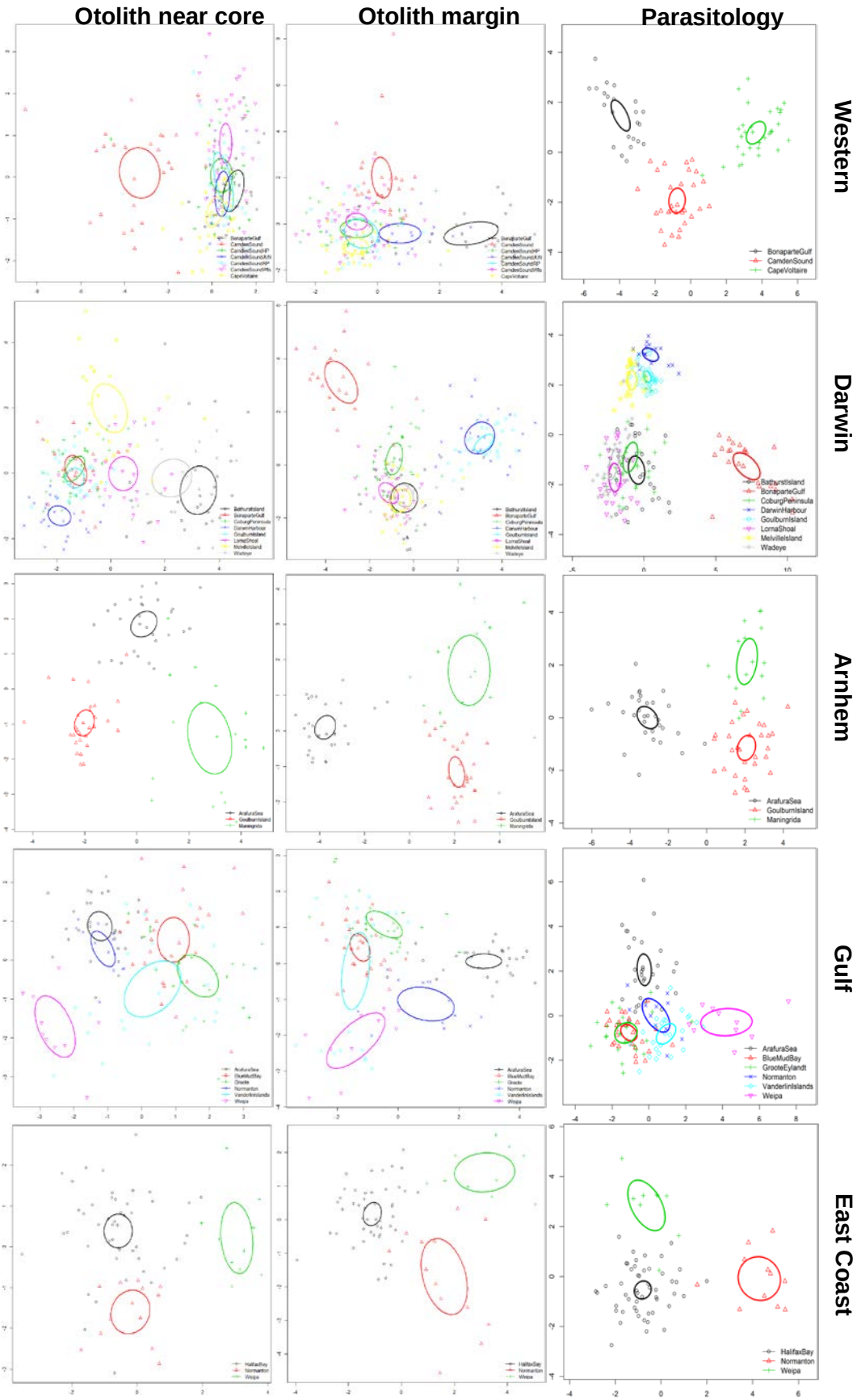

Figure 7. Plots of the first two discriminant function scores showing spatial variation in the parasite assemblage and the multi-elemental otolith near core and margin signatures of Golden Snapper collected from 22 locations within five regions Ellipses are 95% CIs around the group centroid for each location within each region and data points represent individual fish

3.2.2 Parasites

A total of 480 Golden Snapper were examined for the parasitology component of this study. Overall, 98.3% of Golden Snapper were infected with at least one parasite individual; mean abundance was 63.3 (0-561), with the mean parasite species richness 6.5 (1-18) for infected hosts. Most of the uninfected hosts (seven of the eight; mean TL 217.9 (170-265 mm) were collected from Darwin Harbour, with the other uninfected individual (TL 410 mm) collected from Melville Island.

A total of 47 different parasites were identified from the 480 Golden Snapper examined; of these, 15 were excluded from the analyses based on prevalence or issues with identification and/or enumeration (Supplementary Data 1). Removal of these parasites did not affect overall prevalence of infection and only moderately altered mean abundance (61.5) and species richness (5.9; 1-16) for infected hosts. The remaining parasites used in subsequent analyses are presented in Supplementary Data 13.

The parasite assemblage differed significantly among the five broad-scale regions (Western, Darwin, Gulf, Arnhem, Gulf and East Coast) and among locations within each of the regions (MANOVA, $p<0.001$, Table 14). This suggested population structuring of Golden Snapper among locations within each region.

Table 14. Results of the multivariate analysis (MANOVA) investigating spatial variability in parasite fauna of Golden Snapper at two spatial scales: between regions and within regions as defined in the materials and methods section

		Pillai's trace	df	F
Between Regions	All	5.165	17, 454	5.987
Within Regions	Western	1.598	2, 81	12.521
	Darwin	3.675	7, 206	7.301
	Arnhem	1.473	2, 74	7.832
	Gulf	2.106	5, 124	3.965
	East Coast	1.358	2, 69	4.143

All results are significant at the $p < 0.001$ level, unless otherwise indicated.

Discriminant function analysis of the overall parasite assemblage data successfully reclassified 43.6% of fish back to their collection location (in comparison to the proportional chance criterion of Poulin and Kamiya (2015) calculated at 6.2%)) (Table 15). Separation of the analyses into regions gave higher resolution ranging from 61% (Gulf) to 90% (Western) (Table 14). For each of the regions examined, the reclassification success, based on the first two discriminant functions and the parasites that contributed the most to these weightings, are presented in Supplementary Data 15. A total of 10 parasites were the most heavily weighted across the regions. *Hatschekia elongata* affected the weightings of the discriminant functions in all regions.

Table 15. Jack-knife classification success for Golden Snapper to their sample collection location based on parasite assemblage (a) among states and within (b) the Western region, (c) the Darwin region, the (d) Arnhem region, (e) the Gulf region and (f) the East Coast region

		Parasite assemblage
	n	% Correct
(a) Among States		
All Locations	480	58 (6)
(b) Within Western region		
Camden Sound	30	90
Cape Voltaire	31	94
Bonaparte Gulf	23	87
Total	84	90 (34)
(c) Within the Darwin region		
Bonaparte Gulf	23	96
Wadeye	27	70
Lorna Shoal	26	69
Darwin Harbour	25	89
Bathurst Island	31	55
Melville Island	25	100
Coburg Peninsula	35	54
Goulbourn Island	30	87
Total	222	75 (13)
(d) Within the Arnhem region		
Goulburn Island	30	93
Maningrida	16	75
Arafura Sea	31	90
Total	77	88 (36)
(e) Within the Gulf region		
Arafura Sea	31	65
Blue Mud Bay	28	68
Groote	25	44
Vanderlin Islands	25	68
Normanton	11	27
Weipa	10	40
Total	130	57 (19)
(f) Within the East Coast region		
Normanton	11	91
Weipa	10	70
Halifax Bay	51	90
Total	72	88 (54)

The Poulin & Kamiya's (2015) proportional chance criterion is shown in brackets.

3.2.3 Genetics

Genotypes from 10 microsatellites were obtained for 444 individuals of Golden Snapper with 1.17% missing data (Luj082, Luj090, Luj051, Luj072, Luj091, Luj094, Luj114, Luj076, Luj027, Luj068 (Taillebois et al., *In Press*). The number of alleles per locus ranged from 7 (Luj094, Luj051, Luj072) to 31 (Luj090) (Supplementary Data 16). Microchecker indicated the possible occurrence of null alleles at CS for locus Luj068, at BI for locus Luj091 and at HB for loci Luj027 and Luj076 with no stuttering or scoring errors. As there was no evidence of null-alleles at other locations for these loci, all the raw data was checked and we proceeded without removing loci or locations from the dataset. There was no significant test for linkage disequilibrium between pairs of loci across all locations and overall deviations from the Hardy-Weinberg equilibrium (HWE) with excess of heterozygote were detected at two loci Luj027 and Luj076 (p-value=0.0311 and 0.0022, respectively) that was surprising given the small difference between H_O and H_E (0.329 vs 0.328 and 0.789 vs 0.788). Looking at the deviation from HWE with excess of heterozygote

by locus for each population only 10/180 was found to be significant. Heterozygosity was moderate to high for all populations (0.715 +/- 0.184) and generally similar to expectations (around 0.7 in marine species) (DeWoody and Avise, 2000) (Supplementary Data 16).

A pattern of genetic differentiation with very low but significant population pairwise FST (range 0.004-0.024) was observed (Table 16). The pattern revealed that four locations of the sampling area (BG, AS, GE and HB) were genetically distinct from almost all other locations surveyed in the study. The pairwise FST were re-calculated after each step of an iterative approach consisting of pooling adjacent locations that showed no significant differentiation with the nearest location and all the others included in the group. The first round that showed an unambiguous pattern of genetic structuring consisted of the four following groups: CS-CV-BG (Group A), Wa-LS-DH-BI-MI-CoP-GI-Ma (Group B), AS (Group C) and BMB-GE-VI-NR-We-HB (Group D). The pairwise FST between groups were all significant but higher p-values were found for adjacent groups comparisons compared with other pairs of groups (Table 17). We assayed the four-group scenario supported by the pairwise FST with an AMOVA and the grouping explained 0.4% of the genetic variation and was statistically significant.

Bayesian analyses showed a lack of structure among the different localities. Although the optimum number of clusters returned by ΔK statistics was 5, the bar plot corresponding to k=5 did not show any level of genetic differentiation between locations (Figure 8). Increasing the number of clusters did not bring more substantial information and each added cluster was added in proportion to each individual's genotype (Figure 9).

To evaluate the spatial processes that drive population structure and test if there is any IBD effect, we performed a Mantel test in Arlequin. The mantel correlation between G and D was equal to 0.161. Out of the 1000 randomisations performed, 905 were smaller than the observed value, meaning that the chance to obtain a larger value than the observed is 1/905, indicating a non-significant p-value of 0.095.

Table 16. Pairwise FST estimates based on 10 microsatellite data from 444 individuals of Golden Snapper between 18 sampling locations. Lower diagonal, FST estimates; upper diagonal, p-values of the FST estimates, the comparisons that differed significantly from zero are shaded in grey. The boxes show the first round of pooling (see table 18).

	CS	CV	BG	Wa	LS	DH	BI	MI	CoP	GI	Ma	AS	BMB	GE	VI	NR	We	HB
CS	*	0.492	0.627	0.311	0.160	0.438	0.662	0.190	0.824	0.607	0.925	0.144	0.044	0.000	0.145	0.155	0.348	0.004
CV	-0.002	*	0.615	0.334	0.302	0.600	0.518	0.232	0.774	0.801	0.906	0.035	0.147	0.000	0.067	0.413	0.394	0.003
BG	-0.003	-0.002	*	0.010	0.432	0.018	0.028	0.010	0.030	0.121	0.277	0.004	0.019	0.007	0.011	0.073	0.326	0.001
Wa	0.001	0.000	0.011	*	0.340	0.411	0.536	0.096	0.304	0.140	0.574	0.040	0.337	0.000	0.043	0.664	0.923	0.073
LS	0.005	0.001	0.001	0.001	*	0.198	0.349	0.014	0.118	0.119	0.410	0.003	0.416	0.096	0.076	0.562	0.832	0.034
DH	-0.001	-0.002	0.012	-0.001	0.003	*	0.614	0.195	0.497	0.421	0.775	0.009	0.508	0.014	0.241	0.201	0.817	0.064
BI	-0.002	-0.001	0.009	-0.001	0.002	-0.001	*	0.879	0.963	0.770	0.655	0.521	0.641	0.203	0.289	0.494	0.999	0.419
MI	0.003	0.002	0.013	0.005	0.011	0.003	-0.004	*	0.439	0.448	0.098	0.826	0.174	0.102	0.917	0.558	0.735	0.213
CoP	-0.005	-0.003	0.009	0.001	0.005	0.000	-0.005	0.000	*	0.398	0.525	0.172	0.503	0.002	0.165	0.245	0.984	0.211
GI	-0.002	-0.004	0.005	0.004	0.005	0.000	-0.002	0.000	0.001	*	0.659	0.024	0.213	0.019	0.276	0.660	0.911	0.078
Ma	-0.011	-0.007	0.004	-0.002	0.001	-0.005	-0.001	0.008	0.000	-0.002	*	0.134	0.385	0.041	0.093	0.489	0.870	0.040
AS	0.005	0.007	0.014	0.007	0.015	0.012	0.000	-0.004	0.003	0.008	0.006	*	0.011	0.041	0.151	0.156	0.869	0.058
BMB	0.010	0.004	0.011	0.000	0.000	-0.001	-0.002	0.004	-0.001	0.003	0.001	0.011	*	0.159	0.269	0.458	0.896	0.232
GE	0.024	0.016	0.013	0.016	0.005	0.011	0.003	0.005	0.014	0.009	0.010	0.007	0.003	*	0.239	0.143	0.427	0.036
VI	0.006	0.006	0.013	0.007	0.007	0.003	0.003	-0.006	0.004	0.002	0.009	0.004	0.002	0.002	*	0.898	0.396	0.039
NR	0.007	0.000	0.011	-0.004	-0.001	0.005	0.001	-0.002	0.004	-0.002	0.000	0.006	0.000	0.006	-0.007	*	0.655	0.278
We	0.000	0.000	0.004	-0.014	-0.009	-0.010	-0.021	-0.008	-0.015	-0.011	-0.011	-0.010	-0.013	-0.001	0.002	-0.005	*	0.970
HB	0.015	0.011	0.016	0.004	0.007	0.006	0.000	0.002	0.002	0.004	0.009	0.005	0.002	0.006	0.007	0.003	-0.014	*

Table 17. Pairwise FST estimates based on 10 microsatellite data from Golden Snapper for four groups of pooled locations

	Group A	Group B	Group C	Group D
Group A	*	0.034	0.001	0.000
Group B	0.002	*	0.019	0.008
Group C	0.010	0.005	*	0.027
Group D	0.011	0.002	0.005	*

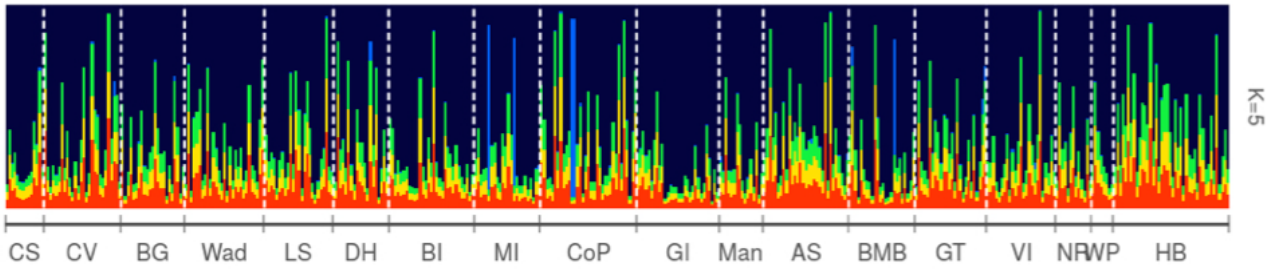

Figure 8. Results from the Bayesian model-based clustering of microsatellite data from Golden Snapper using the software Structure. Each vertical line represents an individual and the posterior probability proportions of its genotype assigned to the different genetic clusters. The number of genetic clusters tested shown is k=5; Population information was used as a prior in the analysis.

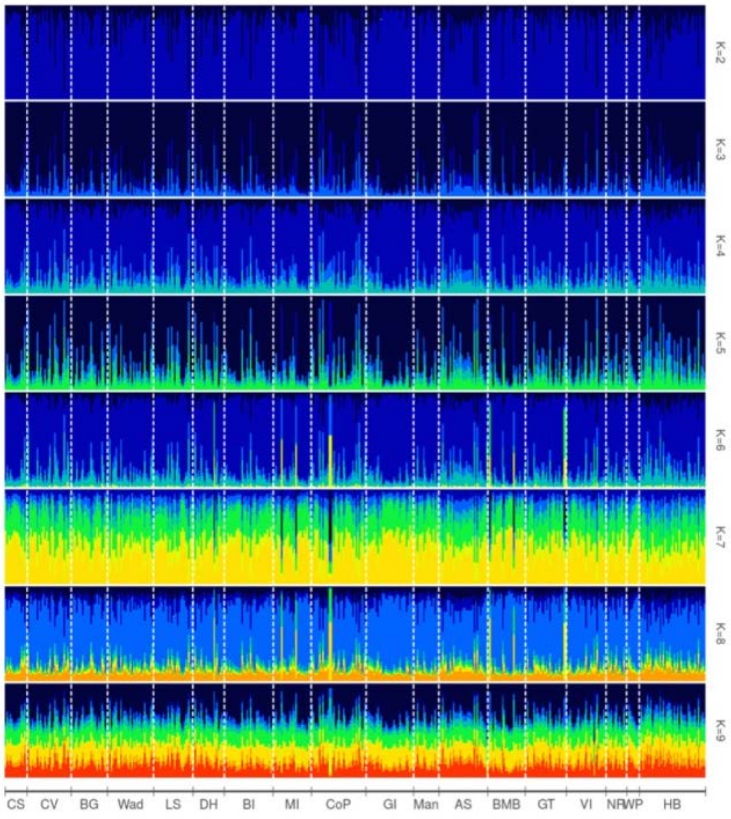

Figure 9. Results from the Bayesian model-based clustering of microsatellite data from Golden Snapper using the software Structure. Each vertical line represents an individual and the posterior probability proportions of its genotype assigned to the different genetic clusters. The number of genetic clusters shown ranges from k=2 to k=10; each plot represents one tested k. Population information was used as a prior in the analysis.

The final set of locations was obtained by pooling adjacent locations that showed no significant differentiation with the nearest location and all the others included in the group until all adjacent groups had significant pairwise FST. Lower diagonal, FST estimates; upper diagonal, p-values of the FST estimates, the comparisons that differed significantly from zero are shaded in grey. Group A = CS-CV-BG, Group B = Wa-LS-DH-BI-MI-CoP-GI-Ma, Group C = AS and Group D = BMB-GE-VI-NR-We-HB.

3.3 Grass Emperor

3.3.1 Otolith chemistry

A total of 329 sections were examined for multi-elemental chemistry signatures. Elements that were not included in the analysis due to them being frequently <LOD were ^{23}Al, ^{49}Ti and ^{53}Cr from the core, near core and margin; ^{60}Ni and ^{66}Zn from the near core and margin and ^{55}Mn from the margin only. Results of the analysis comparing elemental signatures from the near core and margin of individual otoliths among the 13 collection locations indicated that the individual elemental ratios varied over the 13 locations (Supplementary Data 17). Concentrations of ^{7}Li, ^{25}Mg, ^{63}Cu, and ^{55}Mn were consistently higher in the near core, with ^{55}Mn only present in the near core; 88Sr had consistently higher concentrations in the margin while the differences in concentrations of 138Ba between near core and margin were mixed.

The single factor MANOVAs showed significant variation of the multi elemental signatures in the near core and margin of each individual otolith from all collection locations (Table 18). LDFA of the overall otolith microchemistry data across the entire sample range successfully reclassified 29% and 39% of all fish, based on near core and margin microchemistry, respectively back to the location of origin (Table 18). Separation of the analyses into jurisdictional regions gave higher resolutions with 33% (NT) to 63% (Queensland) reclassification based on near core microchemistry and 47% (WA) to 75% (Queensland) based on margin microchemistry (Table 19). Within the jurisdictional regions, results were more variable, ranging from 4% (Roche Reef) to 86% (Halifax Bay) for near core and 17% (Cape Preston) to 86% (Halifax Bay) for margin microchemistry (Table 19). Per cent reclassification of fish between individual locations, based on both near core and margin microchemistry, is presented in Supplementary Data 18.

The scores of the first two discriminant functions of the multi-elemental signatures of otolith near core and margin variations were plotted to visually represent the spatial distribution of the variation within each region (Figure 10). The otolith margin microchemistry results were better discriminators of locations than were the near core microchemistry results. The WA results had considerable overlap in the 95% CI ellipses for the near core microchemistry results, with Cape Voltaire overlapping Camden Sound, Camden Sound overlapping both Locker Point and Cape Preston, Cape Preston and Locker Point overlapping each other and Cape Preston slightly overlapping Dampier Peninsula. Within the margin results for WA, Camden Sound and Cape Preston overlapped substantially, and Cape Voltaire and Cape Preston overlapped slightly; Locker Point and Dampier Peninsula were separated from the other locations. The results were similar for the NT, with the near core results showing substantial overlap between all locations, with the exception of Vanderlin Islands. The margin results showed overlap only between Darwin Harbour and Roche Reef. All of the Queensland results, for both near core and margin were separated, although the Sunshine Coast and Moreton Bay were closer for the near core results. For each of the jurisdictional regions, the elements that contributed most to the weightings of the linear discriminant functions are presented in Supplementary Data 19. ^{7}Li, ^{25}Mg, and ^{55}Mn were among the top weighted elements for the near core; ^{7}Li, ^{25}Mg, ^{88}Sr, and ^{138}Ba for the margin.

Table 18. Results of the MANOVA investigating spatial variability in otolith near core and margin microchemistry of Grass Emperor at two spatial scales: between States and Territories and within each State or Territory

	Near core			Margin		
Source	Source, error df	Pillai's	F	Source, error df	Pillai's	F
All States	72, 1896	0.947	4.936	60, 1580	1.466	10.925
Western Australia	24, 560	0.548	3.706	20, 564	0.650	5.474
Northern Territory	24, 540	0.368	2.281	20, 544	1.151	10.994
Queensland	12, 66	0.918	4.668	10, 68	1.035	7.295

All results are significant at the p <0.001 level.

Table 19. Jack-knife classification success for Grass Emperor to their sample collection location based on multi elemental signatures from the otolith near core and margin (a) among States and within (b) the Western Australia region, (c) the Northern Territory region, and (d) the Queensland region

		Otolith margin	Otolith near core
	n	% correct	% correct
(a) Among States			
All Locations		39	29
(b) Within Western Australia			
Locker Point		63	47
Cape Preston		17	27
Dampier Peninsula		46	61
Camden Sound		59	24
Cape Voltaire		53	50
Total		48	41
(c) Within the Northern Territory			
Wadeye		57	20
Roche Reef		52	4
Darwin Harbour		79	17
Coburg Peninsula		58	58
Vanderlin Islands		50	57
Total		58	33
(d) Within Queensland			
Halifax Bay		86	86
Sunshine Coast		79	57
Moreton Bay		58	42
Total		75	63

3.3.2 Parasites

A total of 341 Grass Emperor (99.7% of all fish collected) were examined for the parasitology component of this study (Table 20). Overall, 100% of examined Grass Emperor were infected with at least one parasite individual; mean abundance was 45.8 (1-274) parasite individuals per host, with the mean parasite species richness 5.1 (1-13). A total of 39 different parasites were identified. Of these, 15 were excluded from the analyses based on prevalence or due to issues with accurate taxonomic identification and/or counts (Supplementary Data 1). Removal of these parasites slightly reduced overall prevalence of infection (95.9%), mean abundance (32.5, 0-250) and species richness (3.6, 0-11). The remaining parasites used in subsequent analyses are presented in Supplementary Data 20.

