Assessing the spawning characteristics and reproductive biology of Pearl Perch (*Glaucosoma scapulare*) in Queensland

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December 2022

FRDC Project No. 2018/074

FRDC
FISHERIES RESEARCH & DEVELOPMENT CORPORATION

CSIRO

UNIVERSITY of TASMANIA

Queensland Government

ISBN 978-0-6456352-3-2

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2022

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In submitting this report, the researcher has agreed to FRDC publishing this material in its edited form.

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Acknowledgments

The authors extend their sincerest thanks to the fishers that contributed fish frames during the routine monitoring program undertaken by Fisheries Monitoring. Thank you to Mal Pearce, Jonathan Staunton-Smith, Jason McGilvray and Darren Smallwood for facilitating the acquisition of biological samples and the various FM staff that assisted with sample processing including Jack Walsh, Nick Stratford, Shannon White, Sam Seghers, and Natalia Robeldo. Lisa Walton assisted with the processing of samples in the laboratory and Michelle Sellin blocked and sectioned otoliths. We also thank Jennifer Larkin and Carlie Heaven from Fisheries Queensland (FQ) for providing relevant data on request. We would also like to thank Derek Lunau for assisting with the acoustic tagging work and Jonathan Lee for facilitating Derek's participation.

Thanks to Steve Campbell, who provided a place for us to start looking for large, spawning Pearl Perch north of Fraser Island. We appreciate the guidance provided by members of the Rocky Reef Working Group in the early stages of project development.

We are grateful to Paul Hickey, Ben Bassingthwaighte, Carmel Barrie and Carmel Coonan for their assistance in project management, administration and development. Special and on-going thanks to Zalee Bates and Pat Abbott for their continued diligence in sourcing and supplying relevant literature and assisting with Endnote challenges.

We are grateful to Fisheries Queensland staff, particularly Michelle Winning, Sian Breen and Chad Lunow, for their support and assistance throughout the initial development of this project.

Peter Kind, Glenn Anderson and Carmel Barrie provided helpful comments on earlier drafts of this report.

This research was undertaken in accord with Great Barrier Reef Marine Park Authority Permit G19/42784.1 and Department of Agriculture and Fisheries General Fisheries Permits 213514 and 186281. Animal ethics approvals were granted under permit numbers CA 2022/04/1597 and CA 2019/07/1297.

Abbreviations

Abbreviation	Definition
CSIRO	Commonwealth Scientific and Industrial Research Organisation
DAF	Department of Agriculture and Fisheries
DArT	Diversity Arrays Technology Pty. Ltd
DNA	Deoxyribonucleic acid
FIS	Fishery-Independent Survey
FL	Fork Length
FM	Fisheries Monitoring
FQ	Fisheries Queensland
GAM	Generalised Additive Model
GSI	Gonosomatic Index
GPS	Global Positioning System
Infofish	Infofish Services Pty. Ltd.
MLS	Minimum Legal Size
PRS	Post-Release Survival
NGS	Next Generation Sequencing
QFB	Queensland Fish Board
RRFF	Rocky Reef Finfish Fishery
RRWG	Rocky Reef Working Group
SAFS	Status of Australian Fish Stocks
TL	Total Length
UQ	University of Queensland
VBGF	von Bertalanffy Growth Function

Executive Summary

Pearl Perch have a long history of exploitation and previous fishery-dependent sampling revealed a lack of spawning fish on the traditional fishing grounds in southern Queensland and northern New South Wales. A quantitative stock assessment published in 2017 indicated that the spawning biomass of Pearl Perch was below sustainable levels, and management intervention was required to rebuild the stock. One recommendation from the stock assessment was the need to understand the spawning dynamics and identify spawning locations.

To address this recommendation, researchers from the Queensland Department of Agriculture and Fisheries (DAF) collected Pearl Perch to determine when and where Pearl Perch spawn. Samples were acquired by Fisheries Queensland's (FQ) Fishery Monitoring (FM) group, as part of their routine monitoring program, and supplemented by fishery-independent sampling undertaken by staff from DAF's Animal Science group. Biological samples were collected from Innisfail in the north, to Coffs Harbour in the south, between July 2018 and June 2022. Spawning fish were collected from deeper (>170 m) waters offshore from the Sunshine Coast and from areas adjacent to the Swain Reefs in Central Queensland.

Movement to and from spawning sites was assessed with both conventional and acoustic tagging. Infofish Australia supplied Pearl Perch tag-recapture information, and this was supplemented with tag-recapture information generated during the current project. Staff from the Commonwealth Scientific and Industrial Research Organisation (CSIRO) provided acoustic tagging equipment with the intention of tagging ~50 Pearl Perch with acoustic tags at spawning locations to determine movement post-spawning.

Initially, an Animal Science geneticist intended to assess the structure of the Pearl Perch stock: however, the DNA extracted was of insufficient quality to enable robust analyses. To provide some information on the importance of the fish spawning adjacent to the Swain Reefs area and the deeper waters offshore of the Sunshine Coast, a researcher from the University of Tasmania analysed the likely dispersal patterns of larvae spawned in these areas based on ocean current data.

This research provides fishery managers with information with which to manage the Pearl Perch stock. The lack of discrete spawning locations and spawning times is challenging, and this research indicates that the current annual spawning closure is inappropriate for Pearl Perch.

Background

Pearl Perch (*Glaucosoma scapulare*) is a recreationally and commercially important species found in schools in depths to at least 250 metres. Pearl Perch are a slow-growing, long-lived (~27 years) species endemic to the east coast between 23°S and 33°S. Although once considered incidental in a multi-species line fishery mainly targeting Snapper (*Chrysophrys auratus*) in southern Queensland, Pearl Perch are now targeted due to a combination of significant decreases in Snapper catch rates and more stringent management arrangements for Snapper in recent years. Recreational and commercial fishers use rod-and-reel (electric, hydraulic and manual) to target Pearl Perch over a variety of habitats including rocky reef, low-relief reef, wrecks and gravel patches where wire weed (Gorgonian soft coral) is present.

In Queensland, logbook data indicate that commercial harvest has decreased from a peak of ~96 t in 2005 to ~14 t in 2019, a decrease of ~85%. In the same period, mean commercial catch rates of Pearl Perch decreased from ~17.5 to ~6 kg boat^{-1} day^{-1}. Similarly, the number of Pearl Perch retained by recreational fishers in Queensland decreased from 54,000 in 2000–01 to 15,000 in 2019–20. The most recent stock assessment demonstrated that the spawning biomass of Pearl Perch

was at low levels, compared to pre-fishing levels. A recommendation from a previous stock assessment was the need for a better understanding of the spawning dynamics of Pearl Perch and areas where they may aggregate to spawn. Previous research found very few animals in spawning condition: however, since 2008, fishery-dependent monitoring conducted by FM has revealed that large fish in spawning condition are caught in the area between Fraser Island and Gladstone, and in deeper waters offshore from the Sunshine Coast. Improved knowledge of the Pearl Perch's spawning dynamics enables fishery managers to make evidence-based decisions regarding harvest strategies that increase egg production and, therefore, increase spawning biomass.

Aims/objectives

The aims of this study are 1) Assess the temporal and spatial trends in the reproductive biology of Pearl Perch, 2) Determine the movement of spawning Pearl Perch using both conventional and acoustic tagging methods, and 3) Identify areas, if any, that support spawning aggregations and determine the relative importance of these aggregations to the sustainability of the Pearl Perch stock.

Methodology

Specimens of Pearl Perch were collected as part of FM's routine fishery monitoring program between July 2018 and June 2022. Fish frames were either donated by commercial and recreational fishers or collected at seafood wholesale outlets. This sampling was supplemented by fishery-independent samples collected during the current study. From these samples, the following biological information was derived: 1) fecundity, 2) gonosomatic index (GSI), 3) gonad stage, 4) age and growth, and 5) age- and length-at-maturity.

Movement of Pearl Perch was assessed using tag-recapture data supplied by Infofish Services, the company responsible for administering the recreational fish tagging program in Queensland. These data were supplemented by tag-recapture information obtained during the current study. Acoustic tags were also used to determine movement adjacent to, and away from, aggregation sites. Pearl Perch were tagged at aggregation sites with Vemco V13 acoustic tags, before Vemco VR2AR receivers were deployed in and around the aggregation sites.

Genetic analyses were used to determine the source of Pearl Perch larvae. Samples were collected throughout the species' distribution to determine the Pearl Perch stock structure. Similarly, larval distribution models were used to determine the dispersal of larvae from known spawning areas.

Results/key findings

The expansion of the fishery, to the north and east of traditional fishing grounds, has resulted in the presence of larger, older Pearl Perch in fishery-dependent samples collected by FM. This expansion was facilitated by increases in fishing power, driven primarily by the uptake of GPS, more powerful fishing finding equipment, and larger vessels with increasing range. The presence of these larger fish improved previous estimates of age and growth in the current study, and improved estimates of length- and age-at-maturity.

Spawning female Pearl Perch were found in April, May, June, and December in the southern region and in September, October, and November in the northern region. Gonosomatic Index was highest on the new moon in the southern region, while lunar phase had no effect on GSI in the northern region. Mean GSI was found to increase in spring in the northern region, reaching a peak in December and January. In contrast, mean GSI increased through summer in the southern region, with a peak in April. Maximum mean GSI (>2%) coincided with sea surface temperatures between 25.26 and 26.32°C. The length- and age-at-maturity of female Pearl Perch was found to be L_{50} =

353 mm FL and t_{50} = 4.42 years. Further, the length- and age-at-95%-maturity were found to be L_{95} = 427 mm and t_{95} = 6.79 years, respectively. Finally, batch fecundity was found to be positively correlated with fork length. These results indicate that a female Pearl Perch at the current minimum legal size of 38 cm (total length, TL) is ~4 years old, has a ~60% chance of being mature, and carries ~315,000 eggs if it is mature.

Pearl Perch were found to live at least 27 years. The von Bertalanffy growth function (VBGF) was found to best fit the observed length-at-age data and the estimate of L_∞ was higher for males (L_∞ = 603 mm fork length, FL), compared to females (L_∞ = 564 mm FL), in the northern region. Further, the estimate of the L_∞ was higher for males in the north (L_∞ = 603 mm FL), compared to males in the south (L_∞ = 561 mm FL).

The tag-recapture data indicated that movement of 3,546 tagged Pearl Perch was restricted to less than 20 km and ~79% of tagged fish moved less than two kilometres from the tagging location. Too few large, mature fish were tagged to determine the movement of pre-spawn Pearl Perch and no tagged fish were captured in areas where spawning is known to occur. The acoustic tagging component demonstrated that some fish exhibited site fidelity, although sample size was low.