MANOVA of the overall parasite assemblage data detected significant variations in infection between locations (Table 21). LDFA of the overall parasite assemblage data across the entire sample range successfully reclassified 56% of fish back to location of origin (in comparison to the proportional chance criterion of Poulin and Kamiya (2015) calculated at 8%) (Table 21).

Table 20. Results of the MANOVA and LDFA investigating spatial variability in parasite assemblage of Grass Emperor at two spatial scales: between States and Territories and within each State or Territory

	Parasite assemblage		
Source	Source, error df	Pillai's	F
All States	12, 328	3.615	5.676
Western Australia	4, 150	1.746	6.240
Northern Territory	4, 141	1.946	11.536
Queensland	2, 37	1.738	8.572

All results are significant at the p <0.001 level.

Table 21. Jack-knife classification success for Grass Emperor to their sample collection location based on the parasite assemblage (a) among states and within (b) the Western Australia region, (c) the Northern Territory region, and (d) Queensland region

		Parasite assemblage
	n	**% Correct**
(a) Among States		
All Locations		56 (8)
(b) Within Western Australia		
Locker Point		68
Cape Preston		46
Dampier Peninsula		64
Camden Sound		93
Cape Voltaire		55
Total		65 (20)
(c) Within the Northern Territory		
Wadeye		67
Roche Reef		79
Darwin Harbour		92
Coburg Peninsula		82
Vanderlin Islands		73
Total		78 (20)
(d) Within Queensland		
Halifax Bay		79
Sunshine Coast		79
Moreton Bay		100
Total		85 (34)

The proportional chance criterion of Poulin and Kamiya (2015) is presented in brackets.

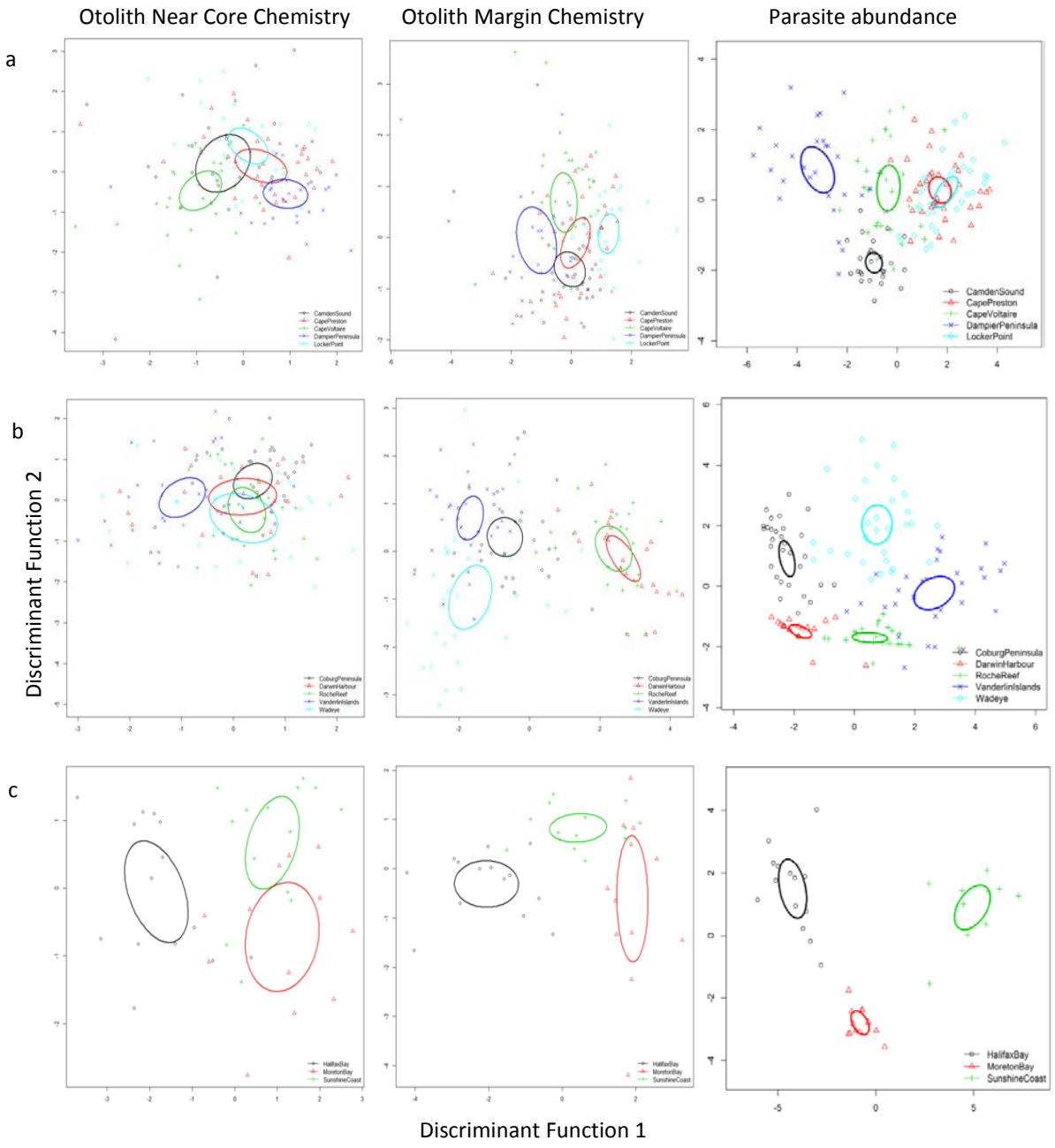

Figure 10. Plot of the first two discriminant function scores showing spatial variation in the otolith near core and margin microchemistry and the parasite assemblages of Grass Emperor (a) within Western Australian fish, (b) within Northern Territory fish, and (c) within Queensland fish. Ellipses are 95% CIs around the group centroid.

Separation of the analyses into jurisdictional regions gave higher resolution with 65% (WA) to 85.0% (Queensland) reclassification success (Table 21). Percent reclassification of fish between individual locations, based on the parasite assemblage, is presented in Supplementary Data 21.

The plots of the scores of the first two discriminant functions of the parasite assemblage variations (Figure 10) showed all locations to be separate from each other within each jurisdictional region, with the exception of Locker Point and Cape Preston in WA, which had substantial overlap in the 95% CI ellipses. For each of the jurisdictional regions, the reclassification success, based on the first two discriminant functions and the parasites that contributed the most to these weightings are presented in Supplementary Data 22. The copepod, *Hatschekia gracilis*, was among the top weighted parasite species for the 1st discriminant function within each jurisdiction.

3.3.3 Genetics

Genotypes from 10 microsatellites were obtained (Lel011, Lel040, Lel033, Lel012, Lel013, Lel032, Lel028, Lel027, Lel044, Lel039 (Taillebois et al., *In Press*) for 279 individuals of Grass Emperor with 1.52% missing data. The number of alleles per locus ranged from 13 (Lel013) to 24 (Lel012) (Supplementary Data 23). Locus Lel012 showed deviations from Hardy-Weinberg equilibrium (HWE) with deficit of heterozygotes at seven locations (Locker Point, Camden Sound, Dampier Peninsula, Cape Voltaire, Roche Reef, Vanderlin Islands and Sunshine Coast). Given the high rate of deviation from HWE, Lel012 was discarded from the dataset for further analyses reducing the number of loci to nine. For the remaining loci, Microchecker indicated the possible occurrence of null alleles at LP for locus Lel040 and at RR for locus Lel032 with no stuttering or scoring errors. Only one out of 45 tests for linkage disequilibrium between pairs of loci (Lel011 x Lel044) was significant (i.e. $p<0.05$) and overall deviation from HWE with excess of heterozygote was detected at a single locus Lel011 ($p=0.001$). Significant deviation from HWE by locus for each population only occurred in seven out of 108 cases. Heterozygosity was high for all populations (0.811 +/- 0.074) and slightly above the expectations (around 0.7 in marine species (DeWoody and Avise, 2000) (Supplementary Data 23).

A pattern of genetic differentiation with low but significant population-pairwise FST (range 0.008-0.046) was observed (Table 22). The pattern revealed that three locations of the sampling area (Vanderlin Islands, Halifax Bay and the Sunshine Coast) were genetically distinct from almost all other locations in the study. Other locations could be grouped into two undifferentiated groups (Locker Point-Cape Voltaire and Wadeye-Coburg Peninsula). The pairwise FST were re-calculated after each step of an iterative approach consisting of pooling adjacent locations that showed no significant differentiation with the nearest location and nor the other locations within the group. The first iteration that showed an unambiguous pattern of genetic structuring consisted of the five following groups: Locker Point-Cape Voltaire (Group A), Wadeye-Coburg Peninsula (Group B), Vanderlin Islands (Group C), Halifax Bay (Group D) and Sunshine Coast (Group E). The comparisons between groups were all significant but higher p-values were found for adjacent group comparisons compared to other pairs of groups (Table 23). We assayed the five-group scenario supported by the pairwise FST with an AMOVA and the grouping explained 1.04% of the genetic variation and was statistically significant.

Bayesian analyses showed a major genetic break between Cape Voltaire and Wadeye locations as revealed by F-statistics. Although the optimum number of clusters returned by ΔK was 3, the different k tested (k=2-9) in Structure were observed to accurately describe the genetic structure of Grass Emperor. A clear separation between Cape Voltaire and Wadeye locations into a western and an eastern group was consistently observed from k=2 to k=9 (Figure 11). From k=5, differences between locations within the western group were revealed. However, above k=5 as each new k was added, did not bring more substantial information.

To evaluate the spatial processes that drive population structure and test if there is any IBD effect, we performed a Mantel test in Arlequin. The mantel correlation between G and D was equal to 0.644. Out of the 1000 randomisations performed, 1000 were smaller than the observed value indicating a significant p-value of 0.

Table 22. Pairwise FST estimates based on nine microsatellite data from 279 individuals of Grass Emperor between 12 sampling locations. Lower diagonal = FST estimates, upper diagonal = p-values of the FST estimates; the comparisons that differed significantly from zero are shaded in grey. The boxes show the first round of pooling (see Table 23).

	LP	CP	CS	DP	CV	Wa	RR	DH	CoP	VI	HB	SC
LP	*	0.730	0.291	0.688	0.659	0.030	0.095	0.349	0.002	0.007	0.001	0.000
CP	-0.001	*	0.427	0.877	0.269	0.066	0.206	0.183	0.268	0.001	0.006	0.001
CS	0.003	0.001	*	0.272	0.125	0.080	0.049	0.042	0.024	0.001	0.000	0.001
DP	-0.001	-0.004	0.002	*	0.215	0.153	0.679	0.177	0.160	0.003	0.033	0.005
CV	-0.001	0.003	0.005	0.003	*	0.003	0.003	0.111	0.006	0.000	0.001	0.000
Wa	0.011	0.007	0.007	0.005	0.015	*	0.930	0.639	0.312	0.186	0.249	0.018
RR	0.007	0.004	0.008	-0.002	0.012	-0.005	*	0.785	0.124	0.288	0.048	0.072
DH	0.002	0.004	0.008	0.003	0.004	-0.002	-0.004	*	0.183	0.372	0.186	0.008
CoP	0.015	0.002	0.009	0.004	0.010	0.002	0.004	0.003	*	0.010	0.301	0.000
VI	0.012	0.014	0.016	0.013	0.019	0.003	0.002	0.000	0.009	*	0.013	0.005
HB	0.029	0.020	0.030	0.013	0.025	0.004	0.012	0.004	0.003	0.016	*	0.010
SC	0.046	0.031	0.032	0.022	0.044	0.020	0.012	0.020	0.032	0.021	0.025	*

Table 23. Pairwise FST estimates for Grass Emperor based on five groups from pooling across the 12 sampling locations. The final set of pooled locations was obtained after pooling adjacent locations that showed no significant differentiation with the nearest location and all the others included in the group until all adjacent groups had significant pairwise FST. Lower diagonal = FST estimates, upper diagonal = p-values of the FST estimates; the comparisons that differed significantly from zero are shaded in grey. Group A = LP-CP-DP-CS-CV, Group B = Wa-RR-DH-CoP, Group C = VI, Group D = HB and Group E = SC.

	Group A	Group B	Group C	Group D	Group E
Group A	*	0.000	0.000	0.001	0.000
Group B	0.006	*	0.049	0.161	0.002
Group C	0.014	0.004	*	0.013	0.005
Group D	0.021	0.005	0.016	*	0.011
Group E	0.034	0.021	0.021	0.025	*

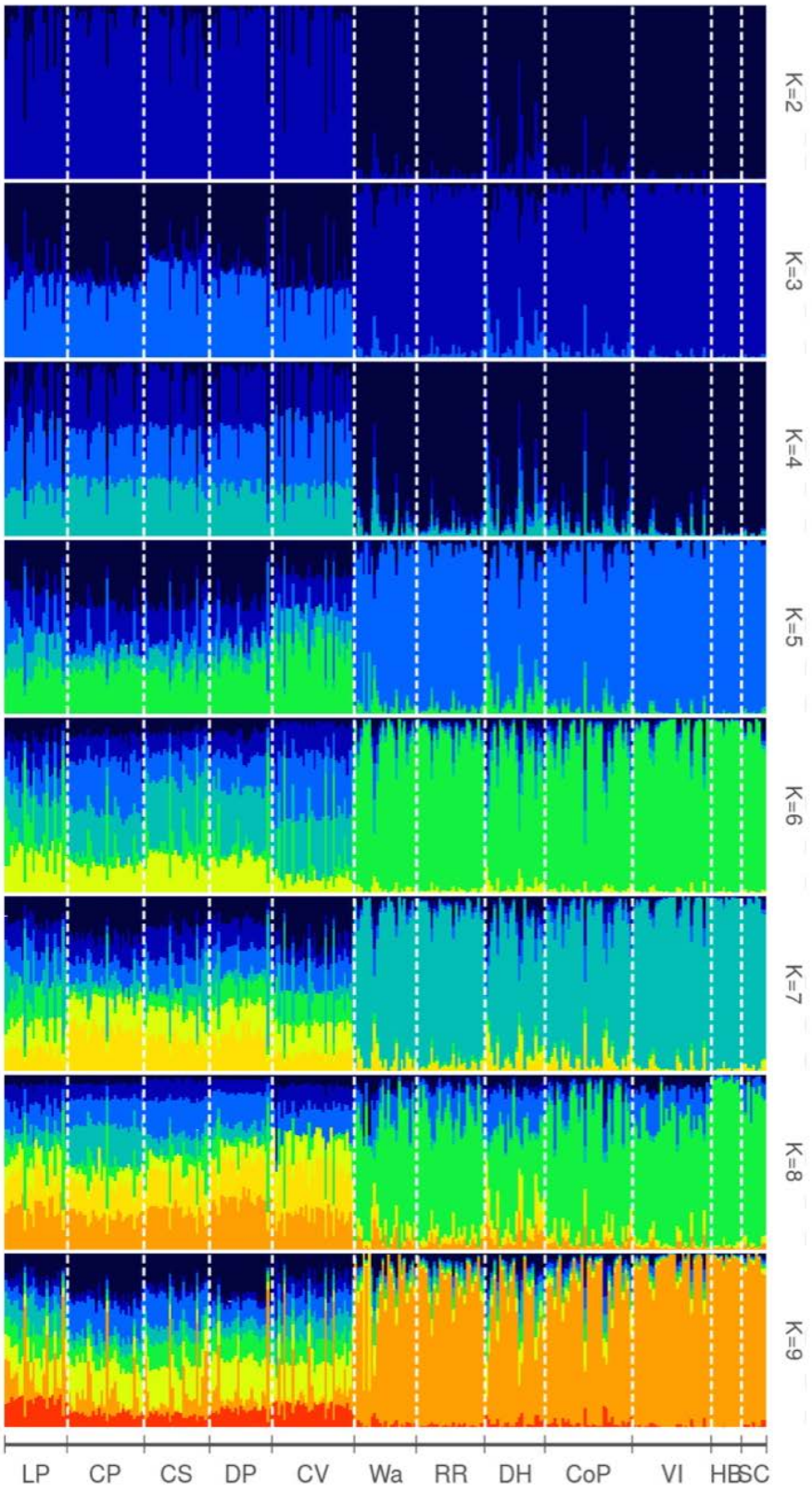

Figure 11. Results from the Bayesian model-based clustering of microsatellite data from Grass Emperor using the software Structure. Each vertical line represents an individual and the posterior probability proportions of its genotype assigned to the different genetic clusters. The number of genetic clusters shown ranges from k=2 to k=9; each plot represents one tested k. Individuals are plotted in order along the sampling gradient from west to east. Population information was used as a prior in the analysis.

3.4 Integration

3.4.1 Black Jewfish

The integration of results from the otolith chemistry, parasite and genetic analyses are presented in a SDM (Table 24). Potential management units that represented separate stocks were identified by looking at the scale of differentiation among sites within the three management regions: Western, Darwin and Arnhem/Gulf (See 2.2.3 for details). The genetic comparison remained among all sites to investigate the scale of genetic connectivity across the distribution of Black Jewfish in Australian waters. The potential management units identified suggested that Black Jewfish stocks primarily existed at the scale samples were collected (Table 25). The exceptions were the sites in WA and western most NT site (Wadeye) that were identified as a 'North West Kimberly' stock and 'Darwin/Tiwi Island stock'. These results suggest that Black Jewfish populations have variable larval connectivity but are generally limited to hundreds of kilometres and adults appear to show movement among sites separated by tens of kilometres but not separated by hundreds of kilometres (Figure 12).

3.4.2 Golden Snapper integration

The integration of results from the otolith chemistry, parasite and genetic analyses are presented in a SDM (Table 26). Potential management units that represented separate stocks were identified by looking at the scale of differentiation among sites within the five management regions: Western, Darwin, Arnhem, Gulf and East Coast. (See 2.2.3 for details). The genetic comparison remained among all sites to investigate the scale of genetic connectivity across the distribution of Golden Snapper in Australian waters. The potential management units identified suggested that Golden Snapper stocks primarily existed at the scale that samples were collected (Table 25). The exception was a 'Western Gulf of Carpentaria' stock that incorporated individuals from Groote Eylandt, Blue Mud Bay and Vanderlin Islands. However, there was some disagreement as to the southern boundary of this stock between the parasite and otolith microchemistry analyses (Table 25). These results suggest that Golden Snapper populations have stronger larval connectivity over larger scales than Black Jewfish (hundreds to thousands of kilometres) but adults appear to show strong site fidelity at the scales examined (Figure 13).

3.4.3 Grass Emperor integration

The integration of results from the otolith chemistry, parasite and genetic analyses are presented in a SDM (Table 28). Potential management units that represented separate stocks were identified by looking at the scale of differentiation among sites within three management regions which coincided with the State or Territory boundaries: WA, NT, and Queensland. (See 2.2.3 for details). The potential management units identified suggested that Grass Emperor stocks primarily existed at the scale that samples were collected (Table 29). The exception was a 'Central WA' stock that incorporated samples from Locker Point and Cape Preston that are towards the southern range of this species on the West Coast. While the genetic results indicated distinct populations across large areas that are likely to be linked by larval connectivity, given the relatively sedentary nature of adults as indicated by the otolith and parasite results, the spatial scale that is appropriate for management is at the finer-scale based on the adult movement (Table 29). These results overall suggest that Grass Emperor populations have larval connectivity generally over very large areas and with a pattern of declining relatedness with distance (isolation by distance); however, once recruited, post-larval fish tend to be relatively site attached (Figure 14).

Table 24. Stock differentiation matrix (SDM) for Black Jewfish showing the results inferred from the regional pairwise comparisons for the three techniques used in this study. Where significantly different results were found for pairwise comparison of the sampling locations, these are indicated by capital letters in bold: G—genetics, P—parasites, O—otolith stable isotopes. Non-significant results are indicated by lowercase letters corresponding to the respective techniques. In those cases where no analysis was carried out, they are denoted by "-". Results for parasites and otolith are from the plots in Figure 4; near core otolith results are used. Results for the genetics are based on the pooled F_{ST}.

	Location	RB	CS	Wy	Wa	Pl	OD	Bl	Ml	Ma	AS	Vl
WA	Roebuck Bay											
WA	Camden Sound	**O P G**										
WA	Wyndham	**O P G**	**O P** g									
NT	Wadeye	o **P G**	**O P** g	**O P** g								
NT	Peron Islands	- - **G**	- - **G**	- - **G**	**O P G**							
NT	Offshore Darwin	- - **G**	- - **G**	- - **G**	o **P G**	**O P** g						
NT	Bathurst Island	- - **G**	- - **G**	- - **G**	**O** p **G**	**O P** g	**O P** g					
NT	Melville Island	- - **G**	- - **G**	- - **G**	**O P G**	**O P** g	o p g	o **P** g				
NT	Maningrida	- - **G**	- - **G**	- - **G**	- - **G**	- - g	- - g	- - g	o **P** g			
NT	Arafura Sea	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	**O P G**	**O P G**		
NT	Vanderlin Islands	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	o **P G**	**O P G**	**O P G**	

Table 25. End-user table that summarises results from all techniques to determine the broadest spatial scale appropriate for management for Black Jewfish, based on sampling locations in this study.