The genetic analyses were unsuccessful. Insufficient quantities of DNA were extracted from Pearl Perch samples to enable Next Generation Sequencing (NGS) analysis. The larval dispersion model indicated that larvae were carried from spawning sites southward, on the East Australian Current (EAC). The highest proportion of larvae settling in each latitude band were spawned in the same area. No larvae spawned south of Fraser Island move northward and very few larvae spawned north of Fraser Island settle in latitudes south of 27°S. All larvae settling in New South Wales are spawned south of Fraser Island.

The increased access by fishers to offshore fishing grounds is concerning. It is likely that the Pearl Perch stock is heavily reliant on spawning animals inhabiting these remote areas. The one-month spawning closure introduced in 2019, occurring annually between July 15 and August 15, provides very little protection for spawning Pearl Perch. The lack of access to offshore grounds prior to 2000, provided refugia for spawning Pearl Perch as evidenced by the lack of spawning fish in fishery-dependent samples collected at this time. Aggregating Pearl Perch are an easy target for commercial fishers, and large catches are possible in a short time. It would be prudent, therefore, to provide these aggregations with some level of protection during spawning periods.

Implications for relevant stakeholders

Knowledge of spawning times and locations provides fishery managers with the ability to develop harvest strategies that minimise impacts on spawning fish and increase egg production. The current temporal spawning closure that occurs between July 15 and August 15, annually, provides no protection for spawning fish. Lunar phase had a variable effect on GSI and, as such, implementing spawning closures like those used to protect spawning coral trout in Queensland, would be inappropriate for Pearl Perch.

The correlation between sea surface temperature and ovary development implies that spawning will likely occur earlier each year due to climate-induced warming. Should temporal spawning closures be implemented to protect spawning fish, the starting date of the closure will need to be reassessed if water temperatures rise as expected.

The estimate of length-at-maturity of L_{50} = 353 mm FL (~372 mm TL) implies that 50% of the fish at this size are mature. Generally, minimum legal sizes (MLSs) allow a fish to spawn at least once before recruiting to the fishery. This is currently the case for Pearl Perch and has been since 2019,

when the MLS was increased from 350 mm TL to 380 mm TL. Prior to 2019, however, the MLS was below L_{50}.

The imposition of a maximum legal size may be beneficial for Pearl Perch given the higher fecundity of larger individuals and the species' resilience to catch-and-release. Prohibiting the retention of large Pearl Perch may deter fishers from accessing large aggregations during the spawning period, providing some protection for spawning fish.

The tag-recapture information generated during this study provides no evidence of spawning migrations. However, the lack of tag returns from areas where Pearl Perch spawn is not evidence that spawning migrations do not occur. Most of the fish tagged to date were immature and spawning migrations are, therefore, not expected. Further, tag loss and non-reporting of recaptures are also likely explanations for the low tag recovery rates.

The inability to recover DNA of sufficient quality for Next Generation Sequencing necessitates further genetic sampling. While genetic analysis failed to determine stock structure, the larval dispersion models provide information on the likely source of larval settlement throughout the fishery. The results indicate fish settling on traditional grounds in southern Queensland and northern New South Wales are spawned south of Fraser Island. The increasing strength of the EAC is likely to transport Pearl Perch larvae further south.

Any future management changes imposed to protect spawning Pearl Perch will necessarily result in the release of captured individuals. Given the number of fish released, significant efforts will be required to educate fishers on methods that maximise the survival of released fish, particularly in the deeper offshore waters where fish caught during the current study exhibited barotrauma symptoms such as exophthalmia. Similarly, sharks were present at offshore grounds and methods that mitigate both depredation and post-release predation should be extended to stakeholders.

Recommendations

1. The results of this study should be used to inform the future harvest strategies such as spatial spawning closures and the imposition of a maximum legal size. Given the increasing fishing effort in areas where spawning aggregations are found, protections should be implemented for spawning Pearl Perch.

2. Estimates of age- and length-at-maturity derived herein should be used in future stock assessments to improve the accuracy of, and confidence in, stock assessment outputs. Given the differences in spawning and growth, consideration should be given to dividing the Queensland portion of the stock into two separate sub-stocks for future stock assessments.

3. Fishery monitoring, with aims of collecting reproductive biology information, should continue. The current study has significantly improved the knowledge of the Pearl Perch's reproductive biology: however, further sample collection will improve estimates of spawning times. Specifically, samples collected during full and new moon periods may lead to improvements in the outputs of the GAM model developed to assess GSI. This monitoring should also include New South Wales to determine if spawning Pearl Perch are present in deeper, offshore waters.

4. The larval dispersion model outputs would benefit from the identification of settlement locations. In the current study, settlement locations were inferred from data collected during trawl and crab bycatch research. Additionally, knowledge of true spawning aggregation areas is currently incomplete and could not be represented accurately in the model. Efforts should be made to quantify these potential inputs to improve larval dispersion models.

5. Genetic sampling should be undertaken, and samples be sent to DArT to ensure DNA of sufficient quality can be extracted for Next Generation Sequencing (NGS).

6. Future research should concentrate tagging effort at large Pearl Perch. Commercial fishers should be engaged to catch large Pearl Perch at likely spawning locations to ensure enough are tagged-and-released to enable robust analyses of tag-recapture data. Further acoustic tagging should be undertaken to determine movement to or from aggregations.

7. Efforts should also be made to determine the effect of climate-driven increases in sea surface temperatures and the strength of the EAC on the transportation of larvae. The effect of these and other environmental factors are currently unknown. The effect of increasing ocean temperature on the distribution of Pearl Perch in Queensland is unknown.

8. Should management changes be introduced, such as a maximum legal size, that result in increased rates of release, resources should be dedicated to educating fishers about maximising the survival of released fish. The Rocky Reef Working Group should be engaged to discuss the most efficient methods of extending information to fishers. The mandatory use of tools that mitigate the effects of barotrauma, such as release weights, venting tools or Coucum's Cages, should be considered by fishery managers and the working group. Further, methods to reduce depredation and post-release predation by sharks should be extended to fishers to maximise the survival of released fish.

9. Fishing power has clearly increased in the rocky reef fishery. Current estimates of fishing power are based on subjective estimates of the effects of a range of technological changes on catches between 1982 and 2012 provided by fishers. The effects of recent advances, such as spot-lock electric motors, digital steering for outboard motors and the use of electric reels with multiple hooks, remain unquantified. Further research is required to empirically derive estimates in fishing power increases.

Keywords

Pearl Perch, *Glaucosoma scapulare*, age-at-maturity (t_{50}), length-at-maturity (L_{50}), larval dispersion, tagging, growth, reproductive biology, Bayesian framework, life history, sea surface temperature, SST

1. Introduction

The Pearl Perch (*Glaucosoma scapulare*) is endemic to the east coast of Australia between Rockhampton (23°20′S) and Port Jackson (33°50′S) (McKay 1997). Along with three other species (*Glaucosoma hebraicum*, *Glaucosoma magnificum* and *Glaucosoma buergeri*), the Pearl Perch is classified within the family Glaucosomatidae, all of which occur in the Indo-Pacific region (McKay 1997). McKay (1997) stated Pearl Perch were found to depths of 90 m: however, sampling undertaken during the current study indicates the species is regularly caught from large schools in depths to at least 250 m in Queensland. Apart from submerged rocky reef areas (McKay 1997), the species is known to aggregate over shipwrecks, gravel substrates and adjacent areas, particularly those where gorgonian sea whips, colloquially known as "wire weed", occur (Grant 2004).

Pearl Perch is considered an excellent table fish (McKay 1997; Grant 2004) and, consequently, is a target for both commercial and recreational fishers. The species has a long history of exploitation (Stewart *et al.* 2013) and was likely caught incidentally by recreational anglers targeting Snapper (*Chrysophrys auratus*) in southern Queensland from the late 1880s (Thurstan *et al.* 2016). Pearl Perch are primarily caught by line fishers using rod-and-reel, and an increasing number of fishers are now using either electric or hydraulic reels in deeper offshore waters. The line fishery accounts for most of the fishing mortality applied to the stock: however, an unknown amount of discard mortality results from the incidental capture of juveniles in trawl (Courtney *et al.* 2007; Rowsell and Davies 2012) and crab (*Portunus armatus*) (Sumpton *et al.* 2003) fisheries.

Despite the long history of exploitation of Pearl Perch throughout its distribution, there is scant biological information on the species in the primary literature. Stewart *et al.* (2013) examined the growth of Pearl Perch using fishery-dependent samples, supplemented by samples of small fish collected by a research trawl vessel. These authors reported that Pearl Perch are long-lived and slow growing, a life history strategy consistent with its congenerics *G. hebraicum* (Hesp *et al.* 2002) and *G. buergeri* (Newman 2002). Further, Stewart (2011) demonstrated that the age distributions of fishery-dependent samples of Pearl Perch were truncated, suggesting that exploitation had removed the older animals from the population. Finally, Campbell *et al.* (2014) quantified the post-release survival of line-caught Pearl Perch and, in contrast to results reported by St. John and Syers (2005) for *G. hebraicum*, found that the Pearl Perch is resilient to catch-and-release.

The Pearl Perch stock is currently classified as depleted by the Status of Australian Fish Stocks report (SAFS, https://fish.gov.au/report/336-Pearl-Perch-2020), which states that fishing mortality exceeds sustainable levels. In Queensland, logbook data (available at https://qfish.fisheries.qld.gov.au/) indicate that commercial harvest has decreased from a peak of ~96 t in 2005 to ~14 t in 2019, a decrease of ~85%. In the same period, commercial catch rates of Pearl Perch decreased from ~17.5 to ~6 kg boat^{-1} day^{-1} (Wortmann 2020). Similarly, the number of Pearl Perch retained by recreational fishers in Queensland decreased from 54,000 in 2000–01 to 15,000 in 2019–20 (data available at: https://www.daf.qld.gov.au/business-priorities/fisheries/monitoring-research/monitoring-reporting/statewide-recreational-fishing-surveys/dashboard). Sumpton *et al.* (2017) indicated that these declines have coincided with a reduction in spawning biomass, compared to pre-fishing levels. This stock assessment used length and age data obtained as part of a routine monitoring program conducted by the Queensland Government's fisheries management agency, Fisheries Queensland (FQ). Since 2006, FQ's Fishery Monitoring group (FM) have collected biological information to assess stock status and develop future harvest strategies for a range of rocky reef-associated species in Queensland, including Pearl Perch. Biological samples for age determination are primarily in the form of processed fish frames, donated by commercial and recreational fishers or collected at seafood wholesale outlets.