	Otoliths (core)	Parasites	Genetics	Management units
WA	Roebuck Bay	Roebuck Bay	Roebuck Bay	Roebuck Bay
WA	Camden Sound	Camden Sound	North west Kimberley	Camden Sound
WA	Wyndham	Wyndham		Wyndham
NT	Wadeye	Wadeye		Wadeye
NT	Peron Islands	Peron Islands	Western Northern Territory	Peron Islands
NT	Offshore Darwin/ Tiwi Islands	Eastern Offshore Darwin		Darwin/Tiwi Islands
NT				
NT		Bathurst Island		
NT	Maningrida	Maningrida		Maningrida
NT	Arafura Sea	Arafura Sea	Arafura Sea	Arafura Sea
NT	Vanderlin Islands	Vanderlin Islands	Vanderlin Islands	Vanderlin Islands

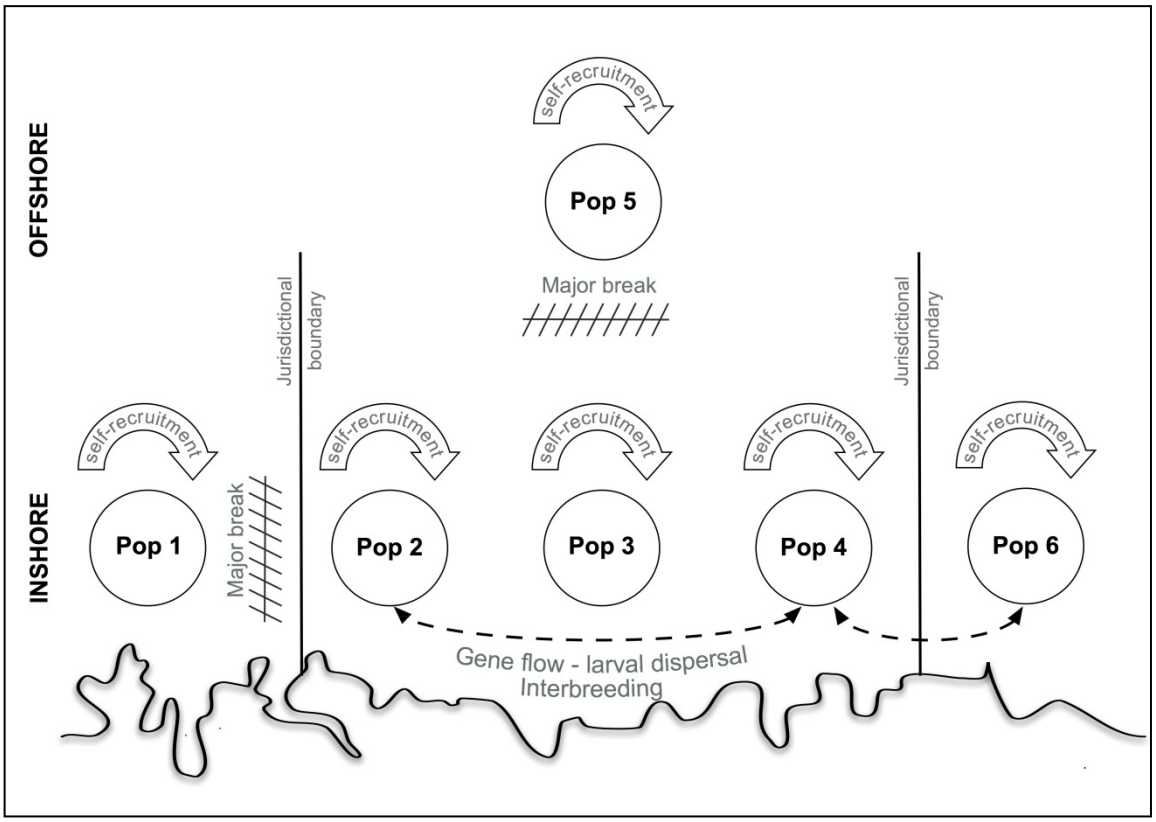

Figure 12. Conceptual model of how populations of Black Jewfish are connected across northern Australia. Each population is self-recruiting with levels of genetic interchange occurring between them. Dashed arrows indicate low levels of genetic interchange. Major breaks indicate that a major geological/biological feature occurs to separate exchange between populations. Based on the results, populations operate at tens to thousands of kilometres that may include a single reef complex or a system of several reefs.

Table 26. Stock differentiation matrix (SDM) for Golden Snapper showing the results generated from the regional pairwise comparisons for the three techniques used in this study. Where significantly different results were found for pairwise comparison of the sampling locations, they are indicated by capital letters in bold: G—genetics, P—parasites, O—otolith stable isotopes. Non-significant results are indicated by lowercase letters corresponding to the respective techniques. In those cases where no analysis was carried out are denoted by "-". Results for parasites and otolith are from the plots in Figure 7; near core otolith results are used. Results for the genetics are based on the pooled F_{ST}.

	Locatiogs	CS	CSWI	CSRP	CSHP	CSJU	CV	BG	WA	LS	DH	BI	MI	CoP	GI	MA	AS	BMB	GE	VI	NR	WE	HB
WA	CS																						
WA	CSWI	**O**--																					
WA	CSRP	**O**--	o--																				
WA	CSHP	**O**--	o--	o--																			
WA	CSJU	**O**--	**O**--	o--	o--																		
WA	CV	**OP**g	**O**--	o--	**O**--	o--																	
NT	BG	**OP**g	**O**--	o--	o--	o--	o**P**g																
NT	WA	--**G**	---	---	---	---	--**G**	**OPG**															
NT	LS	--**G**	---	---	---	---	--**G**	**OPG**	**O**pg														
NT	DH	--**G**	---	---	---	---	--**G**	**OPG**	**OP**g	**OP**g													
NT	BI	--**G**	---	---	---	---	--**G**	**OPG**	o**P**g	**OP**g	**OP**g												
NT	MI	--**G**	---	---	---	---	--**G**	**OPG**	**OP**g	**OP**g	**OP**g	**OP**g											
NT	CoP	--**G**	---	---	---	---	--**G**	o**PG**	**OP**g	**OP**g	**OP**g	**O**pg	**OP**g										
NT	GI	--**G**	---	---	---	---	--**G**	o**PG**	**OP**g	**OP**g	**OP**g	**OP**g	**OP**g	o**P**g									
NT	MA	--**G**	---	---	---	---	--**G**	--**G**	--g	--g	--g	--g	--g	--g	**OP**g								
NT	AS	--**G**	---	---	---	---	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	**OPG**	**OPG**							
NT	BMB	--**G**	---	---	---	---	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	**OPG**						
NT	GE	--**G**	---	---	---	---	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	**OPG**	opg					
NT	VI	--**G**	---	---	---	---	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	**OPG**	o**P**g	o**P**g				
Qld	NR	--**G**	---	---	---	---	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	o**PG**	**OP**g	**OP**g	**O**pg			
Qld	WE	--**G**	---	---	---	---	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	**OPG**	**OP**g	**OP**g	**OP**g	**OP**g		
Qld	HB	--**G**	---	---	---	---	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--**G**	--g	--g	--g	**OP**g	**OP**g	

Table 27. End-user table that summarises results from all techniques to determine the broadest spatial scale appropriate for management for Golden Snapper based on sampling locations in this study

	Otoliths (core)	**Parasites**	**Genetics**	**Management units**
WA	Camden Sound	Camden Sound	Camden Sound	Camden Sound
WA	Woinjabi Islands*			Woinjabi Islands
WA	Hall Point*			Hall Point
WA	Raft Point*			Raft Point
WA	Jungulu*			Jungulu
WA	Cape Voltaire	Cape Voltaire	North west Kimberley	Cape Voltaire
NT	Bonaparte Gulf	Bonaparte Gulf		Bonaparte Gulf
NT	Wadeye	Western Northern Territory		Wadeye
NT	Lorna Shoal			Lorna Shoal
NT	Darwin Harbour	Darwin Harbour		Darwin Harbour
NT	Bathurst Island	Bathurst Island	North western Northern Territory	Bathurst Island
NT	Melville Island	Melville Island		Melville Island
NT	North Northern Territory	Coburg Peninsula		Coburg Peninsula
NT		Goulburn Island		Goulburn Island
NT	Maningrida	Maningrida		Maningrida
NT	Arafura Sea	Arafura Sea	Arafura Sea	Arafura Sea
NT	Western Gulf of Carpentaria	North western Gulf of Carpentaria	North Eastern Australia	Western Gulf of Carpentaria
NT				
NT		Southern Gulf of Carpentaria		
Qld	Normanton			Normanton
Qld	Weipa	Weipa		Weipa
Qld	Halifax Bay	Halifax Bay		Halifax Bay

*Only otoliths were collected from these sites.

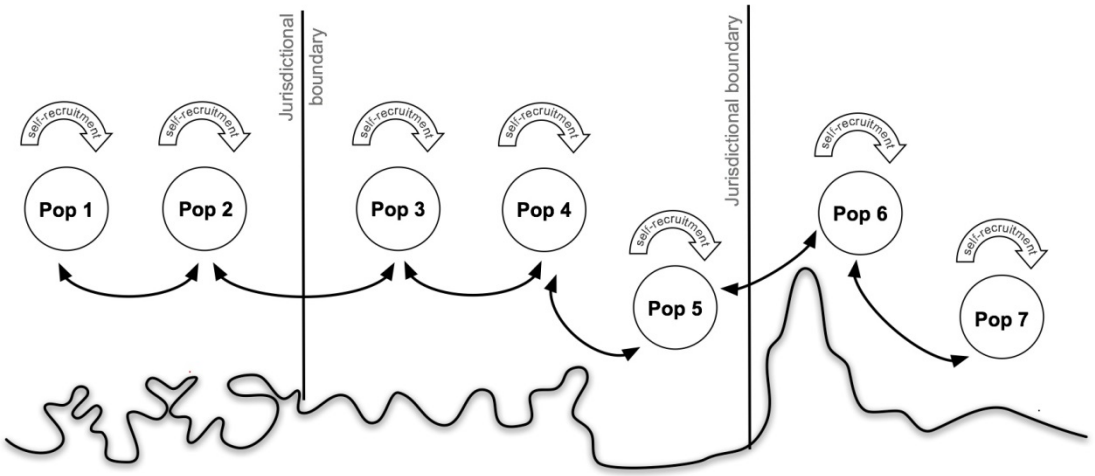

Figure 13. Conceptual model of how populations of Golden Snapper are connected across northern Australia. Each population is self-recruiting with levels of genetic interchange occurring between them. Solid arrows indicate higher levels of exchange between the populations. Based on the results, populations tend to exist at the reef complex level at the scale of tens of kilometres.

Table 28. Stock differentiation matrix (SDM) for Grass Emperor showing the results generated from the regional pairwise comparisons for the three techniques used in this study. Genetic pairwise comparison results were inferred from the final Fst groupings based on pooling adjacent locations. Where significantly different results were found for pairwise comparison of the sampling locations, they are indicated by the capital letters in bold: G—genetics, P—parasites, O—otolith stable isotopes. Non-significant results are indicated by lowercase letters corresponding to the respective techniques. In those cases where no analysis was carried out, they are denoted by "-".Results for parasites and otolith are from the plots in Figure 10; near core otolith results are used. Results for the genetics are based on the pooled F_{ST}.

	Locations	**LP**	**CP**	**DP**	**CS**	**CV**	**Wa**	**RR**	**DH**	**CoP**	**VI**	**HB**	**SC**	**MB**
WA	Locker Point													
WA	Cape Preston	o p g												
WA	Dampier Peninsula	**O P** g	o **P** g											
WA	Camden Sound	o **P** g	o **P** g	**O P** g										
WA	Cape Voltaire	**O P** g	**O P** g	**O P** g	o **P** g									
NT	Wadeye	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**								
NT	Roche Reef	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	o **P** g							
NT	Darwin Harbour	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	o **P** g	o **P** g						
NT	Coburg Peninsula	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	o **P** g	o **P** g	o **P** g					
NT	Vanderlin Islands	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	**O P G**	**O P G**	**O P G**	**O P G**				
Qld	Halifax Bay	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**			
Qld	Sunshine Coast	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	- - **G**	**O P G**		
Qld	Moreton Bay	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	**O P** -	o **P** -	

Table 29. End-user table that summarises results from all techniques to determine the broadest spatial scale appropriate for management of Grass Emperor based on sampling locations in this study

	Otoliths	Parasites	Genetics	Management units
WA	Central Western Australia	Central Western Australia	North Western Australia	Central Western Australia
WA				
WA	Dampier Peninsula	Dampier Peninsula		Dampier Peninsula
WA	Northern Kimberly	Camden Sound		Camden Sound
WA		Cape Voltaire		Cape Voltaire
NT	Western Northern Territory	Wadeye	Western Northern Territory	Wadeye
NT		Roche Reef		Roche Reef
NT		Darwin Harbour		Darwin Harbour
NT		Coburg Peninsula		Coburg Peninsula
NT	Vanderlin Islands	Vanderlin Islands	Vanderlin Islands	Vanderlin Islands
Qld	Halifax Bay	Halifax Bay	Halifax Bay	Halifax Bay
Qld	South East Queensland	Sunshine Coast	Sunshine Coast	Sunshine Coast
Qld		Moreton Bay*		Moreton Bay

* Genetic material was unable to be obtained in sufficient amounts from samples from Moreton Bay.

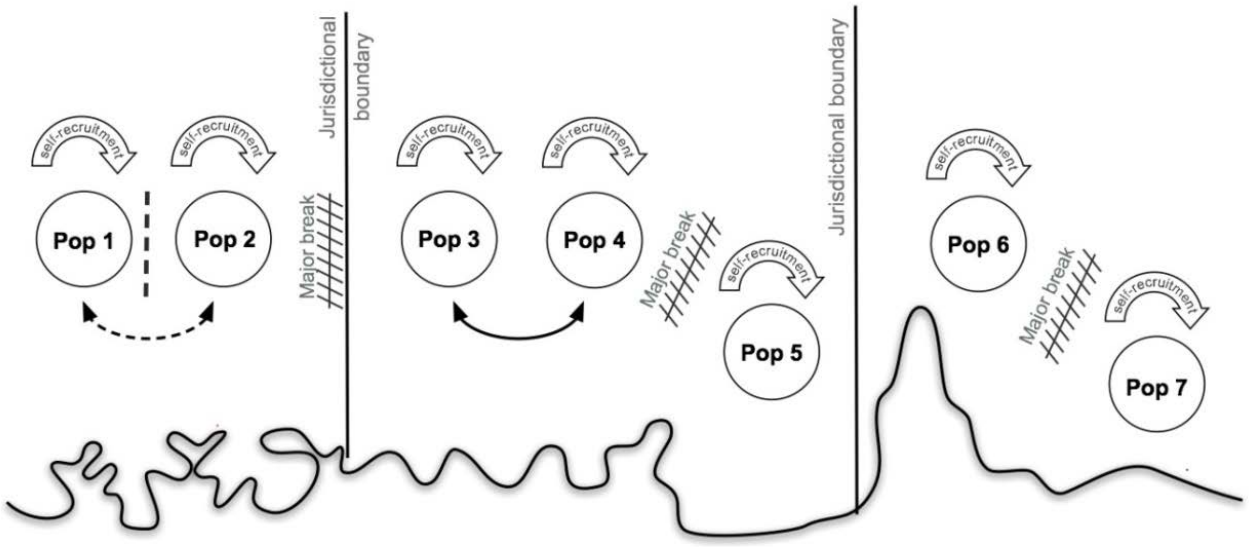

Figure 14. Conceptual model for the future management of stocks of Grass Emperor across northern Australia. Each population is self-recruiting with levels of genetic interchange occurring between them. Dashed arrows indicate low levels of genetic interchange; solid arrows indicate higher levels of exchange between the populations. Major breaks indicate that a major geological/biological feature occurs to separate exchange between populations. Based on the results, populations tend to exist at the reef complex level at the scale of tens of kilometres.

3.5 Indigenous Training

3.5.1 Training course results

All of the students that participated in the course achieved competency on their first attempt. The trainers also conducted a basic, anonymous evaluation of the course by the students, which asked whether they found the course content interesting and whether they thought the trainers had done a good job delivering the course. All of the students completed the evaluation and all of them indicated that the course content was interesting and that the trainers had delivered it well. However, it has been over two years since the completion of the course so there can be several other measures applied to assess its success. Out of the 17 students only one is no longer employed as an IMR; three have been employed as technical officers (two at T1 and one at T4 level) with government research agencies in Darwin; two IMR groups (seven students in total) are currently involved in collecting scientific information for several projects for DPIR on a fee-for-service basis and the other seven students are still working as IMRs. Both of the T1 employees have started a Certificate IV course in Laboratory Techniques. All of the students still in employment as IMRs have had their skills informally re-assessed by research scientists from DPIR approximately six months after the completion of the course. This process included the scientists going out on a routine IMR patrol where they collected fish samples that were taken back to the community offices for dissection. In all cases, the former students were observed to accurately record data on the location where the fish were caught, which was transferred to the datasheets that were used to record the details of the samples collected during the dissection of the fish. The scientists did not need to prompt any of the students during the chain of data collection and only a few former students sought clarification during the dissection process. Given the successful outputs so far from trained IMRs, there are many other Indigenous communities from the NT, WA, Queensland and Torres Strait who want their members to participate in the training. Consequently, another course is scheduled during 2017 to accommodate this interest.

3.5.2 Research activities conducted by students post training

Students have participated in three key areas of providing monitoring information to DPIR subsequent to their training. One of these has been providing samples for the current project. These samples were collected by students from four separate IMR groups and were critical in getting a geographical spread of samples from the remote areas of the NT. Furthermore, two IMR groups have been collecting barramundi flesh and liver samples for a project investigating the factors that influence mercury concentrations in the tissue of this species. The collection of these samples has obvious benefits in understanding the variability in levels of mercury and whether the results indicate consumption limitations to address any health concerns. Finally, several IMR groups have provided fish and water samples when fish kills have happened in waters adjacent to their communities. In all cases, samples were either shipped back to Darwin for analyses or stored in their local freezers for collection by DPIR. All data sheets relating to the sample collection were emailed to DPIR. All of this information could not have been collected within the funding for these projects had DPIR not conducted the sampling.

4 Discussion

4.1 Objective 1: Gain Information on Stock Structure of Key Tropical Reef Fish Species

This project used a holistic approach to determine the stock structure of three key nearshore fishery species of northern Australia: Black Jewfish, Golden Snapper, and Grass Emperor. The three key species represent iconic fish species targeted by all fishery sectors, particularly the recreational fishing sector. Given the importance of these three species to local fisheries and the lack of relevant information for informed management, this project determined their stock structure, which provides the spatial basis for

management of fisheries stocks generally. This will be critically important for Golden Snapper and Black Jewfish as both species have been identified as overfished in some parts of their northern Australian range (e.g. Saunders et al. 2014a and b), while recreational targeting of Grass Emperor indicates that this species is also vulnerable to overfishing.

For each species three different techniques were used concurrently to determine stock structure: microsatellites, otolith chemistry and parasites. These techniques have all been used effectively in the past in identifying fishery species stock structure and have been increasingly combined in holistic studies (Begg and Waldman, 1999; Buckworth et al., 2007; Izzo et al., 2012; Welch et al., 2010, 2011, 2015). The holistic approach is important as it utilises the different characteristics of different techniques, in particular the spatial and temporal scales at which they provide information, to create a more comprehensive picture of species stock structures with greater confidence than is possible with a single technique in isolation (Welch et al., 2015).

The scale of stock structuring differed among the three species and varied with the technique used. Both Grass Emperor and Golden Snapper had generally quite strong genetic connectivity throughout northern Australia with an IBD model applying across hundreds of kilometres. However, Black Jewfish demonstrated much higher genetic segregation in this region with sites in WA in particular, demonstrating genetic separation at the scale of hundreds of kilometres. Grass Emperor and Golden Snapper stocks were identified at the scale of tens of kilometres according to the otolith microchemistry and parasitology analyses indicating strong juvenile/adult site fidelity. However, Black Jewfish appeared to have adult movement among sites separated by tens of kilometres.

The strongest genetic structure was observed in Black Jewfish, in particular between Roebuck Bay in WA and the rest of the sampling range. Although this result may not appear surprising given that there is a distance of ~400 km between Roebuck Bay and the nearest location (Camden Sound), similar or greater distances between other sampling locations did not result in similarly strong genetic breaks. It is more likely that the duality of the geomorphology and hydrodynamics of the WA tropical coastline may help explain this observation. This part of the coastline is divided into the Kimberley and Canning bioregions, separated by the Dampier Peninsula, each with their distinctly different regimes of tidal influence, substrate composition, extent of the river networks and mangrove area (Semeniuk, 1993; Thackway and Cresswell, 1998). The tip of the Dampier Peninsula has been identified as an important biogeographic break for marine species (Hutchins, 1994; Travers et al. 2010; Wilson, 2013) reflecting a pronounced shift in the underlying geology (e.g. from sedimentary sandstone in the north to unconsolidated sand and silt in the south) and associated dominant benthic habitat (e.g. from coral reefs in the north to soft substrate communities in the south), in combination with a prominent increase in tidal currents and associated water turbidity to the north. It is thus relevant that the Kimberley-Canning border is characterised by the largest tropical tidal range (~12 m) and some of the fastest tidal currents in the world (2.5 m s^{-1}), including the input of massive volumes of fresh water in a highly turbid plume from the Fitzroy River during the monsoonal wet season (Wolanski and Spagnol, 2003). The Kimberley bioregion consists of ancient steep mountain ranges with an extensive river system thereby creating a jagged ria coastline with many estuarine areas and extensive mangrove forests. In contrast, the Canning bioregion is characterised by a more contiguous coastline with no rivers. This duality in coastal geomorphology results in discontinuity in the marine habitat that is likely to affect larval dispersal and dictate spatial population structure. Past studies have in fact found that fish assemblages among the two regions are different (Hutchins, 2001; Fox and Beckley, 2005; Travers et al., 2006, 2010). Other recent studies on king and blue threadfins and grey mackerel have also found strong east-west phylogeographic breaks between Roebuck Bay and locations farther to the east (Broderick et al., 2011; Horne et al., 2011).

The Vanderlin Islands, in the Gulf of Carpentaria, were also genetically distinct from other locations. This is not surprising given the results above and given that the islands are geographically isolated from other locations. Further, the Vanderlin Islands lie in the southwestern region of the Gulf of Carpentaria, a shallow semi-enclosed sea with very long flushing timescales and times of residence for particles (Condie, 2011). Conversely, a study on the genetic stock structure of grey mackerel, a mobile pelagic species, found Vanderlin Island fish to be genetically similar to fish throughout the Gulf of Carpentaria and farther

west into the NT (Broderick et al., 2011). An interesting result was the genetic distinctiveness of fish sampled farther offshore in the Arafura Sea. This result further suggests that local hydrodynamics probably play a significant role in larval connectivity but also further confirms that adult mixing can be very low, even in the inshore - offshore continuum.

For Black Jewfish, the otolith microchemistry and parasite analyses indicated stocks that occurred at similar scales to the genetics where sites were separated by tens to hundreds of kilometres. However, there were finer scale differences detected by non-genetic techniques when the scale of separation was only hundreds of kilometres. There was good agreement among these two techniques with the only difference being that the otolith microchemistry grouped both Tiwi Island sites with the offshore Darwin site while the parasite fauna was significantly different in samples collected in Bathurst Island compared with the other two sites.

While the genetic structure for Grass Emperor was substantially less than for Black Jewfish, the results supported a general isolation IBD model whereby sites separated by larger distances were significantly different from each other. However, there was a significant break between Cape Voltaire in Western Australia and Wadeye in the NT. This resulted in a western and an eastern genetic cluster on either side of the jurisdictional border. Local hydrodynamics may help to explain this observation with modelling having shown the existence of a dominant Indonesian-based current that predominantly flows southwest along the WA coast from the Kimberley (D'Adamo et al., 2009). However, *in situ* observations show a more complex current system with the strong Arafura current that flows westward from the Arnhem Coast across the top of the Joseph Bonaparte Gulf, as well as a strong north-east current from Melville Island into the Van Diemen Gulf to the east (Hill et al. 2002; Condie, 2011; Schiller, 2011). As the genetic break appears to be around the Joseph Bonaparte Gulf, it may be relevant that this is a large, relatively shallow body of water characterised by strong currents and high bottom stress (Condie, 2011), which may restrict larval movement between regions either side or reduce the suitability of settlement habitat for fish recruits, respectively. Furthermore, depth and habitat preferences of Grass Emperor may restrict adult movement across this break given their reported maximum depth of ~25 m and the deeper water adjacent to the Kimberley coast (Condie, 2011; Newman and Williams, 1996). There was also a significant genetic break between the sites on the east coast of Queensland and the rest of the sampling indicating that the Gulf of Carpentaria and Torres Strait act as a geographic barrier to larval transport. Additionally, there was a genetic difference between the two east coast samples separated by hundreds of kilometres, which suggests that significant geographic barriers are not necessary to limit gene flow between locations.

For Grass Emperor, both the parasite and otolith chemistry data revealed generally similar results showing that stock structuring of this species can occur at much finer spatial scales (tens to hundreds of kilometres) than indicated by the genetic results (thousands of kilometres). Generally, agreement among the non-genetic techniques was also strong with only a couple of discrepancies. For example, otolith chemistry in fish from Locker Point and Cape Preston was different; however. the parasite assemblages were similar. Similarly, parasite assemblages were different between Dampier Peninsula and Camden Sound; however, the otolith chemical signatures were similar. However, if either of these techniques demonstrates significant differences between sites, it can be assumed that movement of post-larval individuals is restricted between these adjacent populations.

The genetic structure for Golden Snapper was similar in scale to Grass Emperor and again the results supported an IBD model. There were significant differences between the two offshores sites in the NT (Bonaparte Gulf and Arafura Sea) compared with all other samples, indicating that there are geomorphic barriers existing at a scale of hundreds of kilometres. It is unknown whether these barriers are driven by currents or lack of suitable settlement habitat existing between inshore and offshore sites. Unusually, Groote Eylandt in the Gulf of Carpentaria was significantly genetically different to sites in this region separated by only tens of kilometres. While interesting, it seems that there are no good reasons to identify how this separation is occurring as there are numerous reef and island complexes between Groote Eylandt and the closest site (Blue Mud Bay) and no evidence of substantial currents that would inhibit transport of larvae between these locations. Another site that was significantly different from the

others was Halifax Bay on the east coast, which would be due to the Torres Strait geographic barrier inhibiting larval transport between the east coast and the rest of northern Australia.

For Golden Snapper, both the parasite and otolith chemistry data revealed generally similar results showing that stock structuring of this species can occur at much finer spatial scales (tens of kilometres) than indicated by the genetic results. In general, there was agreement among the non-genetic techniques with only a couple of discrepancies. Lorna Shoal and Wadeye samples had significant differences in otolith microchemistry but had similar parasite fauna, while the opposite was true for Coburg Peninsula and Goulbourn Island. Both of these techniques showed a similar grouping of sites in the Gulf of Carpentaria, with sites in the groupings occurring among sites on the western and eastern sides, although the southern boundary of the western grouping was determined to be different by both techniques. While these groupings of sites existed suggesting stocks that occurred over several hundreds of kilometres, mostly all sites were identified as separate stocks even when they were only tens of kilometres apart.

Such fine spatial scale stock structuring is increasingly being observed in tropical and sub-tropical fish species despite their relatively large sizes and a high capacity for large-scale movements. Many of these previously studied species share the same range as those species in this study and include Blue Threadfin (*Eleutheronema tetradactylum*) and King Threadfin (*Polydactylus macrochir*) (Welch et al., 2010), Barramundi (*Lates calcarifer*) (Shaklee and Salini, 1985), Spanish Mackerel (*Scomberomorus commerson*) (Buckworth et al., 2007) and Grey Mackerel (*Scomberomorus semifasciatus*) (Welch et al., 2009). It appears increasingly evident that nearshore/estuarine species tend to limit movement and prefer areas localised to where they settle after the larval phase, although there are some long-distance movements for some species, which appear to be isolated (Welch et al., 2010). The mechanism for this pattern is unclear; however, several studies have demonstrated a close association with the demography and catches of some of these same species and local river systems and/or embayments (Balston, 2009; Halliday et al, 2011; Meynecke and Lee, 2011; Newman et al., 2011). For example, it is hypothesised that *E. tetradactylum* populations are linked to particular river systems throughout their life cycle with site fidelity of adults and sub-adults, as well as a 'circular' swimming pattern of larvae that may be due to cues from 'home' rivers to which they are attracted (Horne et al., 2011; Welch et al., 2010).

4.2 Objective 2- Develop Indigenous Capability in Scientific Monitoring and Participation in Co-management through the Development of a Certified Training Program

4.2.1 Benefits and costs of training Indigenous community members

The main benefit of the training has been the increase in IMRs' research capability across the NT, which has had the effect of IMRs gaining additional funding by conducting research activities on a fee-for-service basis. This allows them to either generate additional ranger positions, purchase capital equipment or conduct additional fieldwork that benefits the community (e.g. compliance patrols and searches for discarded fishing gear). Furthermore, the training has provided students with increased employment opportunities, with three of the participants securing employment as technical officers in research agencies based in Darwin. Without the qualification, they would have had a lesser chance of obtaining these positions. In terms of savings for DPIR, the collection of the samples would cost about $3000 per day for two staff over three days; these figures are equivalent to most research agencies research costs. Additionally, there would be at least two extra days travelling time to get to the communities, which would additionally cost $2500 bringing the total cost to $11 500. In comparison, IMRs charge $1700 per day to conduct sampling; so for the same period of sample collection, it would cost only $5100. This represents more than 55% in savings on research costs. These figures are based on 2015-2016 DPIR salary and daily travel allowance for two Technical Officer 3 positions and estimated operational costs for using a vehicle and boat each day.

4.2.2 Future directions

The short-term goals of the training (increase monitoring capacity of Indigenous communities, improve employment opportunities and reduce the cost of monitoring activities in remote areas) have been achieved more than two years after the course was conducted. However, regarding employment benefits, there is a need for more students to complete the courses to get an indication of how representative the results from this study are. Jobs in most disciplines of biological research are quite rare across Australia, let alone in remote and regional centres of the NT, where many students obtain undergraduate and postgraduate training at universities but are unable to gain employment in their field of study. There has been a great effort to increase the capability of Indigenous communities to engage in natural resource management (e.g. Sithole, 2012); however, the opportunities for employment in communities are extremely limited (May et al., 2010). Consequently, there needs to be a significant increase in funding and government support to increase such employment opportunities (Altman et al., 2011).

The cost savings from IMRs conducting research within their communities have already been substantial from this project and other examples of engaging Indigenous community members in research (e.g. Almany et al., 2010; Prescott et al., 2016). However, these savings could be further optimised if the current model of government agencies running all aspects of aquatic resource management moves to a co-management model whereby both research and management capability resides within Indigenous communities and the management agency takes on a more administrative role with fewer staff based in larger population centres.

The longer-term goal of this training is to utilise the increased research capability within communities to assist with the development of research partnerships to facilitate the move to co-management. The first co-management model being explored between DPIR and Indigenous communities is based on developing Indigenous fisheries in waters adjacent to their communities (DPIR, 2011). Community members that have taken up these licences have aspirations to both provide food to their community and also generate income through the sale of fish locally or in Darwin. While IMRs who participated in the course have already been involved in collecting biological samples from this fishing activity, as these fisheries develop, they will conduct routine monitoring to provide information to DPIR to assess the impacts of harvest on the species being targeted. This research partnership is still in its infancy and there have only been aspirational discussions between DPIR and Indigenous communities near Maningrida and Nhulunbuy (Figure 1) during meetings with Aboriginal Consultative Committees (e.g. DPIR, 2015). However, there is already at least one model developed in northern Australia that can be used as an example to move this research partnership to a co-management system (Dobbs et al., 2016). This study integrated Indigenous and western scientific knowledge in remote wetlands using field-based monitoring activities and workshops, which provided a comprehensive list of management priorities and aspirations that informed the basis of a co-management plan (Dobbs et al., 2016).

While there have been numerous examples of Indigenous community members engaging in monitoring activities associated with aquatic resources (e.g. Almany et al., 2010; Cohen and Steenbergen, 2015; Prescott et al., 2016; Rose et al., 2016), most of these have involved a research partnership where participants are informally trained by scientists. There has been at least one other example of community members undertaking a registered training course in aquaculture to participate in sea ranching trials of (*Holothuria scabra*) in waters off Goulbourn Island in the NT (Fleming et al., 2015; Gould, 2016). The development of that course was based on exactly the same objectives as the training that was undertaken in the current study: increasing Indigenous community capability and providing increased employment opportunities (Fleming et al., 2015). While the aquaculture training was explicitly designed for conducting work on developing enterprises within the community (Fleming et al., 2015) the qualification obtained at the end of the training would have offered similar benefits to students seeking jobs in research agencies outside of the community as is the case in the current study. Given the success of the training in this study, it is intended that this course will become a regular training component for IMRs. However, in addition to training IMRs, it is intended to broaden the course to target teenagers in school, since it has been recognised that training to facilitate increased Indigenous participation in resource management should begin long before students become ‘rangers’ (Altman et al., 2011).

4.3 Objective 3- Identify an Appropriate Spatial Scale of Management for Tropical Reef Fish based on Biological Sustainability and Sectoral Aspirations

The most powerful way to reliably determine stock structure is through the concurrent use of different techniques. This is referred to as a holistic approach and has been increasingly used and advocated in stock structure studies (e.g. Buckworth et al., 2007; Abaunza et al., 2008; Baldwin et al., 2012; Welch et al., 2015). Historically, stock structure studies have employed a single analytical technique to detect differences among populations; however, a major limitation of such approaches is that when no differences are detected, this may merely reflect the discriminating power of the particular technique. It does not necessarily mean they are from the same stock. Using a holistic approach, therefore, greatly increases the likelihood of detecting different stocks where they exist (Begg and Waldman, 1999). The use of several techniques also enables different temporal, spatial and evolutionary scales to be addressed (Welch et al., 2015). A holistic approach therefore provides a 'weight of evidence' approach to more accurately identify individual fish stocks.

The purpose of establishing the stock structure of exploited species is to inform managers and other stakeholders on the appropriate spatial scale at which management of targeted species should occur. Management at this scale thereby provides the basis for ensuring biological sustainability. The use of the three different techniques on each species in this study provides different levels of information on connectivity at different spatial scales generally (larger for genetics and finer-scale for parasites and otolith chemistry), as well as different time scales; genetics provide historical patterns of population connectivity and divergence as well as contemporary connectivity, while parasites and otolith chemistry are more relevant to the actual lifetime connectivity among adults and sub-adults (Welch et al., 2015). While genetic information is an important descriptor of stock structure for fisheries and conservation management, fisheries managers generally are interested in management of stocks on time scales relevant to the lifetime of the species in question. Genetic connectivity can be maintained among stocks through the exchange of several individuals per generation (Palumbi, 2003). However, this level of exchange is demographically insignificant and would not replenish stocks at time scales that are meaningful to fisheries activities. Consequently, the otolith and parasite chemistry results in this study that indicated localised structure would suggest that management for these three species is most appropriate at finer spatial scales.

With this in mind, it is important to note that the 'stocks' defined by the integration technique (Tables 27-29) were determined using a statistically significant 95% CI. A more conservative approach would have been to use the reclassification success in the non-genetic methods, which would have identified separate stocks at each of the sites where samples were collected for all species. Another consideration with the 'stocks' identified, is that there were numerous samples that were hundreds to thousands of kilometres from the closest site. The fact that they were classified as separate stocks does not mean that a line can be drawn half way between them as separate management units. The conceptual models for each species were developed to assist fisheries managers to understand how these stocks operate when there is limited clarity on where the boundary of the stock exists. The suggested approach for delineating a management unit for separate or multiple stocks of these species would be to identify the aggregation areas or reef complexes that are targeted by fishers. If several of these can be managed sustainably together under total allowable catches or effort restrictions (whether they be enforced or occur due to isolation of the stocks) for all sectors, then having a broader management unit can occur. This situation would appear to be pertinent for the stocks of these species that exist in WA and parts of Queensland and the NT where there is relatively little harvest of these species due to the remoteness of these stocks. However, if separate stocks can have relatively unconstrained harvest occurring on them, then management units probably need to occur at the stock level. This situation has been initiated in the Darwin area of the NT as a part of the recovery program for the species in this study. However, the stocks that have been identified in this project indicate that further units of management may need to be implemented to ensure that this overfishing problem does not become more widespread in this region.

In addition to identifying the appropriate scales of management, the results of this study can be more specifically used to improve the performance of stock status assessments and developing harvest strategies. Additionally, the results can assist with resource allocation among different sectors as the fine-scale stock structure for these species provides the option of sectors having 'sole' access to certain stocks to lessen competition and conflict. Examples could include allowing sole access to Indigenous communities to stocks inhabiting waters adjacent to their land and sea country or allowing recreational anglers sole access to stocks located at access locations, such as boat ramps or accommodation.

5 Conclusion

Key Findings

- The project determined that each of the three species showed similar stock structuring with genetically homogeneous populations across distances ranging from hundreds to several thousands of kilometres and likely to be predominantly connected through larval dispersal mechanisms. Further, each species shows that post-larval fish have limited movement resulting in localised adult and sub-adult populations. These populations appear to be limited to areas from tens to a few hundred kilometres. This means that each of these species has an increased risk of localised depletions.
- This study shows that the spatial scale for management of the three study species is generally similar. Based on post-larval movement of each species, the appropriate spatial scale for management is at localised scales. However, the feasibility of regional management, although with considerable potential benefits to biological sustainability and sectoral resource allocation issues, would need to be weighed up against the cost of what is a potentially more resource-intensive management approach.
- The use of a holistic approach to stock structure studies has been advocated for some time and although there are now several examples in northern Australia, globally holistic studies are still relatively limited. The use of the holistic approach was vindicated in the current study for three coastal fish species, whereby likely spatial scales for movement and connectivity among the different life history stages (larval – sub-adult – adult) was ascertained by the different methods.
- Accredited training has led to ongoing contracts with ranger groups and has the potential to significantly reduce research and management costs.
- The Indigenous training course developed in this project has the potential to become a major source of Indigenous capacity building in the area of scientific monitoring. It will be implemented within DPIR's Indigenous training curriculum and broadened to include IMRs and members from other communities in the NT, Queensland, WA and Torres Strait.

Key Outcomes

- The project has filled important information gaps for the three of the most important coastal fishery target species in northern Australia. Fisheries managers and other stakeholders have sufficient information to apply appropriate arrangements for management of the three study species to ensure sustainability and appropriate access and allocation among all sectors. These decisions will pave the way for individual sectors to have future surety on their access rights and catch allocations. That will include increasing or maintaining the value of commercial licences by providing surety on access, ensuring ongoing access to the resource by the recreational sector and providing a framework whereby Indigenous fisheries targeting coastal reef fish species will be able to develop in a sustainable and economically viable manner.
- A Certificate II training course in sampling and analysis (MSL20109) was developed and conducted by DPIR in partnership with the registered training organisation Labtech Training.
- This training has provided an increased scientific monitoring capability to course participants. Three participants have been employed by government research agencies and three Indigenous communities are now participating in scientific monitoring programs on a fee-for-service basis, which provides additional income to these groups to either employ more rangers or fund priority

community projects. This increased monitoring capability will ensure Indigenous communities have the capability to collect the information needed to develop fisheries in their sea country in a sustainable manner and provide the background to participate in co-management.

Implications

The fine-scale stock structure that was found for the three study species has large economic implications for both the management agencies and industries targeting these species. Current management of these fisheries resources in northern Australia is jurisdiction-based, which provides large cost savings to management agencies by not having to conduct monitoring assessments at many different scales, or to monitor the industries that target them as they have a large degree of flexibility to conduct their fishing operations, are not restricted by limitations on GVP from localised total allowable catches (TACs) and have fewer costs passed on from the management agencies.

While it is difficult to put exact figures on the additional costs of fine-scale management, the recent overfishing of these species in the NT can provide some insight into the costs when management has not been conducted at an appropriate scale and a recovery program is implemented. The NT Coastal Line Fishery that targets these species has had a TAC implemented for Black Jewfish and Golden Snapper as well as a tight 'group species' TAC that does not allow them to target other reef fish. They also had areas closed to them and most licences were moved to lightly-fished regions. The lost GVP from these restrictions is close to $1 million based on recent annual averages but would be closer to several million dollars at peak harvest levels. Additionally, licence values have reduced by more than 50% for those fishers moved to other regions. Until recently, ten fishing tour operators targeted these species. The recent declines in TACs have caused losses to most operators. The recovery program for these species has also meant that a large research and monitoring program had to be implemented to measure the effectiveness of these management arrangements, which is estimated to cost over half a million dollars annually. This fishery is quite small even by NT standards, so while these costs do not seem large, they have had significant impacts on the commercial and recreational sectors and DPIR.

If the information from this project had been available ten years ago and management had acted quickly, there would have been additional costs and restrictions to all commercial operations targeting these species as well DPIR. But they would have been less than the current costs of the recovery program.

The increased research capability of the Indigenous participants in the training has provided efficiency dividends in the cost of monitoring for DPIR and provided additional money for IMR groups (see details in 4.2.1).

Recommendations

This project identified that all the three species had fine-scale stock structure needs, which have to be taken into consideration by the management of fisheries that harvest them. The overfishing of these species in the Darwin region highlights their vulnerability to serial depletion of localised stocks. Additionally, it is likely that these species are representative of many tropical reef-associated fish. It is therefore suggested that the management of this species group takes into account that they are likely to have fine-scale stock structure.

Further Development

The longer-term goal of Indigenous training is to assist the development of research partnerships to facilitate the move to co-management. The first co-management model being explored by DPIR and Indigenous communities is based on developing Indigenous fisheries in waters adjacent to their communities. Community members that have taken up these licences have aspirations to both provide food to their community and generate income through the sale of fish locally or to Darwin. As these

fisheries develop, it is hoped that trained community members will conduct routine monitoring to inform DPIR to assess the impacts of this harvest on the species being targeted.

Given the success of the training conducted in this project, it is intended that this course will become a regular training component for IMRs. However, in addition to training IMRs, it is intended to broaden the course to target teenagers in school to improve employment opportunities for them.

The stock structure component of this project collected a large number of samples across the distribution of each species. However, there were numerous 'gaps' in the sample collection as the focus of the research was around the Darwin region because of the recent overfishing of these species in this area. In particular, if catches of these species were to increase significantly in waters off Arnhem Land (NT), the Gulf of Carpentaria and Queensland's east coast, it would be appropriate to better understand the fine-scale stock structures of these species for their sustainable management.

Extension and Adoption

Extension

The stock structures determined for the three species studied have already been presented to the Executive Director of Fisheries, the Director of Fisheries and Aquaculture and Aquatic Resource Managers of the Fisheries Division of DPIR. The results have also been presented to commercial fishers in the NT Coastal Line Fishery and the Recreational Fishing Advisory Committee. Although recent management measures were introduced in 2015 to address the overfishing of coastal reef fish species in NT waters (https://nt.gov.au), many of them were designed to protect specific stocks of Golden Snapper as this species was identified as the most overfished. However, after presenting the results at the above forums, all stakeholders have identified that Black Jewfish aggregations not protected by these recent changes have suffered significant declines recently. Consequently, DPIR prioritised the Coastal Line Fishery as one fishery for which a harvest strategy would be developed within the next year. During this development period, the results of this study will assist in the implementation of specific management reductions on separate stocks of Black Jewfish, such as catch limits and/or temporal and spatial fishing closures. The stock structure determined for the other two species will be used to prepare a harvest strategy for the Coastal Line Fishery and the Offshore Snapper fisheries that catch these species.

The PI for this project will present these results to fisheries managers and researchers in Queensland to assist with their annual stock assessment workshop in 2017. Grass Emperor are the only species of the three studied that are caught in substantial amounts in Queensland and there has been no immediate sustainability concern raised for them. However, the results will assist with the status assessment of this species in Queensland. CI Steve Newman will present the results to fisheries managers in WA. Due to the general remoteness of the coastline that these species inhabit in this jurisdiction, there are current sustainability concerns for these species. However, these results will assist in updating harvest strategies and contribute to any third party accreditation (Marine Stewardship Council) processes for the fisheries that catch these species in Western Australia.

The additional capability provided to Indigenous communities that had participants in the training program has already enabled several students to successfully apply for research positions within government agencies. Additionally, several IMR groups are conducting fisheries monitoring activities on a fee-for-service basis, which provide the dual benefit of income to the community and cost savings to DPIR by not having to send staff from Darwin to remote areas to conduct these activities. The measuring and analysis training course that was developed in this project will also become part of the regular Indigenous training curriculum conducted by DPIR. Indigenous ranger groups from WA, Queensland and Torres Strait are interested to send students to future courses.

One of the specific longer-term outcomes of this training was to provide Indigenous communities the necessary skills to collect information on species targeted in community-based fisheries. It is envisaged that this first step in participating in research will assist the development of ongoing research

partnerships between Indigenous communities and DPIR to form the basis for future co-management. However, the development of Indigenous fisheries has been slower than anticipated, which has delayed the participation of trained community members in monitoring activities associated with their fishery harvest.

Communication

As discussed above, there has already been substantial communication with stakeholders in the NT and this will be extended to WA and Queensland in the near future. The results will also contribute information to jurisdictional status reports for these species as well as to the national Status of Australian Fish Stocks Report from 2016 onwards. There was substantial media coverage around the success of the training course and the PI and Simon Xuereb have published an article detailing its outcomes in a special issue of *Reviews in Fish Biology and Fisheries*. Additionally, these investigators had numerous meetings with Indigenous ranger groups and relevant researchers in the NT, WA, Queensland and Torres Strait on providing participants for the next scheduled training course in 2017.

CI's Dave Crook, Di Barton and Laura Taillebois presented the results of the stock structure component of the project at the Australian Society of Fish Biology Conference in 2016. Additionally, the stock structure results from this study will be published in several international scientific journals in the next six to 12 months.

The results of the project will also be communicated to other relevant forums, such as steering committees for the Northern Research Partnership, Research Providers Network, Indigenous Reference Group and Research Advisory Committees in the NT, Queensland and WA.

Project coverage

Articles on the Indigenous training course were published in FRDC's *FISH Magazine* and DPIR's Chief Executive's Newsletter in 2015.

Project Materials Developed

The Certificate II in Measuring and Analysis under the Australian Vocational Education Training Scheme.