Prior to 2010, the age frequencies of fish collected by FM were truncated as described by Stewart (2011), with very few fish >10 years in age (Sumpton *et al.* 2017; Fig. 35, page 49), despite a lifespan

of at least 19 years (Stewart *et al.* 2013). In recent years, however, FM has collected significant numbers of Pearl Perch at ages not previously observed in fishery-dependent samples. The presence of older Pearl Perch in samples is a direct result of the expansion of the fishery that occurred throughout the early 2000s. Prior to this time, fishers were mostly restricted to depths (<100 m) in the area south of Fraser Island: however, the increasing use of larger vessels equipped with Global Positioning Systems (GPS) and powerful fish finders, combined with decreasing catch rates on traditional fishing grounds, encouraged fishers to explore deeper (>100–200 m) waters offshore from the Sunshine Coast and Fraser Island (see Figure 1), and in waters adjacent to the Swain Reefs. In these more remote, lightly fished areas, significant numbers of large Pearl Perch were caught by fishers targeting tropical snappers such as Ruby Snapper (*Etelis coruscans*), Rosy Jobfish (*Pristipomoides filamentosus*), and Goldband Snapper (*Pristipomoides multidens*). These grounds are now regularly accessed by both commercial and recreational fishers.

Previous research (Sumpton *et al.* 1998; Stewart 2011; Stewart *et al.* 2013) failed to find any fish in spawning condition which led Stewart *et al.* (2013) to hypothesise that Pearl Perch migrated northward to spawn. Some spawning fish were found in samples collected by Sumpton *et al.* (2013a) from areas north of Fraser Island, which prompted Sumpton *et al.* (2017) to recommended research to understand the spawning dynamics and identify spawning locations. This knowledge would allow FQ to develop harvest strategies designed to protect spawning fish and increase egg production. In 2019, the Rocky Reef Working Group (RRWG) considered a suite of measures to reduce the total harvest of Pearl Perch, considered to be appropriate to enhance spawning fish stocks, and cease the ongoing decline in spawning biomass. Following a round of consultation, FQ introduced the following changes to the management of Pearl Perch: 1) 15 t total allowable commercial catch, 2) increased minimum legal size (MLS) from 35 cm (total length, TL) to 38 cm TL, 3) a reduction in the recreational in-possession limit from five to four, and 4) an annual one month no-take period commencing on 15 July, annually. The current study was developed to inform the future management of Pearl Perch, specifically through the development of harvest strategies based on reproductive information that improve egg production and spawning biomass.

2. Objectives

1. Assess the temporal and spatial trends in the reproductive biology of Pearl Perch.

2. Determine the movement of spawning Pearl Perch using both conventional and acoustic tagging methods.

3. Identify areas, if any, that support spawning aggregations and determine the relative importance of these aggregations to the sustainability of the Pearl Perch stock.

3. Method

3.1 Growth

Specimens of Pearl Perch were collected as part of FQ's routine fishery monitoring program between January 2020 and December 2021. Fish frames were either donated by commercial and recreational fishers or collected at seafood wholesale outlets and stored in freezers located at the EcoSciences Precinct in Brisbane, Queensland. This sampling was supplemented by fishery-independent samples collected in the same period as part the current study, which included sub-legal fish collected under permit in an attempt to produce an unbiased estimate of age-at-maturity. Based on preliminary results indicating spatial and temporal differences in spawning, the fishery was divided into two spatial regions at the 24.5°S line of latitude in the current study (see Figure 1).