Published papers

1. Barton, D. P. and Morgan, J. A. T. (2016). A morphological and genetic description of pentastomid infective nymphs belonging to the family Sebekidae Sambon 1922 in fish in Australian waters. *Folia Parasitologica*, **63:** 026 doi: 10.14411/fp.2016.026.
2. Moravec, F. and Barton, D. P. (2015). Two gonad-infecting species of Philometra Costa, 1845 (Nematoda: Philometridae) from marine fishes off the northern coast of Australia. *Parasite*, **22:**4.
3. Moravec, F. and Barton, D. P. (2016). New tissue-dwelling species of Philometra Costa, 1845 and Philometroides Yamaguti, 1935 (Nematoda: Philometridae) from marine perciform fishes off the northern coast of Australia. *Systematic Parasitology*, **93:** 623-637.
4. Taillebois, L., Dudgeon, C., Maher, S., Crook, D. A., Saunders, T. M., Barton, D. P., Taylor, J. A., Welch, D. J., Newman, S. J., Travers, M. J., Saunders, R. J. and Ovenden, J. (2016). Characterization, development and multiplexing of microsatellite markers in three commercially exploited reef fish and their application for stock identification. *Peer J.* **4:**e2418.
5. Saunders, T and Xuereb, S. (2016) Optimising the monitoring of tropical aquatic resources through the development of Indigenous scientific capability. *Reviews in Fish Biology and Fisheries*, 26(4), 727-736

Appendices

Appendix 1 – Staff

Name	Organisation
Thor Saunders	Department of Primary Industry and Resources (NT) (Principal Investigator)
David Welch	C2O Consulting
David Crook	Charles Darwin University
Laura Taillebois	Charles Darwin University
Jenny Ovenden	University of Queensland
Steve Newman	Department of Fisheries (WA)
Mike Travers	Department of Fisheries (WA)
Richard Saunders	Queensland Department of Forestry and Fisheries
Safia Maher	University of Queensland
Christine Dudgeon	University of Queensland
Di Barton	Department of Primary Industry and Resources (NT)
Jon Taylor	Department of Primary Industry and Resources (NT)
Mark Hearnden	Department of Primary Industry and Resources (NT)
Simon Xuereb	Department of Primary Industry and Resources (NT)
Chris Errity	Department of Primary Industry and Resources (NT)
Bryan Mcdonald	Department of Primary Industry and Resources (NT)
Robert Carne	Department of Primary Industry and Resources (NT)
Quentin Allsop	Department of Primary Industry and Resources (NT)
Dan Schmidt	Griffiths University

Appendix 2 – Intellectual property

No patentable or marketable products or processes have arisen from this research. All results will be published in scientific and non-technical literature. For the stock structure component the raw data from field sampling remains the intellectual property of DPIR. Intellectual property of the samples collected from fish (otoliths, parasites, fin clips and muscle tissue) and that accruing from their analysis and interpretation vests jointly with DPIR, CDU and the University of Queensland. For the Indigenous training component, intellectual property of the course content remains the property of DPIR and Labtech Training.

Appendix 3. - References

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Appendix 4 – Parasite experts consulted

This is a list of experts who provided assistance in the identifications of parasites. Institute locations are in Australia unless indicated otherwise.

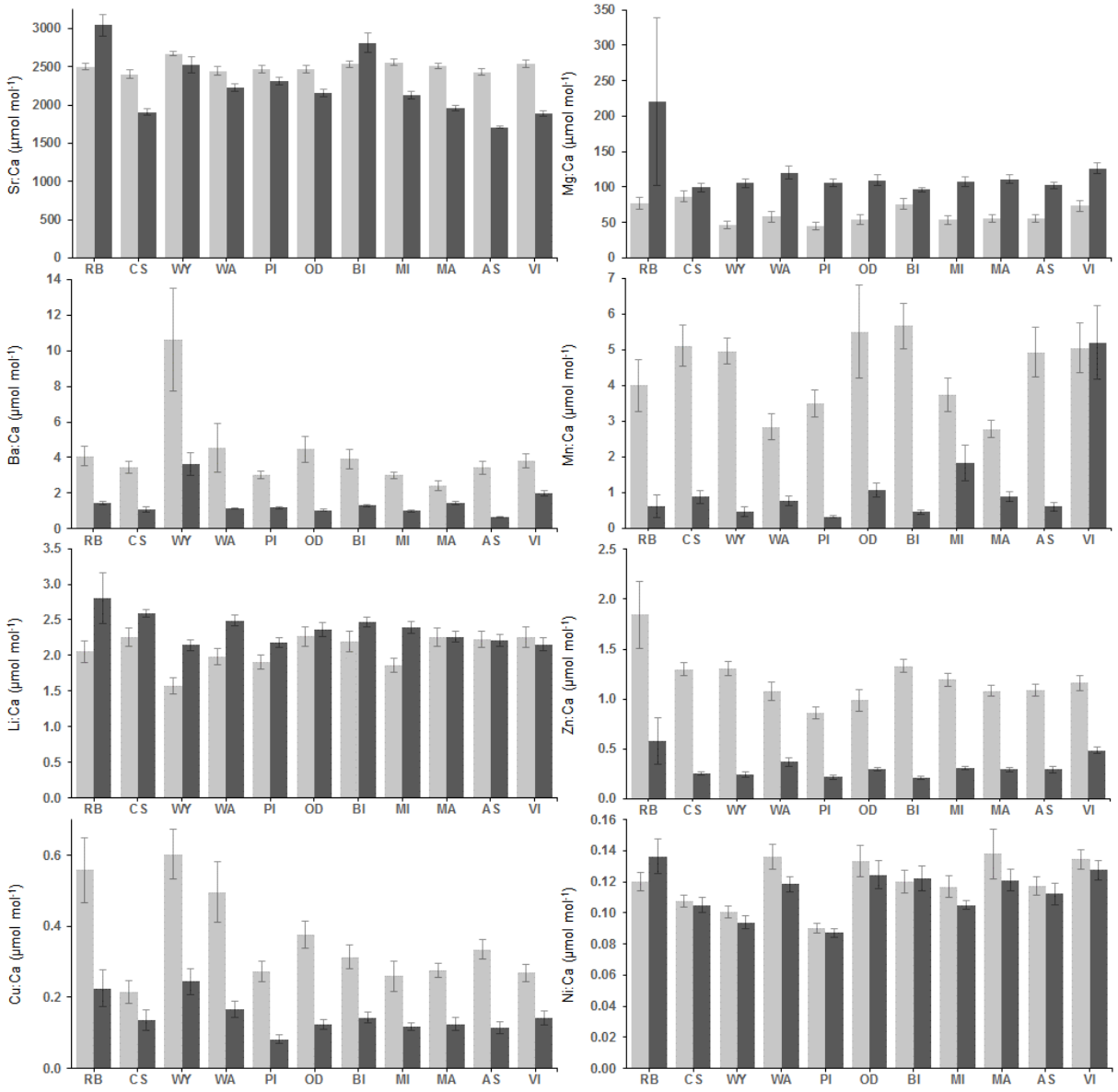
Expert	Institute	Parasite
Dr Frantisek Moravec	Czech Institute for Parasitology, Czech Republic	Philometrid nematodes
Dr Ian Beveridge	University of Melbourne	Trypanorhynch cestode larvae
Dr Lesley Smales	South Australian Museum, Adelaide	Acanthocephalans
Dr Marty Deveny	South Australia Research and Development Institute, Adelaide	Capsalid monogeneans
Dr Delane Kritsky	Idaho State University, USA	Ancyrocephaline & Diplectanid Monogenea
Dr Geoff Boxshall	British Museum of Natural History, England	Copepods
Dr Niel Bruce	Queensland Museum, Townsville	Isopods
Dr Lexa Grutter	University of Queensland, Brisbane	gnathid isopods
Dr Jose Luque	Federal Rural University of Rio de Janeiro, Brazil	Cucullanid nematodes
Dr Shokoofeh Shamsi	Charles Sturt University, Wagga Wagga	Ascarid nematodes
Mr Storm Martin	PhD candidate, University of Queensland, Brisbane	Opecoelid digeneans
Dr Michael Hammer	Northern Territory Museum and Art Gallery, Darwin	pseudoparasitic eels
Dr Jess Morgan	Queensland Alliance for Agriculture and Food Innovation, Brisbane	genetic analysis

Appendix 5 – Supplementary data

Supplementary Data 1. A list of parasites that were collected but were subsequently not used in analyses as their prevalence of infection was never ≥ 10% in at least one sample location or they were removed from analyses due to issues with accurate counts and/or identifications, which rendered them unsuitable for inclusion as a biological tag.

Host species	Parasite group	Parasite identification	Location in host
Grass Emperor	Copepoda	*Caligus* sp. 1	Gills
		Caligus sp. 5	Gills
		Unknown Copepods	Gills
	Isopoda	Gnathidae praniza larva	Gills
	Monogenea	*Benedenia* sp.	Gills
	Digenea	Opecoelidae	Intestine
		Unknown Digenea	Intestine
		Didymozoidae	Gill wash
	Cestoda	*Pterobothrium sp. 1*	Body cavity mesenteries
		Nybelinia sp. 3	Body cavity mesenteries
		Nybelinia sp. 4	Body cavity mesenteries
		Dasyrhynchus sp.	Tissues near gills
		Undifferentiated Cestode Larvae	Body cavity mesenteries
	Nematoda	Gnathostomidae sp.	Body cavity mesenteries
	Acanthocephala	Adult	Intestine
Golden Snapper	Copepoda	*Argulus* sp.	Gills
		Unknown Copepods	Gills
	Isopoda	Adult Isopods	Gills
		Gnathidae praniza larva	Gills
	Digenea	Acanthocolpidae metacercaria	Gills
		Opecoelidae	Intestine
		Didymozoidae	Stomach wall
		Transversotrema sp.	Gill wash
		Unknown Digenea	Intestine
	Cestoda	*Pterobothrium* sp. 3	Body cavity mesenteries
		Unknown Cestode Larva sp. 1	Body cavity mesenteries
		Unknown Cestode Larva sp. 2	Body cavity mesenteries
	Nematoda	Camallanidae	Intestine
	Pentastomida	*Alofia merki*	Body cavity mesenteries
	Teleostei	Pseudoparasitic eel (Fam. Opichthidae)	Body cavity mesenteries
Black Jewfish	Copepoda	*Copepod* sp. 5	Gills
	Isopoda	Gnathidae praniza larva	Gills
		Adult Isopod	Gills
	Monogenea	Ancyrocephalidae & Diplectanidae	Gills
		Polyopisthocotylidea	Gills
	Digenea	Didymozoidae	Gills
		Bucephalidae	Intestine
		Opecoelidae	Intestine
		Unidentified Digenea	Intestine
	Cestoda	Proteocephalidae	Body cavity mesenteries
	Nematoda	Capillaridae	Intestine
		Goezia sp.	Intestine
		Anisakidae	Body cavity mesenteries
		Unknown Nematodes	Intestine
	Acanthocephala	Larval Acanthocephala	Body cavity mesenteries

Supplementary Data 2. Mean concentrations of element:^{43}Ca ratios from the near core (light grey) and margin (dark grey) of Black Jewfish otoliths collected from 11 locations across northern Australia. See Table 1 for location codes.



Supplementary Data 3. Jack-knife reclassification success for the otolith trace elements of Black Jewfish sampled from the various management jurisdictions for this study for a) near core and b) margin. Data is presented as the number of fish captured from regions (rows) that are classified by discriminant functions into the various regions (columns). Bold values indicate successful reclassification to the location of origin.

a)

Group	RB	CS	Wy	Wa		Wa	PI	OD	BI	MI		MI	Ma	AS	VI
RB	**17**	4	6	7											
CS	2	**11**	3	2											
Wy	5	0	**22**	3											
Wa	9	0	5	**10**											
Wa						**9**	2	3	4	6					
PI						2	**18**	1	4	4					
OD						3	5	**3**	3	3					
BI						3	2	1	**13**	8					
MI						2	8	1	6	**12**					
MI												**12**	8	4	5
Ma												10	**12**	3	5
AS												1	7	**5**	7
VI												7	5	4	**12**

b)

Group	RB	CS	Wy	Wa		Wa	PI	OD	BI	MI		MI	Ma	AS	VI
RB	**26**	1	0	7											
CS	0	**12**	2	4											
Wy	1	3	**23**	3											
Wa	5	5	0	**14**											
Wa						**8**	4	2	5	4					
PI						0	**27**	0	1	1					
OD						4	1	**3**	1	9					
BI						4	4	0	**17**	2					
MI						3	3	3	2	**18**					
MI												**23**	1	4	1
Ma												8	**14**	2	6
AS												0	1	**19**	0
VI												0	5	0	**23**

Supplementary Data 4. Element:^{43}Ca ratios from the otolith near core and margin for Black Jewfish listed by region of analysis that were found to be the more heavily weighted discriminating factors for the first two Linear Discriminants (LD1 and LD2, respectively). +/- indicates whether the factor was weighted in a positive or negative direction.

	Near core				**Margin**			
	LD1		LD2		LD1		LD2	
Region	Element: ^{43}Ca	Proportion of Trace	Element: ^{43}Ca	Proportion of Trace	Element: ^{43}Ca	Proportion of Trace	Element: ^{43}Ca	Proportion of Trace
Western	- Cu + Ni + Ba	54.3	+ Mn - Ni + Mg	31.0	+ Ba - Sr	56.0	+ Zn + Sr	43.2
Darwin	- Mn - Mg	42.7	+ Ni	34.1	+ Mn - Sr	52.3	+ Sr + Li	32.6
Arnhem/ Gulf	+ Mg - Li - Zn	50.5	+ Mg + Sr - Li	31.8	+ Ba - Sr	71.1	- Sr	21.9

Supplementary Data 5. Parasites found infecting Black Jewfish sampled from 11 locations across northern Australia used in the analyses for this study. Data is presented as mean abundance with prevalence in parentheses. Data presented is untransformed. Only parasites used in analyses are included.

	Collection locations	RB	CS	Wy	Wa	PI	OD	BI	MI	Ma	AS	VI
	Sample size	**36**	**20**	**34**	**25**	**22**	**17**	**28**	**30**	**29**	**19**	**29**
Gills	*Caligus haemulonis* & *Caligus* sp. 2 combined	0.3 (19)		0.2 (9)	0.04 (4)	0.5 (32)	0.1 (6)	0.04 (4)	0.1 (10)	3.2 (59)		0.1 (7)
	Caligus sp. 3							0.3 (18)				
	Lernanthropus cruciatus	4.6 (83)		0.9 (32)	2.2 (56)	1.4 (59)	0.4 (24)	6.3 (82)	1.2 (43)	1.4 (59)	1.0 (42)	2.3 (86)
	Acanthocolpidae metacercaria	0.5 (22)	0.6 (10)						0.7 (10)	0.1 (14)		3.3 (41)
Body cavity, mesenteries, tissues & ovaries	*Pseudogilquinia* sp.		0.1 (10)	0.3 (6)				0.04 (4)	0.03 (3)			
	Pterobothrium sp. 1	0.6 (22)	1.6 (50)	9.3 (62)	3.0 (24)	9.7 (96)	1.1 (29)	5.5 (79)	1.3 (23)	0.03 (3)	0.3 (21)	
	Pterobothrium sp. 3	0.1 (11)	0.3 (20)	3.6 (62)	0.2 (12)	0.2 (9)		0.3 (14)	0.03 (3)	0.03 (3)		
	Pterobothrium sp. 5	0.1 (6)	0.1 (5)	0.4 (18)	0.2 (12)	0.1 (5)		0.2 (11)	0.1 (7)	0.1 (3)		
	Otobothrium sp.		0.1 (5)	0.1 (9)	0.04 (4)	0.2 (14)		0.2 (21)	0.1 (10)	0.03 (3)		
	Paratobothrium sp.	9 (64)		0.7 (21)		0.1 (5)				0.5 (24)		
	Nybelinia spp.	0.1 (8)	0.1 (5)	0.1 (9)	0.04 (4)	0.1 (5)	1.5 (29)	0.1 (7)	0.2 (17)	0.03 (3)	0.1 (5)	0.03 (3)
	Dasyrhynchus sp.	0.3 (19)		19.9 (97)	3.2 (76)	3.0 (77)		9.6 (75)	1.6 (17)	0.1 (3)		
	Poecilanstrium sp.	7.9 (92)	3.1 (80)	5.7 (85)	4.7 (92)	12.1 (100)	1.8 (47)	11.4 (89)	3.2 (50)	0.6 (28)	0.4 (32)	0.2 (17)
	Callitetrarhynchus sp.	1.4 (61)	0.1 (50)	0.4 (27)	0.7 (24)	2.0 (64)	0.1 (12)	2.3 (68)	0.6 (17)	0.1 (14)	10.4 (90)	0.3 (24)
	Philometra protonibeae	0.04 (4.0)	0.1 (12.5)	0.18 (23.1)	0.12 (25.0)	0.41 (69.2)		0.36 (66.7)	0.13 (33.3)	0.03 (8.3)		
	Philometroides stomachus								0.2 (3)		0.3 (32)	
	Gnathostomidae sp.	1.4 (53)		1.1 (35)		0.4 (18)		0.4 (14)	0.1 (3)	0.6 (38)		
	Serrasentis sagittifer	0.1 (3)			0.2 (8)	0.1 (9)			0.5 (33)	0.2 (21)	0.8 (53)	0.2 (17)
	Sebekidae spp.			0.8 (24)				0.1 (4)		0.03 (3)		

	Collection locations	RB	CS	Wy	Wa	PI	OD	BI	MI	Ma	AS	VI
	Sample size	**36**	**20**	**34**	**25**	**22**	**17**	**28**	**30**	**29**	**19**	**29**
	Pseudoparasitic eel (Fam. Opichthidae)	0.6 (36)	0.1 (10)	0.1 (6)						0.03 (3)		
Intestinal canal	*Orientodiploproctodaeum* sp.	12.2 (86)	7.8 (95)	24.7 (88)	46.8 (76)	54.4 (96)	8.8 (71)	52.7 (93)	28.8 (67)	6.8 (90)	0.1 (5)	22.0 (100)
	Pleorchis sp.	1.3 (36)	0.1 (5)		0.5 (20)		2.9 (47)	0.2 (7)	1.8 (47)	0.1 (7)	0.3 (11)	
	Stephanostomum sp.	0.5 (11)	2 (65)	3.2 (38)	10.2 (92)	6.5 (59)	10.4 (35)	21.5 (75)	5.0 (67)	0.1 (10)	0.1 (5)	1.8 (41)
	Hemiuridae sp.	7.4 (64)	0.1 (5)			0.1 (5)	0.1 (6)	0.1 (4)	0.3 (23)	0.03 (3)		0.3 (21)
	Dichelyne spinigerus		1.3 (65)	6.7 (62)	13.2 (88)	4.1 (73)	10.0 (71)	9.0 (79)	4.5 (73)			0.1 (10)
	Camallanidae sp.			0.1 (12)	0.04 (4)	0.1 (5)			0.1 (10)			
	Ascaridae sp. 1			0.41 (20.6)								
	Ascaridae sp. 2				0.2 (8)	0.1 (9)		0.04 (4)	0.4 (23)	12.2 (72)	5.5 (11)	0.03 (3)
	Acanthocephala	0.1 (6)		0.4 (12)			0.1 (6)			0.03 (3)	0.1 (5)	

Supplementary Data 6. Jack-knife reclassification success for the overall parasite assemblage of Black Jewfish sampled from the various management jurisdictions for this study. Data is presented as the number of fish captured from regions (rows) that are classified by discriminant functions into the various regions (columns). Bold values indicate successful reclassification to the location of origin.

Group	% Correct	RB	CS	Wy	Wa		Wa	PI	OD	BI	MI		MI	Ma	AS	VI
RB	86.1	**31**	5	0	0											
CS	95.0	0	**19**	0	1											
Wy	67.6	0	3	**23**	8											
Wa	80.0	0	3	2	**20**											
Wa	56.0						**13**	4	1	3	3					
PI	72.7						3	**16**	1	2	0					
OD	64.7						0	2	**11**	1	3					
BI	42.9						9	2	5	**12**	0					
MI	50.0						2	2	7	4	**5**					
MI	80.0												**24**	0	0	6
Ma	89.7												1	**26**	0	2
AS	89.5												0	1	**17**	1
VI	96.6												1	0	0	**28**

Supplementary Data 7. Parasite species listed by region of analysis that were found to be the more heavily weighted discriminating factors for the first two linear discriminants (LD1 and LD2, respectively). +/- indicates whether the factor was weighted in a positive or negative direction.

	LD1		LD2	
Region	**Parasite species**	**Proportion of trace**	**Parasite species**	**Proportion of trace**
Western	+ *Dasyrhynchus* sp.	0.66	- *Stephanostomum* sp. + *Ascaridae* sp. 1	0.20
Darwin	+ *Poecilanstrium* sp.	0.41	+ *Stephanostomum* sp. - *Pterobothrium* sp. 1 + *Dasyrhynchus* sp.	0.31
Arnhem/Gulf	- *Callitetrarhynchus* sp. + *Orientodiploproctodaeum* sp.	0.50	- Gnathostomidae sp. + *Pterobothrium* sp. 1 + *Dichelyne spinigerus*	0.31

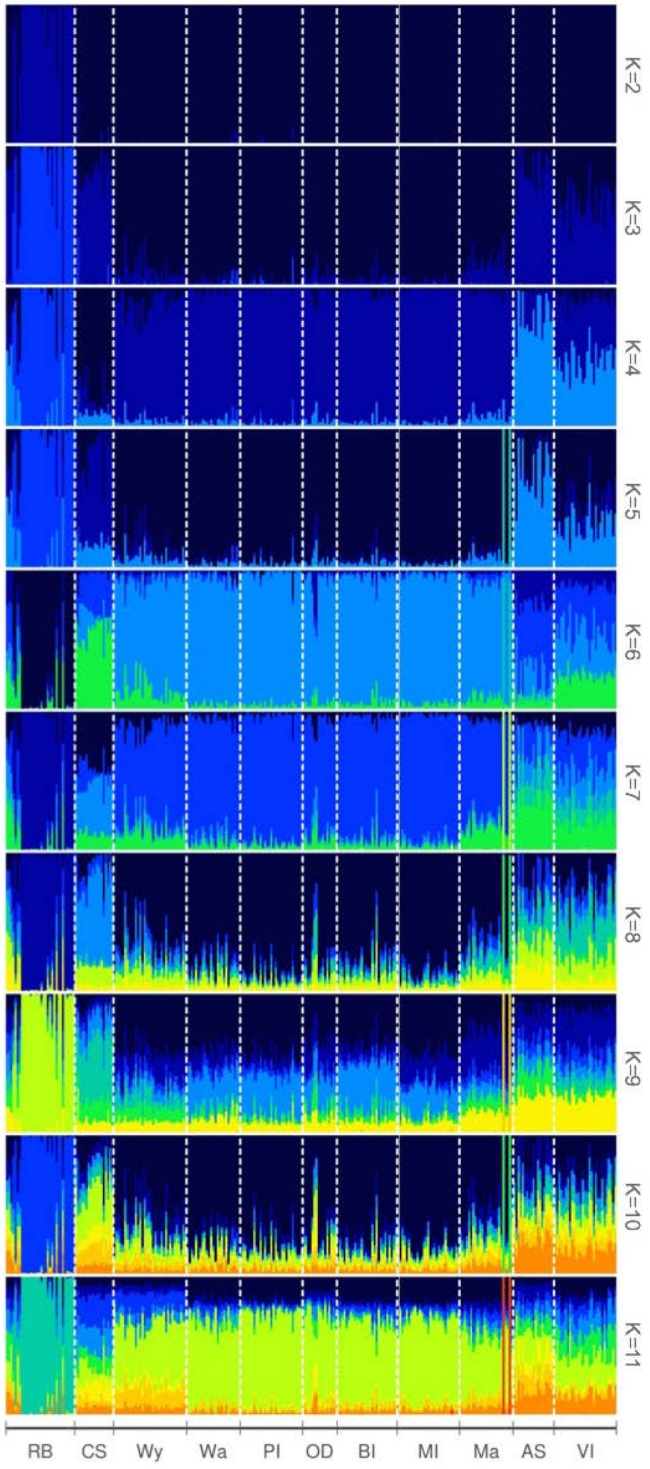
Supplementary Data 8. Summary statistics of 11 microsatellite loci for Black Jewfish from 284 individuals sampled from 11 locations across northern Australia. n = sample size, *#A* = number of alleles, A_R = allelic richness, *I* = Shannon's Information Index, H_E = expected heterozygosity, H_O = observed heterozygosity, and *F* = fixation index $(H_E\text{-}H_O)/H_E$.

Pop		*Prd044*	*Prd023*	*Prd042*	*Prd012*	*Prd046*	*Prd018*	*Prd020*	*Prd045*	*Prd049*	*Prd036*	*Prd024*
RB	***n***	32	32	32	29	32	30	32	32	32	32	32
	#A	5	8	5	12	4	12	6	6	3	6	5
	A_R	3.298	5.044	4.154	6.648	1.645	6.081	3.543	1.533	1.171	1.653	3.225
	I	1.344	1.805	1.487	2.124	0.777	2.057	1.418	0.744	0.313	0.854	1.286
	H_O	0.594	0.719	0.625	0.759	0.375	0.833	0.781	0.344	0.094	0.281	0.656
	H_E	0.697	0.802	0.759	0.850	0.392	0.836	0.718	0.348	0.146	0.395	0.690
	F	0.148	0.104	0.177	0.107	0.044	0.003	-0.088	0.011	0.358	0.288	0.049
CS	***n***	18	18	18	15	18	14	18	13	18	18	18
	#A	8	7	6	10	4	8	7	6	4	6	5
	A_R	4.025	5.684	3.340	6.164	1.333	5.600	2.746	2.641	1.493	2.365	3.812
	I	1.630	1.850	1.409	2.018	0.535	1.871	1.348	1.302	0.647	1.091	1.421
	H_O	0.778	0.944	0.667	0.933	0.278	0.571	0.667	0.769	0.278	0.444	0.722
	H_E	0.752	0.824	0.701	0.838	0.250	0.821	0.636	0.621	0.330	0.577	0.738
	F	-0.035	-0.146	0.048	-0.114	-0.111	0.304	-0.049	-0.238	0.159	0.230	0.021
Wy	***n***	34	34	34	32	34	34	33	33	34	34	34
	#A	8	8	5	16	5	8	8	5	4	10	6
	A_R	3.932	5.598	3.095	9.846	1.609	4.797	4.445	2.344	1.127	3.163	3.238
	I	1.564	1.854	1.286	2.488	0.817	1.779	1.714	1.109	0.285	1.517	1.417
	H_O	0.735	0.794	0.824	0.906	0.324	0.971	0.970	0.515	0.118	0.765	0.618
	H_E	0.746	0.821	0.677	0.898	0.378	0.792	0.775	0.573	0.113	0.684	0.691
	F	0.014	0.033	-0.217	-0.009	0.145	-0.226	-0.251	0.102	-0.042	-0.118	0.106
Wa	***n***	25	25	25	23	25	25	25	23	25	25	25
	#A	8	8	5	12	4	7	7	7	4	7	5
	A_R	4.340	5.580	3.247	8.397	1.649	3.788	3.541	2.388	1.337	2.706	2.577
	I	1.690	1.871	1.348	2.263	0.759	1.511	1.477	1.208	0.539	1.331	1.178
	H_O	0.720	0.840	0.680	0.739	0.440	0.680	0.720	0.609	0.280	0.640	0.720

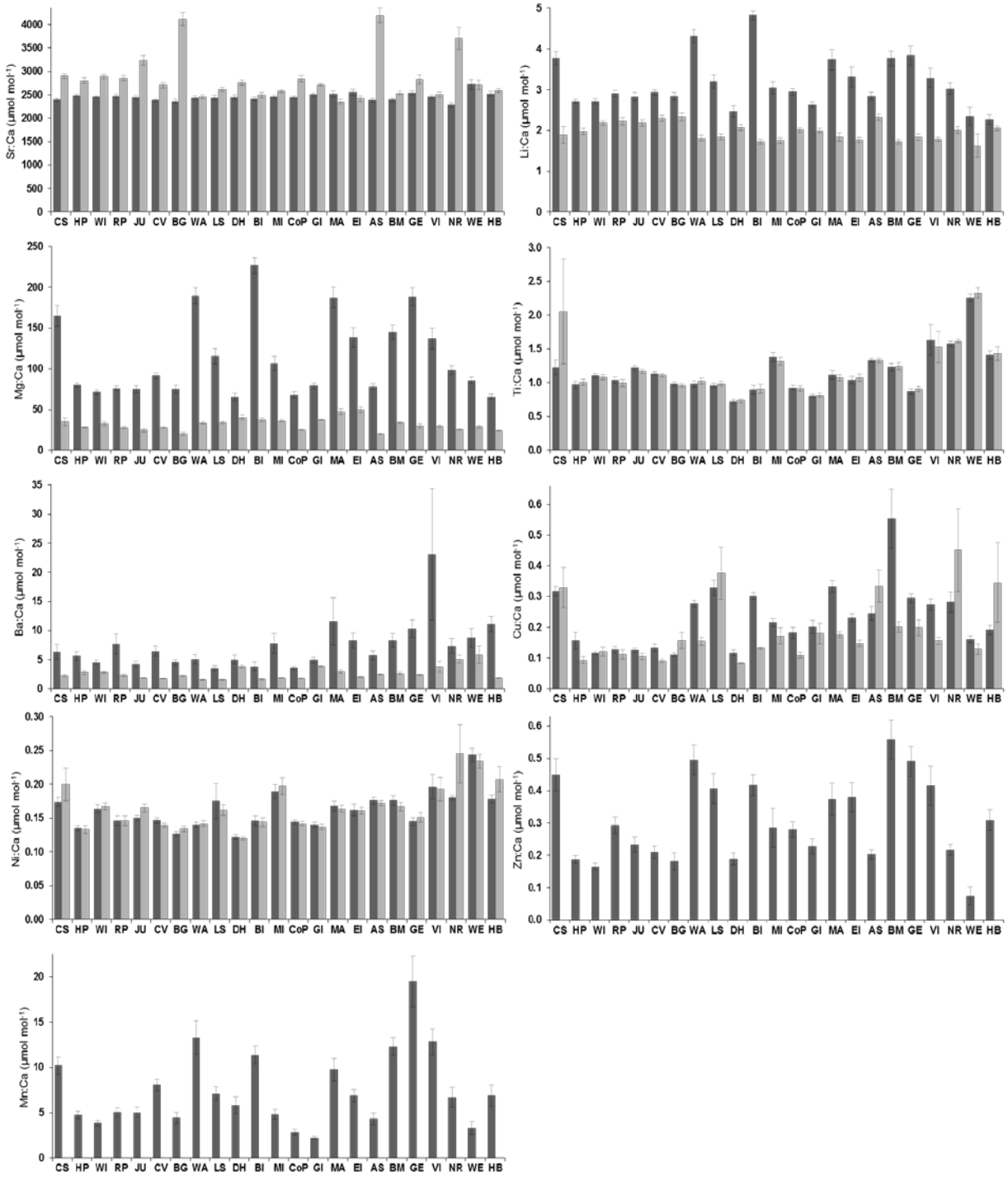
Pop		*Prd044*	*Prd023*	*Prd042*	*Prd012*	*Prd046*	*Prd018*	*Prd020*	*Prd045*	*Prd049*	*Prd036*	*Prd024*
	H_E	0.770	0.821	0.692	0.881	0.394	0.736	0.718	0.581	0.252	0.630	0.612
	F	0.064	-0.023	0.017	0.161	-0.118	0.076	-0.003	-0.047	-0.111	-0.015	-0.176
PI	***n***	29	28	29	25	29	28	29	26	29	29	29
	#A	8	8	5	15	5	7	8	5	4	7	6
	A_R	4.083	5.560	3.260	8.993	2.541	4.994	3.995	1.791	1.330	2.817	2.288
	I	1.649	1.873	1.352	2.422	1.220	1.717	1.571	0.905	0.525	1.312	1.101
	H_O	0.759	0.786	0.690	1.000	0.690	0.857	0.862	0.538	0.276	0.724	0.552
	H_E	0.755	0.820	0.693	0.889	0.606	0.800	0.750	0.442	0.248	0.645	0.563
	F	-0.005	0.042	0.005	-0.125	-0.137	-0.072	-0.150	-0.219	-0.113	-0.123	0.020
OD	***n***	16	16	16	14	16	16	16	13	16	16	16
	#A	6	8	4	12	4	7	8	3	4	7	5
	A_R	4.031	5.953	2.926	9.116	1.690	4.697	5.224	1.888	1.213	2.829	2.522
	I	1.559	1.906	1.156	2.333	0.787	1.701	1.828	0.821	0.414	1.434	1.147
	H_O	0.813	0.875	0.438	1.000	0.500	0.750	0.563	0.462	0.188	0.563	0.688
	H_E	0.752	0.832	0.658	0.890	0.408	0.787	0.809	0.470	0.176	0.646	0.604
	F	-0.081	-0.052	0.335	-0.123	-0.225	0.047	0.304	0.019	-0.067	0.130	-0.139
BI	***n***	28	28	28	24	28	28	28	28	28	28	28
	#A	9	8	5	15	3	7	9	4	4	6	6
	A_R	4.272	6.938	3.621	9.600	1.602	3.778	4.000	1.570	1.344	2.708	3.200
	I	1.749	1.997	1.383	2.441	0.667	1.566	1.682	0.725	0.539	1.271	1.377
	H_O	0.750	0.821	0.679	0.917	0.393	0.679	0.714	0.357	0.286	0.750	0.643
	H_E	0.766	0.856	0.724	0.896	0.376	0.735	0.750	0.363	0.256	0.631	0.688
	F	0.021	0.040	0.063	-0.023	-0.046	0.077	0.048	0.016	-0.117	-0.189	0.065
MI	***n***	29	29	29	21	29	29	29	29	29	29	29
	#A	8	9	5	10	4	7	7	5	4	6	6
	A_R	4.174	6.444	3.419	7.056	1.606	4.034	3.384	2.222	1.194	3.311	2.580
	I	1.673	1.960	1.338	2.086	0.753	1.594	1.388	1.102	0.385	1.382	1.189
	H_O	0.724	0.931	0.793	0.857	0.414	0.759	0.828	0.655	0.138	0.966	0.690
	H_E	0.760	0.845	0.707	0.858	0.378	0.752	0.705	0.550	0.162	0.698	0.612
	F	0.048	-0.102	-0.121	0.001	-0.096	-0.009	-0.175	-0.191	0.150	-0.383	-0.126

Pop		*Prd044*	*Prd023*	*Prd042*	*Prd012*	*Prd046*	*Prd018*	*Prd020*	*Prd045*	*Prd049*	*Prd036*	*Prd024*
Ma	***n***	25	25	25	19	25	25	24	24	25	25	25
	#A	10	8	5	13	5	8	6	5	4	6	6
	A_R	4.386	6.158	3.264	9.890	2.189	4.562	2.946	2.931	1.178	2.927	2.828
	I	1.781	1.918	1.335	2.407	1.061	1.733	1.262	1.307	0.362	1.331	1.306
	H_O	0.720	0.880	0.720	0.684	0.680	0.760	0.583	0.625	0.160	0.680	0.560
	H_E	0.772	0.838	0.694	0.899	0.543	0.781	0.661	0.659	0.151	0.658	0.646
	F	0.067	-0.051	-0.038	0.239	-0.252	0.027	0.117	0.051	-0.058	-0.033	0.134
AS	***n***	19	19	19	17	19	19	19	19	19	19	19
	#A	8	7	5	11	4	11	7	8	4	8	5
	A_R	5.554	5.597	3.703	7.811	1.462	5.388	4.102	4.376	1.660	3.267	3.861
	I	1.859	1.820	1.414	2.209	0.624	1.966	1.620	1.700	0.799	1.538	1.431
	H_O	0.789	0.842	0.632	0.882	0.211	0.789	1.000	0.737	0.474	0.842	0.947
	H_E	0.820	0.821	0.730	0.872	0.316	0.814	0.756	0.771	0.398	0.694	0.741
	F	0.037	-0.025	0.135	-0.012	0.333	0.031	-0.322	0.045	-0.192	-0.214	-0.279
VI	***n***	28	29	29	26	29	29	28	28	29	29	29
	#A	11	8	5	16	4	6	6	7	3	8	6
	A_R	5.917	5.881	2.905	7.308	1.528	4.092	3.240	3.039	1.503	3.780	2.813
	I	2.005	1.877	1.208	2.341	0.659	1.533	1.320	1.425	0.569	1.634	1.220
	H_O	0.750	0.862	0.724	0.846	0.310	0.690	0.821	0.679	0.276	0.793	0.759
	H_E	0.831	0.830	0.656	0.863	0.345	0.756	0.691	0.671	0.335	0.735	0.644
	F	0.097	-0.039	-0.104	0.020	0.102	0.087	-0.188	-0.011	0.176	-0.078	-0.177
All populations	***n***	283	283	284	245	284	277	281	268	284	284	284
	#A	14	9	7	21	5	14	12	10	6	10	6
	A_R	4.365	5.858	3.358	8.257	1.714	4.710	3.742	2.429	1.323	2.866	2.995
	I	1.682	1.885	1.338	2.285	0.787	1.730	1.512	1.123	0.489	1.336	1.279
	H_O	0.739	0.845	0.679	0.866	0.419	0.758	0.774	0.572	0.233	0.677	0.687
	H_E	0.765	0.828	0.699	0.876	0.399	0.783	0.724	0.550	0.233	0.636	0.657
	F	0.034	-0.020	0.027	0.011	-0.033	0.031	-0.069	-0.042	0.013	-0.046	-0.046

Supplementary Data 9. Results from the Bayesian population assignment of microsatellite data from Black Jewfish using the software Structure. Location prefixes follow Table 1. Each vertical line represents an individual and the posterior probability proportions of its genotype assigned to the different genetic clusters. The number of genetic clusters shown ranges from k=2 to k=11; each plot represents one tested k. Population information was used as a prior in the analysis.



Supplementary Data 10. Mean concentrations (± s.e.) of element:^{43}Ca ratios from the near core (dark bars) and margin (lighter bars) of Golden Snapper otoliths collected from 22 locations across northern Australia. See Table 2 for location codes.



Supplementary Data 11. Jack-knife reclassification success for the otolith trace elements of Golden Snapper sampled from the various management jurisdictions for this study for a) near core and b) margin. Data is presented as the number of fish captured from regions (rows) that are classified by discriminant functions into the various regions (columns). Bold values indicate successful reclassification to the location of origin.

a)

Group	CS	CSWI	CSRP	CSHP	CSJU	CV	BG	BG	Wa	LS	DH	BI	MI	CoP	GI	GI	Ma	AS	AS	BMB	GE	VI	NR	We	NR	We	HB
CS	**19**	2	0	1	1	4	0																				
CSWI	0	**27**	0	9	0	5	5																				
CSRP	0	4	**3**	6	2	2	1																				
CSHP	1	11	0	**13**	1	5	4																				
CSJU	0	6	3	2	**1**	6	2																				
CV	1	6	1	2	1	**15**	3																				
BG	0	3	1	5	1	3	**9**																				
BG								**21**	0	0	3	0	1	5	2												
Wa								6	**10**	3	0	6	2	0	2												
LS								1	3	**13**	1	1	3	3	0												
DH								0	0	1	**16**	0	0	4	1												
BI								0	3	1	0	**21**	2	1	1												
MI								2	1	2	0	2	**15**	2	1												
CoP								0	0	7	3	0	0	**15**	4												
GI								0	0	3	1	0	0	5	**19**												
GI																**28**	0	1									
Ma																2	**13**	3									
AS																2	0	**27**									
AS																			**22**	1	0	3	2	1			
BMB																			5	**11**	6	6	1	0			
GE																			4	1	**18**	2	0	0			
VI																			2	3	7	**6**	1	4			
NR																			8	0	0	1	**4**	0			
We																			1	0	0	0	1	**8**			
NR																									**6**	0	7
We																									0	**10**	0
HB																									4	4	**40**

b)

Group	**CS**	**CSWI**	**CSRP**	**CSHP**	**CSJU**	**CV**	**BG**		**BG**	**Wa**	**LS**	**DH**	**BI**	**MI**	**CoP**	**GI**		**GI**	**Ma**	**AS**		**AS**	**BMB**	**GE**	**VI**	**NR**	**We**		**NR**	**We**	**HB**
CS	**18**	7	1	1	0	0	0																								
CSWI	4	**29**	1	7	3	2	0																								
CSRP	0	7	**0**	2	2	7	0																								
CSHP	1	12	0	**12**	1	8	1																								
CSJU	1	5	0	1	**9**	2	2																								
CV	1	1	0	5	0	**21**	1																								
BG	0	1	0	1	2	1	**17**																								
BG									**19**	0	0	0	0	0	3	0															
Wa									0	**7**	0	0	7	3	4	0															
LS									0	3	**10**	0	8	1	4	0															
DH									0	0	0	**11**	1	0	3	10															
BI									0	2	0	0	**17**	5	3	2															
MI									0	4	0	1	3	**15**	2	0															
CoP									1	4	1	0	2	0	**24**	0															
GI									0	0	1	8	0	0	0	**20**															
GI																		**29**	0	0											
Ma																		6	**12**	0											
AS																		1	0	**28**											
AS																						**26**	0	1	2	0	0				
BMB																						0	**20**	4	5	0	0				
GE																						2	6	**17**	0	0	0				
VI																						0	3	11	**0**	0	9				
NR																						4	1	0	3	**5**	0				
We																						0	3	0	3	0	4				
NR																												**8**	2	3
We																												0	**8**	2
HB																												1	0	**47**

Supplementary Data 12. Element:^{43}Ca ratios from the otolith near core and margin for Golden Snapper listed by region of analysis that were found to be the more heavily weighted discriminating factors for the first two linear discriminants (LD1 and LD2, respectively). +/- indicates whether the factor was weighted in a positive or negative direction.

	Near core				**Margin**			
	LD1		LD2		LD1		LD2	
Region	**Element:^{43}Ca**	**Proportion of trace**	**Element:^{43}Ca**	**Proportion of trace**	**Element:^{43}Ca**	**Proportion of trace**	**Element:^{43}Ca**	**Proportion of trace**
Western	+ Mg + Cu	71.5	- Ni	11.4	+ Ba	52.4	+ Li - Cu	28.9
Darwin	+ Mg	63.7	- Ti	14.6	+ Ba - Sr	58.6	- Sr - Ba	58.9
Arnhem	+ Mg + Ti	61.8	+ Ti - Mg	38.2	+ Sr + Li	87.8	+ Mg + Ti	12.2
Gulf	- Ti	60.9	+ Mg + Ti	21.1	- Sr + Ba	71.8	+ Ti + Ba	20.0
East Coast	- Ti + Cu	72.8	+ Ni - Mg	27.2	-Cu + Ti	76.5	- Sr + Ti	23.5

Supplementary Data 13. Parasites found infecting Golden Snapper sampled from 18 locations across northern Australia. Data is presented as mean abundance with prevalence in parentheses. Data presented is untransformed. Only parasites used in analyses are included.

	Location	CS	CV	BG	Wa	LS	DH	BI	MI	CoP	GI	Ma	AS	BMB	GE	VI	NR	We	HB
	Sample size/Species	**30**	**31**	**23**	**27**	**26**	**25**	**31**	**25**	**35**	**30**	**16**	**31**	**28**	**25**	**25**	**11**	**10**	**51**
Gills and pharyngeal teeth	*Hatschekia elongata*	0.77 (40.0)	15.45 (93.5)	0.57 (17.4)	20.37 (100)	16.19 (100)		10.16 (100)	0.36 (32.0)	14.80 (91.4)		0.19 (18.8)	5.48 (90.3)	27.25 (96.4)	35.68 (100)	13.84 (56.0)	83.18 (81.8)	19.70 (60.0)	31.08 (98.0)
	Caligus spp.	1.37 (56.7)	0.35 (29.0)	0.48 (43.5)	2.44 (70.4)	1.65 (50.0)	0.84 (36.0)	4.39 (87.1)	0.28 (24.0)	2.69 (60.0)	4.60 (90.0)	19.25 (93.8)	1.13 (41.9)	2.00 (67.9)	1.12 (60.0)	2.32 (56.0)	7.00 (72.7)	8.20 (100)	5.71 (80.4)
	Lernanthropus pillai		0.06 (6.5)	0.04 (4.3)		0.04 (3.8)		0.10 (9.7)	0.12 (12.0)		0.17 (13.3)	0.19 (12.5)	0.10 (9.7)	0.11 (7.1)					0.02 (2.0)
	Euryhaliotrema spp.	0.50 (26.7)	0.39 (9.7)	13.96 (100)		0.69 (19.2)	26.12 (68.0)	5.03 (48.4)	0.28 (12.0)	8.26 (65.7)	3.77 (76.7)	2.88 (62.5)	3.71 (58.1)	6.07 (42.9)	2.00 (16.0)	8.88 (60.0)	17.73 (63.6)	19.60 (70.0)	3.69 (39.2)
	Capsalidae		1.42 (12.9)	9.13 (69.6)													0.18 (9.1)		11.10 (60.8)
	Polyopisthocotylean			0.13 (13.0)															
	Didymozoidae	1.10 (16.7)	0.10 (6.5)	0.61 (47.8)	0.11 (7.4)	0.31 (23.1)		0.13 (12.9)	0.76 (32.0)	0.34 (28.6)		0.13 (12.5)	0.19 (19.4)	0.57 (7.1)	0.12 (12.0)	0.16 (12.0)	2.18 (27.3)	0.20 (20.0)	1.55 (43.1)
Body cavity, mesenteries & tissues	*Pseudogilquinia* sp	7.17 (76.7)	8.00 (83.9)	21.74 (100)	1.19 (59.3)	5.00 (76.9)	0.16 (12.0)	6.13 (96.8)	0.12 (4.0)	3.86 (80.0)	6.87 (90.0)	1.31 (50.0)	1.87 (51.6)	1.04 (46.4)	2.68 (80.0)	6.92 (80.0)	11.73 (81.8)	7.70 (100)	26.18 (100)
	Pterobothrium sp. 1	0.73 (20.0)	4.52 (51.6)	18.22 (100)	1.41 (59.3)	0.81 (34.6)	0.16 (12.0)	0.23 (19.4)	0.28 (20.0)	2.51 (57.1)			0.77 (35.5)	0.21 (14.3)	0.52 (20.0)	0.32 (16.0)	0.55 (36.4)	0.10 (10.0)	0.10 (7.8)
	Pterobothrium sp. 2	0.10 (10.0)	0.13 (3.2)		0.48 (14.8)	0.85 (11.5)													
	Pterobothrium sp. 4	0.20 (6.7)	2.81 (71.0)		0.04 (3.7)	0.15 (7.7)		0.13 (6.5)		0.23 (11.4)		0.13 (12.5)			0.04 (4.0)	0.16 (12.0)	0.09 (9.1)	0.10 (10.0)	0.20 (15.7)
	Pterobothrium sp. 5	2.33 (46.7)		0.22 (8.7)	0.07 (7.4)	0.19 (7.7)		0.42 (32.3)	0.40 (24.0)	0.26 (11.4)		0.31 (6.3)			0.04 (4.0)	0.04 (4.0)		1.90 (40.0)	0.33 (21.6)
	Paratobothrium sp.		0.42 (6.5)	1.09 (17.4)	0.04 (3.7)			0.32 (9.7)		0.43 (2.9)		0.13 (12.5)	0.06 (3.2)					3.60 (20.0)	0.02 (2.0)
	Nybelinia spp.		0.06 (6.5)	0.09 (8.7)	0.30 (11.1)	0.12 (11.5)		0.23 (19.4)	0.04 (4.0)	0.11 (8.6)			0.29 (19.4)	0.82 (14.3)	0.08 (4.0)	3.80 (32.0)	0.09 (9.1)		0.75 (31.4)
	Callitetrarhynchus sp.	1.17 (73.3)	0.55 (16.1)	7.70 (100)	0.04 (3.7)	0.27 (19.2)		0.61 (32.3)	0.04 (4.0)	0.86 (22.9)		0.13 (12.5)	3.39 (77.4)	0.46 (42.9)	1.96 (60.0)	1.08 (28.0)	2.36 (81.8)	0.70 (40.0)	0.35 (21.6)
	Proteocephalidae			0.09 (8.7)				0.10 (6.5)		0.11 (8.6)	0.13 (6.7)			0.32 (10.7)	0.00	0.72 (12.0)			0.02 (2.0)