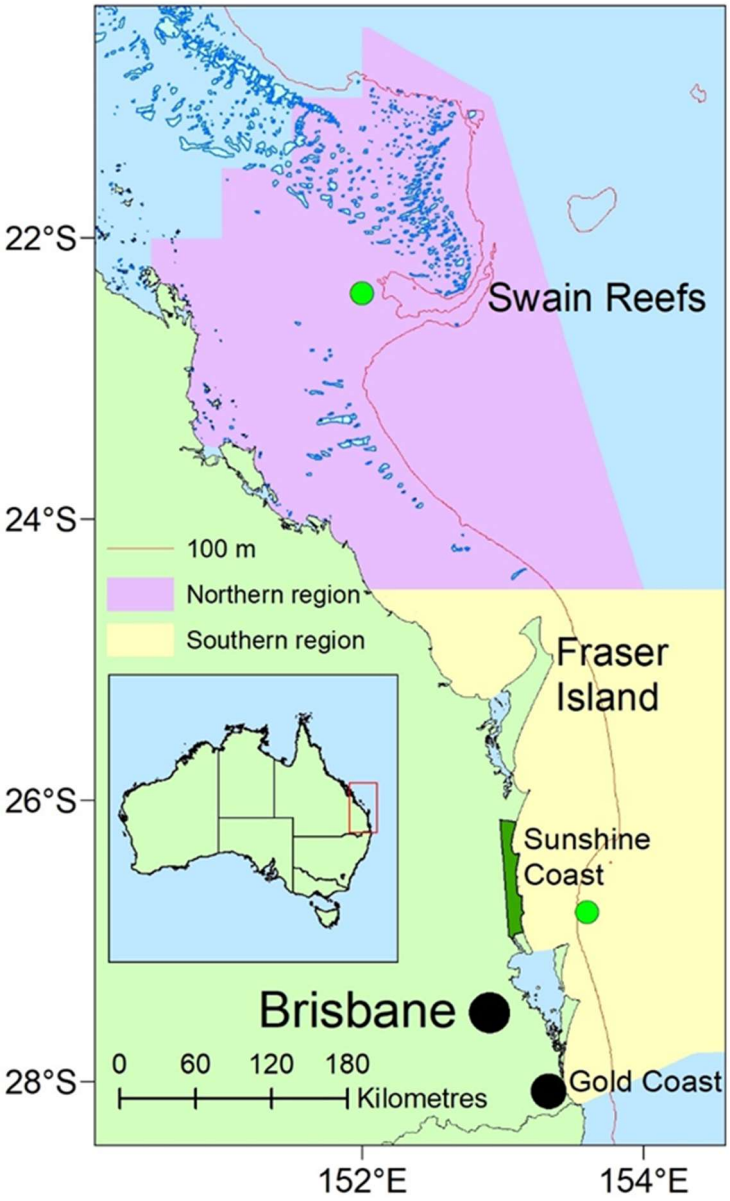


Figure 1: Spatial extent of the northern and southern regions from which Pearl Perch were caught between July 2018 and June 2022. The two green dots represent the locations used to assess the effect of sea surface temperature (SST) on gonad development and are the approximate midpoint of locations from which Pearl Perch were sampled from the northern (22.4°S, 152°E) and southern (26.8°S, 153.6°E) regions.

Laboratory processing

All Pearl Perch were thawed, sexed, and measured (fork length, FL, ± 1 mm). Sagittal otolith pairs were removed from each individual, cleaned, wiped dry and placed into labelled vials. After drying, the left otolith was embedded in polyester resin and sectioned with a Buehler IsoMet Low Speed cutting saw (www.buehler.com\\isoMet-low-speed-cutter.php), at a width of 350 μm, and mounted on a microscope slide. Each otolith section was examined with a Leica M6Z stereo microscope (https://www.leica-microsystems.com/products/stereo-microscopes-macroscopes/p/leica-mz6/) at a magnification of 8x, under reflected light on a matt black background. A digital image of the section was acquired with a Leica IC90 E digital camera (https://www.leica-microsystems.com/products/microscope-cameras/p/leica-ic90-e/).

Ageing

The protocol used to interpret age for Pearl Perch was similar to that used by Stewart *et al.* (2013). The age of each individual was based on the number of opaque zones visible along the dorsal sulcul ridge between the primordium and the otolith edge. Age was determined without prior knowledge of the length, sex or capture date of the individual. Readability of each section was based on a qualitative assessment of the reader's confidence in their interpretation, similar to the assessment described by Officer *et al.* (1996).

Prior to interpreting the otoliths in the current study, familiarisation of the incremental macrostructure of Pearl Perch was undertaken with the use of a reference collection. Subsequently, the reader's competency was tested with species-specific qualification criteria, which prevents long-term drift in interpretation of the otoliths ensuring consistency of age estimation over time by experienced readers. Once competency was achieved all otoliths were read before a sub-sample of 500 was randomly selected and aged again by the same reader to provide a measure of consistency between reads. Bias and precision were tested using: 1) average percent error (APE, Beamish and Fournier 1981), 2) age bias plot with 95% confidence intervals, and 3) Bowker's test of symmetry.

Marginal increment ratio

To determine the periodicity of opaque zone formation, marginal increment ratio (MIR) was calculated following Natanson *et al.* (1995), who defined MIR as $MIR = (OR - OR_n)/(OR_n - OR_{n-1})$, where OR is the otolith radius, OR_n is the radius of the final complete opaque zone and OR_{n-1} is the radius of the penultimate complete opaque zone. Given this method, MIR was calculated only for animals aged ≥2 years. Following Simpfendorfer *et al.* (2000), MIR was compared between months using the Kruskal–Wallis one way analysis of variance on ranks.

Edge type was qualitatively assessed to provide further evidence the periodicity of opaque zone formation (Cailliet *et al.* 2006) and was classified into three levels, namely, 'new', 'intermediate' and 'wide'. A 'new' edge was one where an opaque zone occurred at the distal edge of the sectioned otolith, irrespective of the width of the opaque band. The edge of an otolith section with a continuous band of translucent material visible beyond the last complete opaque zone was categorised as 'intermediate' (i.e., MIR > 0). An edge was classified as 'wide' where the width of the translucent zone beyond the last complete opaque zone was equal to or more than 2/3 of its expected width when fully complete (i.e., MIR ≥ 0.66). A chi-square test was used to compare the observed frequency of each edge type, as a function of month, with the expected frequencies. In this case, the null hypothesis of the test was that the frequency of edge type was not dependent on month of capture.

Growth

Three growth functions were used to estimate mean length-at-age: von Bertalanffy growth function (VBGF), Logistic growth function and Gompertz growth function (Table 1) (Smart *et al.* 2016). In all cases, the length-at-age-zero (L_0) was estimated rather than the age-at-zero-length (t_0). Growth

was estimated in a Bayesian framework using Markov chain Monte Carlo (MCMC) using the 'BayesGrowth' package (Smart 2020, accessed 11 July 2022) in R statistical software (Version 4.0.2, R Foundation for Statistical Computing, Vienna, Austria, see https://www.R-project.org/, accessed 11 July 2022), in accord with methods described by Smart and Grammer (2021). Four MCMC chains with 10,000 simulations, with a burn in period of 5,000 simulations, were used to determine parameter posterior distributions. Model convergence was assessed using the Gelman-Rubin test and diagnostic plots generated using the 'Bayesplot' package (Gabry 2020, accessed 11 July 2022) in R.