	Location	CS	CV	BG	Wa	LS	DH	BI	MI	CoP	GI	Ma	AS	BMB	GE	VI	NR	We	HB
	Sample size/Species	**30**	**31**	**23**	**27**	**26**	**25**	**31**	**25**	**35**	**30**	**16**	**31**	**28**	**25**	**25**	**11**	**10**	**51**
	Serrasentis sagitiifer			0.78 (56.5)	0.04 (3.7)	0.12 (11.2)				0.09 (8.6)			0.23 (16.1)			0.04 (4.0)			0.39 (21.6)
	Gorgorhynchoides sp.			0.00	0.00	0.00				0.00		0.19 (12.5)							1.63 (27.5)
	Philometra sp.	0.07 (6.7)	0.00	0.00	0.15 (14.8)	0.08 (7.7)		0.16 (16.1)		0.06 (5.7)		0.06 (6.3)	0.32 (32.3)	0.07 (7.1)	0.04 (4.0)	0.04 (4.0)	0.27 (27.3)	0.10 (10.0)	0.12 (11.8)
	Philometra gracilis		0.39 (25.8)							0.40 (28.6)								0.20 (20.0)	1.47 (49.0)
	Philometroides branchiarum										0.17 (13.3)								
	Anisakidae spp.	10.33 (80.0)	28.39 (100)	44.78 (100)	10.63 (77.8)	29.62 (92.3)	0.12 (8.0)	14.84 (83.9)	3.88 (80.0)	12.69 (94.3)	9.60 (96.7)	11.25 (81.3)	43.55 (100)	11.86 (89.3)	13.24 (72.0)	10.80 (68.0)	12.73 (72.7)	24.80 (100)	51.43 (100)
	Gnathostomidae spp.		0.03 (3.2)							0.03 (2.9)		0.06 (6.3)		0.11 (10.7)	1.12 (24.0)			0.20 (10.0)	0.33 (11.8)
Intestinal canal	*Siphoderina* sp.	0.37 (30.0)	0.13 (12.9)	0.52 (39.1)	1.04 (25.9)	0.65 (26.9)	1.32 (24.0)	1.84 (54.8)	0.28 (24.0)	2.89 (62.9)	0.80 (30.0)	0.06 (6.3)	0.35 (25.8)	2.11 (64.3)	2.52 (52.0)	1.04 (44.0)	7.45 (63.6)	3.30 (30.0)	2.08 (37.3)
	Stephanostomum sp.			0.04 (4.3)		0.04 (3.8)				0.17 (11.4)		0.19 (6.3)	0.06 (6.5)	0.07 (7.1)	0.04 (4.0)		0.18 (9.1)		
	Helicometrina sp.		0.03 (3.2)	0.00		0.00		1.39 48.4)							0.12 (8.0)				
	Hemiuridae			0.04 (4.3)	0.11 (11.1)			0.03 (3.2)		0.03 (2.9)		0.06 (6.3)	0.16 (6.5)	0.04 (3.6)	0.12 (8.0)				0.35 (17.6)
	Cucullanus bourdini	0.77 (53.3)	0.39 (25.8)	0.65 (34.8)	0.04 (3.7)		0.04 (4.0)	0.29 (22.6)		0.03 (2.9)			0.81 (45.2)				0.91 (54.5)		0.22 (17.6)
	Dichelyne spinigerus	0.03 (3.3)		0.09 (8.7)	0.07 (7.4)	0.19 (19.2)		0.29 (19.4)		0.37 (11.4)		0.13 (6.3)	0.32 (22.6)				0.18 (9.1)		0.33 (13.7)
	Capillaridae			0.13 (13.0)	0.07 (3.7)			0.10 (9.7)		0.03 (2.9)			0.00						0.00
	Ascaridae			1.26 (43.5)							0.10 (6.7)	0.13 (12.5)	0.03 (3.2)			0.04 (4.0)			0.67 (15.7)
	Rhadinorhynchus sp.		0.06 (6.5)			0.04 (3.8)				0.06 (5.7)	0.03 (3.3)								0.16 (11.8)

Supplementary Data 14. Jack-knife reclassification success for the overall parasite assemblage of Golden Snapper sampled from the five regions across northern Australia. Data is presented as the number of fish captured from regions (rows) that are classified by discriminant functions into the various regions (columns). Bold values indicate successful reclassification to the location of origin.

Group	CS	CV	BG	BG	Wa	LS	DH	BI	MI	CoP	GI	GI	Ma	AS	AS	BMB	GE	VI	NR	We	NR	We	HB
CS	**27**	0	3																				
CV	2	**29**	0																				
BG	3	0	**20**																				
BG				**22**	0	0	0	0	0	0	1												
Wa				0	**19**	5	0	0	2	0	1												
LS				0	4	**18**	0	0	0	4	0												
DH				0	0	0	**16**	0	2	0	0												
BI				0	2	4	0	**17**	1	4	3												
MI				0	0	0	0	0	**24**	0	0												
CoP				0	6	4	3	2	0	**19**	1												
GI				0	0	0	0	0	4	0	**26**												
GI												**28**	2	0									
Ma												4	**12**	0									
AS												3	0	**28**									
AS															**20**	4	3	1	2	1			
BMB															1	**19**	6	1	1	0			
GE															2	10	**11**	1	0	1			
VI															1	5	2	**17**	0	0			
NR															1	2	1	0	**3**	4			
We															0	0	0	4	2	**4**			
NR																					**10**	0	1
We																					0	**7**	3
HB																					1	4	**46**

Supplementary Data 15. Parasite species infecting Golden Snapper listed by region of analysis that were found to be the more heavily weighted discriminating factors for the first two linear discriminants (LD1 and LD2, respectively). +/- indicates whether the factor was weighted in a positive or negative direction.

	LD1		LD2	
Region	**Parasite species**	**Proportion of trace**	**Parasite species**	**Proportion of trace**
Western	- *Hatschekia elongata* + *Euryhaliotrema* spp.	81.4	- *Pterobothrium* sp. 5	18.6
Darwin	+*Callitetrarhynchus* sp.	47.8	+*Hatschekia elongata*	23.0
Arnhem	-*Hatschekia elongata* +*Caligus* spp.	81.6	+*Caligus* spp. + *Pterobothrium* sp. 4 -*Pseudogilquinia* sp.	18.4
Gulf	+ *Hatschekia elongata* - *Pterobothrium* sp. 5	45.4	+ Anisakidae spp.	29.8
East Coast	-*Callitetrarhynchus* sp. +*Pseudogilquinia* sp.	71.4	-*Hatschekia elongate* +*Paratobothrium* sp.	28.6

Supplementary Data 16. Summary statistics of 10 microsatellite loci for Golden Snapper from 444 individuals sampled from 18 locations across northern Australia. n is the sample size, #A is the number of alleles, A_R is the allelic richness, H_E is the expected heterozygosity, H_O is the observed heterozygosity, and F is the fixation index $(H_E-H_O)/H_E$.

Pop		*GS027*	*GS094*	*GS076*	*GS068*	*GS090*	*GS051*	*GS114*	*GS091*	*GS072*	*GS082*
CS	***n***	14	14	12	14	14	14	14	11	14	14
	#A	4	2	6	16	12	2	8	6	5	8
	A_R	1.347	1.153	4.645	12.250	9.116	1.960	3.843	3.507	3.267	4.506
	I	0.559	0.257	1.632	2.633	2.326	0.683	1.636	1.477	1.300	1.721
	H_O	0.286	0.143	1.000	0.714	0.857	0.857	0.857	0.818	0.786	0.714
	H_E	0.258	0.133	0.785	0.918	0.890	0.490	0.740	0.715	0.694	0.778
	F	-0.109	-0.077	-0.274	0.222	0.037	-0.750	-0.159	-0.145	-0.132	0.082
CV	***n***	28	28	27	28	28	28	27	24	27	26
	#A	7	3	8	16	19	5	10	10	4	10
	A_R	1.533	1.427	5.207	11.615	13.754	2.477	5.028	4.000	3.019	8.346
	I	0.843	0.527	1.773	2.579	2.767	1.067	1.879	1.819	1.156	2.198
	H_O	0.393	0.357	0.704	1.000	0.964	0.571	0.815	0.750	0.704	0.962
	H_E	0.348	0.299	0.808	0.914	0.927	0.596	0.801	0.750	0.669	0.880
	F	-0.130	-0.194	0.129	-0.094	-0.040	0.042	-0.017	0.000	-0.052	-0.092
BG	***n***	23	23	23	23	23	23	23	23	23	23
	#A	4	3	8	14	15	5	8	13	3	9
	A_R	1.311	1.476	4.232	8.966	9.281	2.543	5.371	5.658	2.792	6.080
	I	0.519	0.563	1.677	2.381	2.427	1.112	1.806	2.114	1.062	1.968
	H_O	0.261	0.348	0.783	0.826	0.783	0.652	0.870	0.826	0.652	0.826
	H_E	0.237	0.322	0.764	0.888	0.892	0.607	0.814	0.823	0.642	0.836
	F	-0.100	-0.079	-0.025	0.070	0.123	-0.075	-0.069	-0.003	-0.016	0.011
Wad	***n***	29	29	29	29	29	28	29	28	27	27
	#A	7	3	8	15	18	5	8	12	3	10
	A_R	1.507	1.761	4.672	9.894	8.760	2.694	4.247	4.368	2.876	5.786
	I	0.812	0.711	1.724	2.473	2.476	1.205	1.633	1.908	1.077	1.986
	H_O	0.345	0.414	0.759	0.931	0.931	0.679	0.828	0.821	0.778	0.889

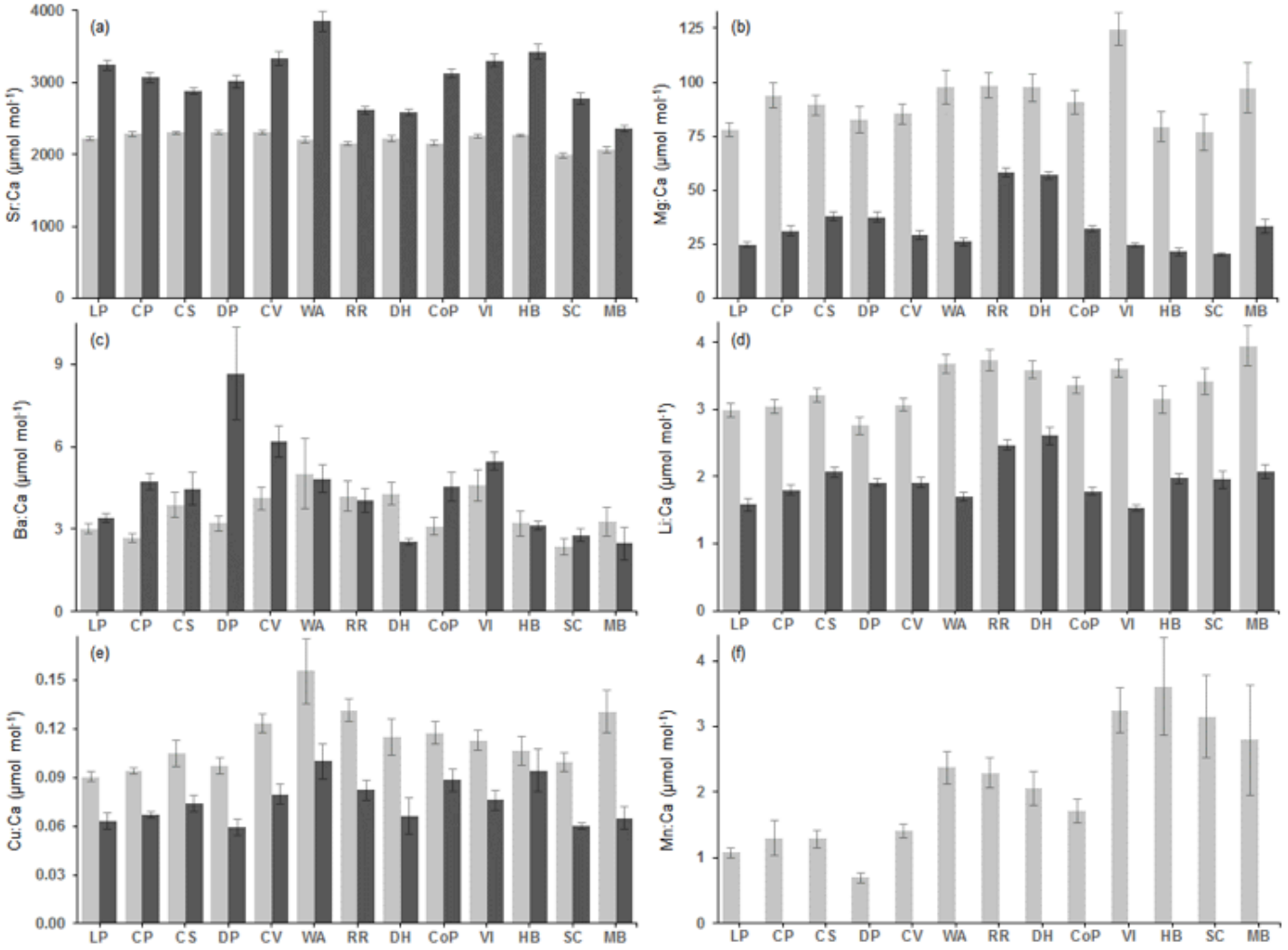
Pop		*GS027*	*GS094*	*GS076*	*GS068*	*GS090*	*GS051*	*GS114*	*GS091*	*GS072*	*GS082*
	H_E	0.337	0.432	0.786	0.899	0.886	0.629	0.765	0.771	0.652	0.827
	F	-0.025	0.043	0.035	-0.036	-0.051	-0.079	-0.082	-0.065	-0.192	-0.075
LS	***n***	25	25	25	25	25	25	25	25	24	24
	#A	7	3	9	16	19	6	8	11	4	10
	A_R	1.474	1.857	3.754	10.331	14.045	2.759	5.556	5.841	2.946	5.512
	I	0.784	0.717	1.681	2.524	2.772	1.215	1.832	2.043	1.148	1.927
	H_O	0.360	0.440	0.720	0.960	0.960	0.520	0.800	0.840	0.708	0.833
	H_E	0.322	0.462	0.734	0.903	0.929	0.638	0.820	0.829	0.661	0.819
	F	-0.119	0.047	0.019	-0.063	-0.034	0.184	0.024	-0.014	-0.072	-0.018
DH	***n***	20	20	19	20	20	20	20	20	20	20
	#A	7	4	10	14	16	3	10	11	4	9
	A_R	1.636	1.839	6.624	10.526	9.412	2.228	4.372	6.667	3.065	6.557
	I	0.910	0.827	2.058	2.465	2.471	0.891	1.768	2.106	1.174	2.026
	H_O	0.450	0.550	0.789	1.000	0.900	0.450	0.900	0.950	0.700	0.900
	H_E	0.389	0.456	0.849	0.905	0.894	0.551	0.771	0.850	0.674	0.848
	F	-0.158	-0.205	0.070	-0.105	-0.007	0.184	-0.167	-0.118	-0.039	-0.062
BI	***n***	31	31	31	31	31	31	31	31	31	31
	#A	6	4	9	17	21	5	10	8	3	9
	A_R	1.686	1.996	5.523	12.165	13.631	2.464	4.841	5.571	2.864	6.407
	I	0.877	0.904	1.882	2.621	2.782	1.083	1.876	1.891	1.074	1.988
	H_O	0.355	0.548	0.774	0.968	0.903	0.548	0.774	0.645	0.742	0.806
	H_E	0.407	0.499	0.819	0.918	0.927	0.594	0.793	0.820	0.651	0.844
	F	0.128	-0.099	0.055	-0.054	0.025	0.077	0.024	0.214	-0.140	0.044
MI	***n***	24	24	23	23	24	24	23	24	24	24
	#A	6	4	7	15	19	5	9	10	3	9
	A_R	1.426	2.141	5.598	10.687	13.395	2.141	3.779	3.282	2.844	5.938
	I	0.700	0.922	1.805	2.494	2.764	0.924	1.672	1.670	1.072	1.927
	H_O	0.333	0.583	1.000	0.913	0.958	0.625	0.652	0.667	0.750	0.792
	H_E	0.299	0.533	0.821	0.906	0.925	0.533	0.735	0.695	0.648	0.832
	F	-0.116	-0.094	-0.217	-0.007	-0.036	-0.173	0.113	0.041	-0.157	0.048

Pop		*GS027*	*GS094*	*GS076*	*GS068*	*GS090*	*GS051*	*GS114*	*GS091*	*GS072*	*GS082*
CoP	***n***	35	35	35	35	35	35	35	35	35	35
	#A	7	4	10	16	18	4	8	11	3	11
	A_R	1.594	1.826	5.506	11.343	9.919	2.256	4.344	5.506	2.963	7.704
	I	0.871	0.855	1.907	2.553	2.565	0.943	1.705	2.027	1.092	2.188
	H_O	0.314	0.371	0.857	0.886	0.886	0.457	0.800	0.829	0.771	0.943
	H_E	0.373	0.452	0.818	0.912	0.899	0.557	0.770	0.818	0.662	0.870
	F	0.157	0.179	-0.047	0.029	0.015	0.179	-0.039	-0.012	-0.165	-0.083
GI	***n***	30	30	30	30	30	30	30	30	30	30
	#A	6	4	7	11	18	4	10	12	4	11
	A_R	1.773	1.846	4.569	9.574	10.526	2.135	4.358	4.775	2.995	5.980
	I	0.920	0.830	1.648	2.312	2.620	0.839	1.782	1.968	1.148	2.027
	H_O	0.467	0.533	0.700	0.800	1.000	0.600	0.800	0.800	0.567	0.833
	H_E	0.436	0.458	0.781	0.896	0.905	0.532	0.771	0.791	0.666	0.833
	F	-0.070	-0.164	0.104	0.107	-0.105	-0.129	-0.038	-0.012	0.149	-0.001
Man	***n***	16	16	16	16	16	16	16	16	15	15
	#A	5	2	6	12	14	5	9	10	3	9
	A_R	1.391	1.358	4.303	9.846	10.240	2.909	4.231	4.452	2.980	5.921
	I	0.642	0.433	1.615	2.369	2.464	1.235	1.732	1.855	1.095	1.943
	H_O	0.313	0.188	0.750	0.938	1.000	0.625	0.875	0.688	0.533	0.800
	H_E	0.281	0.264	0.768	0.898	0.902	0.656	0.764	0.775	0.664	0.831
	F	-0.111	0.289	0.023	-0.043	-0.108	0.048	-0.146	0.113	0.197	0.037
AS	***n***	30	31	31	31	31	31	31	31	30	29
	#A	8	5	10	16	16	6	8	10	4	11
	A_R	1.540	2.103	5.754	12.242	7.845	2.673	3.214	3.463	2.857	6.494
	I	0.840	0.956	1.922	2.616	2.393	1.216	1.548	1.686	1.123	2.051
	H_O	0.333	0.419	0.903	0.903	0.871	0.774	0.742	0.774	0.633	0.724
	H_E	0.351	0.524	0.826	0.918	0.873	0.626	0.689	0.711	0.650	0.846
	F	0.049	0.200	-0.093	0.016	0.002	-0.237	-0.077	-0.089	0.026	0.144
BMB	***n***	24	24	23	24	23	24	22	23	24	24
	#A	4	4	8	13	16	5	7	10	3	10

Pop		*GS027*	*GS094*	*GS076*	*GS068*	*GS090*	*GS051*	*GS114*	*GS091*	*GS072*	*GS082*
	A_R	1.297	2.141	4.600	9.521	10.076	2.346	4.964	4.898	2.776	6.940
	I	0.514	0.922	1.725	2.405	2.515	1.005	1.723	1.902	1.056	2.111
	H_O	0.250	0.542	0.696	0.917	0.913	0.625	0.909	0.783	0.708	0.875
	H_E	0.229	0.533	0.783	0.895	0.901	0.574	0.799	0.796	0.640	0.856
	F	-0.091	-0.016	0.111	-0.024	-0.014	-0.089	-0.138	0.017	-0.107	-0.022
GT	***n***	26	26	26	26	26	26	26	25	24	24
	#A	8	4	8	13	18	5	9	11	4	11
	A_R	1.452	2.401	4.447	10.242	10.646	2.508	4.777	5.556	2.803	6.295
	I	0.788	0.989	1.722	2.423	2.588	1.070	1.819	2.018	1.118	2.027
	H_O	0.308	0.615	0.692	0.923	0.962	0.769	0.885	0.880	0.750	0.792
	H_E	0.311	0.584	0.775	0.902	0.906	0.601	0.791	0.820	0.643	0.841
	F	0.012	-0.054	0.107	-0.023	-0.061	-0.279	-0.119	-0.073	-0.166	0.059
VI	***n***	25	25	25	25	25	25	25	25	24	24
	#A	4	4	7	17	17	5	7	10	3	11
	A_R	1.400	2.495	5.342	12.136	11.364	2.437	2.880	4.529	2.902	5.675
	I	0.613	1.040	1.772	2.652	2.617	1.052	1.370	1.904	1.081	2.012
	H_O	0.280	0.600	0.800	0.920	0.800	0.600	0.720	0.800	0.667	0.750
	H_E	0.286	0.599	0.813	0.918	0.912	0.590	0.653	0.779	0.655	0.824
	F	0.020	-0.001	0.016	-0.003	0.123	-0.018	-0.103	-0.027	-0.017	0.090
NR	***n***	13	13	13	13	13	13	13	13	13	13
	#A	3	4	9	12	12	3	8	7	3	11
	A_R	1.489	2.580	5.045	8.895	8.450	2.432	4.694	3.756	2.620	6.145
	I	0.619	1.100	1.842	2.315	2.289	0.963	1.799	1.624	1.026	2.095
	H_O	0.231	0.462	0.769	1.000	0.846	0.615	0.923	0.692	0.692	0.923
	H_E	0.328	0.612	0.802	0.888	0.882	0.589	0.787	0.734	0.618	0.837
	F	0.297	0.246	0.041	-0.127	0.040	-0.045	-0.173	0.056	-0.120	-0.102
WP	***n***	8	7	7	7	8	8	8	7	8	8
	#A	4	2	5	11	8	2	8	6	4	6
	A_R	1.488	1.508	3.161	9.800	5.565	1.753	5.120	3.920	3.122	5.565
	I	0.689	0.520	1.369	2.342	1.873	0.621	1.836	1.574	1.228	1.754

Pop		*GS027*	*GS094*	*GS076*	*GS068*	*GS090*	*GS051*	*GS114*	*GS091*	*GS072*	*GS082*
	H_O	0.375	0.429	0.857	1.000	0.750	0.375	0.875	0.857	0.500	0.875
	H_E	0.328	0.337	0.684	0.898	0.820	0.430	0.805	0.745	0.680	0.820
	F	-0.143	-0.273	-0.254	-0.114	0.086	0.127	-0.087	-0.151	0.264	-0.067
HB	***n***	42	42	42	42	42	42	41	40	42	41
	#A	7	6	8	18	19	5	10	14	3	11
	A_R	1.637	2.443	4.225	12.000	7.964	2.300	5.025	4.533	2.729	7.168
	I	0.895	1.094	1.662	2.634	2.454	1.041	1.821	2.011	1.050	2.126
	H_O	0.262	0.714	0.643	0.952	0.810	0.667	0.902	0.825	0.667	0.902
	H_E	0.389	0.591	0.763	0.917	0.874	0.565	0.801	0.779	0.634	0.860
	F	0.327	-0.209	0.158	-0.039	0.074	-0.180	-0.127	-0.059	-0.052	-0.049
All populations	***n***	443	443	437	442	443	443	439	431	435	432
	#A	12	7	16	22	31	7	15	16	7	14
	A_R	1.499	1.908	4.845	10.668	10.222	2.390	4.480	4.682	2.912	6.279
	I	0.744	0.787	1.745	2.488	2.509	1.009	1.735	1.867	1.116	2.004
	H_O	0.329	0.459	0.789	0.919	0.894	0.612	0.829	0.791	0.684	0.841
	H_E	0.328	0.449	0.788	0.905	0.897	0.575	0.770	0.778	0.656	0.838
	F	-0.010	-0.026	-0.002	-0.016	0.004	-0.067	-0.077	-0.018	-0.044	-0.003

Supplementary Data 17. Mean concentrations (± s.e.) of element:^{43}Ca ratios from the near core (lighter bars) and margin (darker bars) of Grass Emperor otoliths collected from 13 locations across northern Australia. See Table 3 for location codes.