Models were fit to length-at-age data for both sexes combined, females only and males only in each region. Each model was fit with a normal residual error structure (σ). The prior distribution of the L_∞ parameter of each growth function was $L_\infty \sim N(700, 35)$ based on a maximum size of 700 mm TL (McKay 1997). The prior distribution of the L_0 parameter was $L_0 \sim N(0, 0.001)$ (Smart and Grammer 2021). A non-informative prior was used for σ and a common non-informative prior was used for the growth coefficients of the three candidate models (k, g_1 and g_2, Table 1). An upper bound was nominated for the uniform distributions of σ and k of 100 and 0.5 year^{-1}, respectively. The common non-informative prior for the growth coefficients allowed for comparison of the three candidate growth functions, each with identical priors. Leave-one-out-information-criterion weights (LOOICw), calculated within the 'BayesGrowth' package using the 'loo' R package (Vehtari *et al.* 2020), were used to determine the most appropriate candidate model. As with the Akaike weights in the frequentist approach, the candidate model with the highest LOOICw was considered the most appropriate.

Differences in growth parameters between sexes and regions were assessed by comparing 10,000 posterior estimates of L_∞, k and L_0. A frequency histogram of a vector, representing the difference between the two vectors of interest (e.g., male L_∞ and female L_∞), was generated and a significant difference was detected if zero was not within the 95% confidence interval of the distribution of this vector (Campbell and Rigby 2022).

Table 1: Equations of the three candidate growth functions used to assess the growth of Pearl Perch (n = 1062). L_t is the length at age t; L_∞ is the asymptotic length; L_0 is the length at t = 0; and k, g_1 and g_2 are coefficients of the respective growth functions to be estimated.

Model	Growth function
Von Bertlanffy	$L_t = L_0 + (L_\infty - L_0)(1 - e^{-kt})$
Gompertz function	$L_t = L_0 \times e^{\left(Ln\left(\frac{L_\infty}{L_0}\right)\left(1-e^{-g_1 t}\right)\right)}$
Logistic function	$L_t = \frac{L_\infty \times L_0\left(e^{(g_2 t)}\right)}{L_\infty \times L_0(e^{(g_2 t-1)})}$

3.2 Reproduction

Specimens of Pearl Perch were collected as part of Fisheries Queensland's routine fishery-dependent monitoring program between July 2018 and June 2022. Fish frames were either donated by commercial fishers and recreational anglers or collected at seafood wholesalers and stored in freezers located at the EcoSciences Precinct in Brisbane, Queensland. These samples were supplemented by fishery-independent sampling conducted as part of the current study, which included sub-legal fish collected under permit to produce an unbiased estimate of age-at-maturity.

Laboratory processing

In the laboratory, after sagittal otolith pairs were removed to determine age, female gonad pairs were staged (Table 2), removed, and weighed (±0.0001 g). Where appropriate, a section of one gonad was also removed and fixed in 10% neutral buffered formalin for estimates of batch fecundity.

Gonadosomatic index

Gonadosomatic index (GSI) was calculated for females identified as Stage 2 or higher, using the equation $GSI = [W_o / W_t] * 100$, where W_o is the total weight of a gonad pair (g) and W_t is the whole weight of the animal (g). For processed fish collected from fishers and wholesalers, W_t was estimated from fork length according to the equation $W_t = 0.04 \times FL^{2.787} + \sigma$, (Sumpton *et al.* 1998, p. 47) where σ is the error from the regression.

Table 2: Macroscopic stages of female Pearl Perch gonads.

Stage	Classification	Description of gonads
0	Unknown sex	Small translucent ribbons, sex indistinguishable.
1	Immature	Gonads thin and firm, pale or translucent pink.
2	Resting	Gonads more rounded, pale pink or red. No oocytes visible. Approximately 1/4–1/3 length of the body cavity.
3	Developing	Gonads enlarged, pale orange or pink, blood vessels noticeable. Oocytes visible, small. Approximately 1/3–2/3 length of the body cavity.
4	Developed	Gonads enlarged, orange or yellow but not speckled. Oocytes large and clearly visible.
5	Spawning	Gonads much enlarged, translucent pale orange. Hydrated clear oocytes visible giving speckled appearance. Blood vessels prominent.
6	Spent	Gonads bloody and flaccid.

Generalised additive models (GAM) were used to examine factors influencing GSI in Pearl Perch. Much of these analyses were guided by previous work utilising GAMs in examining reproductive periodicity (Fisher *et al.* 2018). Models were fit with the 'FSSgam' package (Fisher 2020, https://github.com/beckyfisher/FSSgam, accessed 15 August 2022) in R statistical software (Version 4.2.1, R Foundation for Statistical Computing, Vienna, Austria, see https://www.R-project.org/, accessed 15 August 2022) with GSI modelled as a gamma distribution. The GAM quantifies changes in GSI between years and months, and within months (lunar scale), and allows for the inclusion of a spatial component to test differences in GSI across the Pearl Perch's distribution.