Supplementary Data 18. Jack-knife reclassification success for the core, near core and margin otolith microchemistry results for Grass Emperor sampled from the three jurisdictional management units. Data is presented as the percentage of fish captured from regions (rows) that are classified by discriminant functions into the various regions (columns) for analysis within that region only. Bold values indicate successful reclassification to the location of origin.

Ablation zone	Group	LP	CP	DP	CS	CV	Wa	RR	DH	CP	VI	HB	SC	MB
NEAR CORE	LP	**47**	17	17	13	7								
	CP	23	**27**	33	7	10								
	DP	0	29	**61**	4	7								
	CS	21	17	10	**24**	28								
	CV	13	20	7	10	**50**								
	Wa						**20**	10	13	33	23			
	RR						36	**4**	16	36	8			
	DH						13	4	**17**	42	25			
	CoP						12	9	6	**58**	15			
	VI						10	0	13	20	**57**			
	HB											**86**	0	14
	SC											7	**57**	36
	MB											17	42	**42**
MARGIN	LP	**63**	20	0	3	13								
	CP	33	**17**	13	23	13								
	DP	0	18	**46**	21	14								
	CS	0	21	14	**59**	7								
	CV	10	17	7	13	**53**								
	Wa						**57**	7	0	17	20			
	RR						0	**52**	36	12	0			
	DH						0	17	**79**	4	0			
	CoP						9	6	0	**58**	27			
	VI						17	0	0	33	**50**			
	HB											**12**	2	0
	SC											1	**11**	2
	MB											0	5	**7**

Supplementary Data 19. Element:^{43}Ca ratios from the otolith near core and margin listed by region of analysis for Grass Emperor that were found to be the more heavily weighted discriminating factors for the first two linear discriminants (LD1 and LD2, respectively). +/- indicates whether the factor was weighted in a positive or negative direction.

	Near Core				Margin			
	LD1		LD2		LD1		LD2	
Region	Element:^{43}Ca	Proportion of Trace	Element:^{43}Ca	Proportion of Trace	Element:^{43}Ca	Proportion of Trace	Element:^{43}Ca	Proportion of Trace
Western Australia	+ ^{7}Li:^{43}Ca - ^{25}Mg:^{43}Ca + ^{55}Mn:^{43}Ca	57.81	- ^{7}Li:^{43}Ca + ^{25}Mg:^{43}Ca - ^{63}Cu:^{43}Ca	29.19	- ^{7}Li:^{43}Ca + ^{88}Sr:^{43}Ca - ^{138}Ba:^{43}Ca	65.68	- ^{25}Mg:^{43}Ca + ^{88}Sr:^{43}Ca + ^{138}Ba:^{43}Ca	19.73
Northern Territory	+ ^{7}Li:^{43}Ca - ^{25}Mg:^{43}Ca - ^{55}Mn:^{43}Ca	62.47	- ^{7}Li:^{43}Ca + ^{25}Mg:^{43}Ca - ^{63}Cu:^{43}Ca	24.47	- ^{7}Li:^{43}Ca - ^{25}Mg:^{43}Ca + ^{63}Cu:^{43}Ca	88.81	+ ^{25}Mg:^{43}Ca + ^{88}Sr:^{43}Ca - ^{138}Ba:^{43}Ca	8.14
Queensland	+ ^{7}Li:^{43}Ca - ^{55}Mn:^{43}Ca - ^{88}Sr:^{43}Ca	85.44	- ^{25}Mg:^{43}Ca + ^{55}Mn:^{43}Ca - ^{63}Cu:^{43}Ca	14.56	+ ^{7}Li:^{43}Ca - ^{88}Sr:^{43}Ca + ^{138}Ba:^{43}Ca	87.25	+ ^{7}Li:^{43}Ca - ^{25}Mg:^{43}Ca - ^{88}Sr:^{43}Ca	12.75

Supplementary Data 20. Parasites found infecting Grass Emperor sampled from 13 locations across northern Australia that were used in analyses. Data is presented as mean abundance with prevalence in parentheses. Data presented is untransformed.

		Location	**LP**	**CP**	**DP**	**CS**	**CV**	**Wa**	**RR**	**DH**	**CoP**	**VI**	**HB**	**SC**	**MB**
	Parasite type	**Sample size**	**34**	**35**	**28**	**29**	**29**	**30**	**29**	**24**	**33**	**30**	**14**	**14**	**12**
Gills and pharyngeal teeth	Copepoda	*Hatschekia gracilis*	1.21 (61.8)	1.89 (62.9)	20.07 (100)	4.07 (89.7)	3.97 (93.1)	6.47 (93.3)	7.59 (93.1)	0.33 (16.7)	0.09 (9.1)	16.33 (96.7)		3.86 (78.6)	3.75 (91.7)
		Sagum vespertilio		0.06 (2.9)										0.50 (28.6)	
	Isopoda	Adult					0.03 (3.4)	0.10 (10.0)							
	Monogenea	*Haliotrema* spp.	24.32 (97.1)	27.54 (100)	9.36 (46.4)	4.24 (31.0)	10.28 (89.7)	15.70 (93.3)	0.76 (20.7)	1.50 (54.2)	22.30 (87.9)	8.63 (46.7)	5.07 (85.7)	0.50 (21.4)	7.50 (58.3)
		Diplectanidae spp.	24.88 (97.1)	12.29 (94.3)	4.93 (50.0)	2.52 (27.6)	6.07 (48.3)	13.53 (96.7)	0.03 (3.4)		12.61 (84.8)	17.93 (73.3)	1.29 (14.3)	2.86 (14.3)	
		Encotyllabe sp.	0.21 (17.6)	0.17 (11.4)	2.32 71.4)		1.07 (58.6)						2.07 (71.4)	0.07 (7.1)	
Body cavity, mesenteries & tissues	Cestoda	*Pseudogilquinia* sp.	1.24 (38.2)	4.40 (37.1)	6.57 (53.6)	0.86 (31.0)	0.79 (24.1)	0.80 (36.7)		0.04 (4.2)	0.03 (3.0)		1.00 (21.4)	0.21 (21.4)	
		Paratobothrium sp.		0.03 (2.9)	0.04 (3.6)									1.14 (28.6)	
		Nybelinia sp. 1	0.50 (8.8)	1.09 (31.4)	0.89 (21.4)		0.10 (10.3)	0.07 (6.7)	0.03 (3.4)	0.17 (12.5)		0.50 (33.3)		0.43 (14.3)	
		Nybelinia sp. 2		0.34 (17.1)	0.18 (10.7)		0.28 (27.6)	0.03 (3.3)				0.03 (3.3)			
		Nybelinia sp. 5											0.14 (14.3)	2.43 (71.4)	
		Nybelinia sp. 6					0.07 (3.4)							0.57 (14.3)	
		Nybelinia sp. 7	0.65 (8.8)	0.34 (14.3)											
		Callitetrarhynchus sp.		0.03 (2.9)			0.14 (10.3)	0.03 (3.3)							
		Proteocephalidae spp.	0.09 (8.8)	2.51 (22.9)			2.59 (27.6)	0.03 (3.3)	0.17 (3.4)		0.33 (9.1)				
	Digenea	Didymozoidae ex stomach wall	0.35 (32.4)	0.09 (5.7)	0.29 (286)		0.38 (24.1)	0.20 (13.3)			0.21 (21.2)	0.10 (10.0)	0.29 (14.3)		

		Location	LP	CP	DP	CS	CV	Wa	RR	DH	CoP	VI	HB	SC	MB
	Parasite type	**Sample size**	**34**	**35**	**28**	**29**	**29**	**30**	**29**	**24**	**33**	**30**	**14**	**14**	**12**
	Nematoda	Anisakidae spp.	0.97 (55.9)	3.17 (74.3)	3.71 (50.0)	0.24 (17.2)	2.17 (65.5)	3.63 (56.7)	0.21 (13.8)	0.04 (4.2)	0.15 (12.1)	0.23 (23.3)	4.00 (78.6)	9.07 (71.4)	0.42 (8.3)
	Acanthocephala	*Corynosoma* sp.												0.14 (14.3)	
		Serrasentis sagitiffer		0.06 (5.7)								0.03 (3.3)		0.36 (35.7)	
Intestinal canal	Digenea	Acanthocolpidae sp.	0.03 (2.9)	0.11 (11.4)		0.14 (6.9)	0.14 (10.3)							0.21 (7.1)	0.25 (25.0)
		Fairfaxia sp.	0.12 (8.8)	0.17 (11.4)	0.04 (3.6)	0.03 (3.4)			0.14 (3.4)			0.03 (3.3)			
		Hemiuridae sp.	0.50 (14.7)	0.46 (22.9)	0.07 (7.1)		0.07 (6.9)	0.40 (23.3)						0.93 (50.0)	0.42 (8.3)
		Bucephalidae sp.	0.03 (2.9)		0.11 (10.7)		0.03 (3.4)				0.03 (3.0)	0.20 (20.0)	0.07 (7.1)		
	Nematoda	*Cucullanus laurotravassosi*		0.23 (20.0)	0.64 (42.9)					0.13 (12.5)	0.12 (6.1)	0.57 (30.0)	0.50 (35.7)		

Supplementary Data 21. Jack-knife reclassification success for the parasite assemblage of Grass Emperor sampled from the three jurisdictional management units. Data is presented as the percentage of fish captured from regions (rows) that are classified by discriminant functions into the various regions (columns) for analysis within that region only. Bold values indicate successful reclassification to the location of origin.

Group	Locker Point	Cape Preston	Dampier Pen.	Camden Sound	Cape Voltaire	Wadeye	Roche Reef	Darwin Harbour	Coburg Pen.	Vanderlin Is.	Halifax Bay	Sunshine Coast	Moreton Bay
Locker Point	**68**	26	0	6	0								
Cape Preston	40	**46**	0	3	11								
Dampier Pen.	0	0	**64**	21	14								
Camden Sound	7	0	0	**93**	0								
Cape Voltaire	3.5	14	3.5	24	**55**								
Wadeye						**67**	3	0	17	13			
Roche Reef						0	**79**	21	0	0			
Darwin Harbour						0	8	**92**	0	0			
Coburg Pen.						0	0	18	**82**	0			
Vanderlin Is.						3	20	3	0	**74**			
Halifax Bay											**79**	7	14
Sunshine Coast											7	**79**	14
Moreton Bay											0	0	**100**

Supplementary Data 22. Parasite species infecting Grass Emperor listed by region of analysis that were found to be the more heavily weighted discriminating factors for the first two Linear Discriminants (LD1 and LD2, respectively). +/- indicates whether the factor was weighted in a positive or negative direction.

Region	**LD1**		**LD2**	
	Parasite species	**Proportion of trace**	**Parasite species**	**Proportion of trace**
Western Australia	+ *Hatschekia gracilis* - *Haliotrema* spp.	0.70	- *Encotyllabe* sp.	0.16
Northern Territory	-*Hatschekia gracilis* + *Haliotrema* spp.	0.54	- Diplectanidae spp.	0.33
Queensland	+ *Nybelinia* sp. 5 + *Serrasentis sagitiffer* + *Hatschekia gracilis* - Diplectanidae spp.	0.83	- *Serrasentis sagittifer* + *Nybelinia* sp. *6* - *Encotyllabe* sp.	0.17

Supplementary Data 23. Summary statistics of 10 microsatellite loci for Grass Emperor from 279 individuals sampled from 12 locations across northern Australia. *n* is the sample size, #A is the number of alleles, A_R is the allelic richness, *I* is Shannon's Information Index, H_E is the expected heterozygosity, H_O is the observed heterozygosity, and *F* is the fixation index $(H_E-H_O)/H_E$.

Pop		***Lel011***	***Lel040***	***Lel030***	***Lel012***	***Lel013***	***Lel032***	***Lel028***	***Lel027***	***Lel044***	***Lel039***
LP	***n***	22	23	22	17	23	21	23	22	23	23
	#A	9	11	15	12	7	11	9	17	8	8
	A_R	3.281	8.015	8.881	5.898	5.264	9.093	6.224	11.524	5.111	3.806
	I	1.543	2.226	2.410	2.084	1.733	2.290	1.972	2.622	1.792	1.628
	H_O	0.636	0.696	0.864	0.647	0.696	0.810	0.783	0.818	0.739	0.739
	H_E	0.695	0.875	0.887	0.830	0.810	0.890	0.839	0.913	0.804	0.737
	F	0.085	0.205	0.027	0.221	0.141	0.090	0.068	0.104	0.081	-0.003
CP	***n***	28	28	28	27	27	28	27	28	28	27
	#A	12	12	15	13	8	12	11	14	8	11
	A_R	3.950	5.074	11.701	7.839	5.420	8.253	6.178	11.281	5.620	3.701
	I	1.786	2.041	2.567	2.273	1.817	2.287	2.064	2.513	1.831	1.708
	H_O	0.643	0.786	0.893	0.778	0.778	0.786	0.852	0.857	0.857	0.593
	H_E	0.747	0.803	0.915	0.872	0.816	0.879	0.838	0.911	0.822	0.730
	F	0.139	0.021	0.024	0.108	0.046	0.106	-0.016	0.059	-0.043	0.188

Pop		*Lel011*	*Lel040*	*Lel030*	*Lel012*	*Lel013*	*Lel032*	*Lel028*	*Lel027*	*Lel044*	*Lel039*
CS	***n***	24	24	24	23	24	23	24	22	24	24
	#A	9	11	19	14	8	10	11	14	6	9
	A_R	3.008	6.194	13.395	6.491	5.053	7.399	8.056	10.522	4.571	3.218
	I	1.461	2.051	2.744	2.254	1.788	2.116	2.224	2.476	1.649	1.531
	H_O	0.583	0.875	0.833	0.652	0.750	0.870	0.875	1.000	0.750	0.708
	H_E	0.668	0.839	0.925	0.846	0.802	0.865	0.876	0.905	0.781	0.689
	F	0.126	-0.043	0.099	0.229	0.065	-0.005	0.001	-0.105	0.040	-0.028
DP	***n***	22	23	23	21	23	23	23	23	22	22
	#A	8	15	17	14	7	11	11	14	8	9
	A_R	3.653	6.373	9.706	6.533	5.454	9.043	6.696	9.796	5.762	4.889
	I	1.573	2.254	2.531	2.272	1.810	2.284	2.053	2.444	1.857	1.829
	H_O	0.773	0.870	0.870	0.667	0.870	0.957	0.957	0.870	0.773	0.682
	H_E	0.726	0.843	0.897	0.847	0.817	0.889	0.851	0.898	0.826	0.795
	F	-0.064	-0.031	0.031	0.213	-0.065	-0.075	-0.124	0.032	0.065	0.143
CV	***n***	30	30	30	29	30	30	30	30	30	30
	#A	11	15	16	14	10	11	10	14	10	11
	A_R	3.896	9.677	11.250	8.327	5.590	7.895	5.788	10.465	6.207	4.147
	I	1.781	2.473	2.542	2.358	1.915	2.179	2.002	2.455	2.001	1.787
	H_O	0.733	0.833	0.900	0.828	0.900	0.867	0.900	0.933	0.767	0.700
	H_E	0.743	0.897	0.911	0.880	0.821	0.873	0.827	0.904	0.839	0.759
	F	0.013	0.071	0.012	0.059	-0.096	0.008	-0.088	-0.032	0.086	0.078
Wa	***n***	23	23	23	23	23	23	23	22	23	20
	#A	7	10	14	13	8	9	9	14	10	6
	A_R	3.094	3.527	10.907	4.215	5.911	6.531	6.870	11.388	5.111	4.762
	I	1.370	1.737	2.490	1.877	1.886	1.983	2.019	2.523	1.936	1.626
	H_O	0.565	0.783	1.000	0.783	0.739	0.783	0.783	0.909	0.870	0.800
	H_E	0.677	0.716	0.908	0.763	0.831	0.847	0.854	0.912	0.804	0.790
	F	0.165	-0.092	-0.101	-0.026	0.110	0.076	0.084	0.003	-0.081	-0.013
RR	***n***	25	25	24	24	25	24	25	25	25	25
	#A	6	14	12	10	8	10	10	14	8	8

Pop		*Lel011*	*Lel040*	*Lel030*	*Lel012*	*Lel013*	*Lel032*	*Lel028*	*Lel027*	*Lel044*	*Lel039*
	A_R	3.019	5.482	9.443	4.923	5.896	6.982	8.117	10.684	5.708	4.596
	I	1.262	2.168	2.346	1.849	1.879	2.102	2.175	2.480	1.862	1.722
	H_O	0.600	0.840	0.875	0.625	0.840	0.708	0.840	1.000	0.840	0.880
	H_E	0.669	0.818	0.894	0.797	0.830	0.857	0.877	0.906	0.825	0.782
	F	0.103	-0.027	0.021	0.216	-0.012	0.173	0.042	-0.103	-0.018	-0.125
DH	***n***	21	21	22	21	22	22	22	22	22	20
	#A	5	10	12	11	8	15	10	13	8	9
	A_R	2.410	4.500	9.132	5.313	5.694	8.643	6.722	10.298	4.227	4.278
	I	1.113	1.840	2.313	1.973	1.849	2.385	2.043	2.431	1.707	1.723
	H_O	0.714	0.762	0.864	0.810	0.864	0.909	0.955	0.909	0.773	0.800
	H_E	0.585	0.778	0.890	0.812	0.824	0.884	0.851	0.903	0.763	0.766
	F	-0.221	0.020	0.030	0.003	-0.048	-0.028	-0.121	-0.007	-0.012	-0.044
CoP	***n***	31	32	31	31	31	32	32	32	32	30
	#A	6	11	16	14	8	13	10	15	8	8
	A_R	2.715	3.287	11.306	5.772	5.384	9.225	5.107	10.952	5.447	4.569
	I	1.202	1.665	2.572	2.136	1.817	2.368	1.900	2.512	1.803	1.705
	H_O	0.613	0.688	0.935	0.935	0.806	0.875	0.813	0.938	0.813	0.733
	H_E	0.632	0.696	0.912	0.827	0.814	0.892	0.804	0.909	0.816	0.781
	F	0.030	0.012	-0.026	-0.132	0.010	0.019	-0.010	-0.032	0.005	0.061
VI	***n***	29	29	29	28	29	29	29	27	29	29
	#A	7	11	14	14	6	13	9	13	8	6
	A_R	2.620	4.711	9.191	5.580	3.903	7.377	6.675	8.890	5.021	3.511
	I	1.217	1.910	2.393	2.130	1.510	2.210	1.980	2.327	1.784	1.424
	H_O	0.759	0.862	0.931	0.714	0.724	0.931	0.862	0.889	0.793	0.655
	H_E	0.618	0.788	0.891	0.821	0.744	0.864	0.850	0.888	0.801	0.715
	F	-0.227	-0.094	-0.045	0.130	0.026	-0.077	-0.014	-0.002	0.010	0.084
HB	***n***	11	11	10	11	9	11	11	10	11	11
	#A	5	4	8	7	5	7	9	9	5	7
	A_R	2.420	2.180	6.250	3.903	3.375	4.939	5.378	8.333	3.507	4.172
	I	1.147	1.010	1.943	1.590	1.353	1.743	1.917	2.155	1.388	1.633

Pop		*Lel011*	*Lel040*	*Lel030*	*Lel012*	*Lel013*	*Lel032*	*Lel028*	*Lel027*	*Lel044*	*Lel039*
	H_O	0.545	0.545	0.900	0.545	0.667	0.818	0.909	0.900	0.909	0.909
	H_E	0.587	0.541	0.840	0.744	0.704	0.798	0.814	0.880	0.715	0.760
	F	0.070	-0.008	-0.071	0.267	0.053	-0.026	-0.117	-0.023	-0.272	-0.196
SC	***n***	9	9	8	9	9	9	9	9	9	9
	#A	4	6	8	6	5	9	7	12	5	6
	A_R	3.057	3.176	5.565	4.050	3.000	6.480	3.857	9.000	2.531	3.951
	I	1.223	1.377	1.890	1.538	1.301	2.029	1.629	2.351	1.164	1.542
	H_O	0.889	0.556	0.875	0.556	0.778	1.000	0.889	0.889	0.778	0.778
	H_E	0.673	0.685	0.820	0.753	0.667	0.846	0.741	0.889	0.605	0.747
	F	-0.321	0.189	-0.067	0.262	-0.167	-0.182	-0.200	0.000	-0.286	-0.041
All locations	***n***	275	278	274	264	275	275	278	272	278	270
	#A	16	20	23	24	13	17	14	20	14	16
	A_R	3.093	5.183	9.727	5.737	4.995	7.655	6.306	10.261	4.902	4.133
	I	1.390	1.896	2.395	2.028	1.721	2.165	1.998	2.441	1.731	1.655
	H_O	0.671	0.758	0.895	0.712	0.784	0.859	0.868	0.909	0.805	0.748
	H_E	0.668	0.773	0.891	0.816	0.790	0.865	0.835	0.902	0.784	0.754
	F	-0.047	0.028	-0.016	0.037	0.025	0.028	-0.025	-0.017	-0.036	0.031