The effect of month (1:12, examining season periodicity) was modelled with cyclic cubic splines and the lunar cycle (0:1, a measure of the moon's brightness, where 0 is new moon and 1 is full moon) was modelled with cubic regression splines, while region (north or south) was included as a categorical factor. All variable interactions were considered to identify potential differences in month and lunar periodicity among and between regions. As this study had a large sample size (n = 897) and two continuous predictors, models with up to a maximum of three predictors were included. The number of knots (k) was restricted in all GAM fits to reduce overfitting by including unnecessary splines, and providing an optimal smoothed relationship (Fisher *et al.* 2018). The most appropriate model was selected according to the Akaike Information criterion (AIC) value and the coefficient of determination (R^2).

Given the association between sea surface temperature (SST) and GSI in *G. hebraicum* (Lenanton *et al.* 2009), the effect of SST on Pearl Perch GSI was assessed. It should be noted that SST was not

included in the analysis above due to the dependence of SST on both month and region, and the need to retain month in the model to inform potential management changes to protect spawning Pearl Perch. Daily SST data, derived from observations from the Advanced Very High Resolution Radiometers (AVHRR) on board National Oceanic and Atmospheric Administration (NOAA) polar-orbiting satellites, were downloaded from the Integrated Marine Observing System (IMOS, https://imos.org.au/data), via the Australia Ocean Data Network (AODN) portal. The SST at two sites only, representing the approximate midpoint of locations from which Pearl Perch were sampled from the northern (22.4°S, 152°E) and southern (26.8°S, 153.6°E) regions (Figure 1) during the current study, were used to assess the effect of SST on GSI. This approach was required as the exact location of each catch was not provided by fishers when donating samples. The effect of mean daily SST on GSI was assessed via a second GAM (hereafter referred to as the "reduced GAM") in R using the 'mgcv' package (Wood 2017), where GSI was the response variable and SST was added as a continuous explanatory variable with a cubic regression spline.

Maturity

The length-at-maturity (L_{50}) and age-at-maturity (t_{50}) of female Pearl Perch were quantified using generalised linear modelling (GLM) in R, via a binomial distribution with a logit link function. Maturity (0 = immature, 1 = mature) was the response variable and FL (mm) or adjusted age (years) was added as a continuous explanatory variable. The ages derived in Section 3.1 were adjusted for growth beyond the last complete opaque zone by the marginal increment ratio (MIR, Campbell *et al.* 2021b). All immature fish were collected during fishery-independent sampling conducted offshore from Brisbane and the Sunshine Coast and, as such, maturity was assessed for fish caught in these areas only to minimise any bias in the estimates of t_{50} and L_{50} resulting from the under-sampling of immature animals in other areas. The age- and length-at-95%-maturity (L_{95} and t_{95}) were also estimated.

Batch fecundity

To obtain estimates of batch fecundity, samples were removed from female gonads categorised as developed or spawning (Table 2). After each gonad pair was weighed, three small masses of eggs were removed from connective tissue, and each placed in separate labelled 80mm x 120mm petri dishes and weighed (±0.0001 g). Each sample was examined with a Leica M6Z stereo microscope at a magnification of 8x, under reflected light on a matt black background. A digital image of the sample was acquired with a Leica IC90 E digital camera. The resultant images were then loaded into ImageJ software (Rasband 2022, accessed 17 June 2022) to enable egg counts. Batch fecundity (F) was calculated as $F = [E_n / W_s] \times W_o$, where E_n is the number of eggs; W_s is the sample weight (g); and W_o is the total weight of both gonads (g). This resulted in three measures of F for each gonad pair, from which a point estimate and a standard error were derived. Mean batch fecundity, as a function of fork length, was estimated via linear regression, after the natural logarithm transformation of each variable, in R.

3.3 Movement

Conventional tagging

To determine the movement of Pearl Perch, tag-recapture data were acquired from Infofish Services. Infofish Services (hereafter referred to as 'Infofish') administers a community-based recreational fish tagging program known as 'Suntag' (Stenekes and Sahlqvist 2011). Infofish consult with a range of stakeholders to promote the return of tags from recaptured fish including the Queensland government, fishing clubs and participants at fishing events. Fishers are supplied with dart tags with which to tag a range of species, including Pearl Perch. Once a fish is tagged, anglers submit a form to Infofish containing relevant information such as location, date, and fish size. Each tag has a unique identifier and a phone number so that a recapture can be reported. Infofish were approached to provide tag-

recapture information for Pearl Perch in Queensland. Once supplied, cases with incomplete data were removed from the dataset.

The Infofish data were supplemented by tag-recapture data generated during the current study. Project staff purchased dart tags from Hallprint (https://hallprint.com/fish-tag-products/2014/8/26/plastic-tipped-dart-tags) and provided these to charter operators and recreational anglers. Further, project staff tagged Pearl Perch during fishery-independent field work conducted off Brisbane, the Sunshine Coast and the Gold Coast in south-east Queensland.

Acoustic tagging

Project staff were informed by DAF's Animal Ethics Committee that performing surgical procedures on animals does not comply with current regulations under the *Veterinary Surgeons Act* 1936.

In order to comply with the act, a DAF veterinarian, Derek Lunau, was engaged to insert acoustic tags. Mr Lunau accompanied project staff aboard the Tom Marshall for a tagging trip undertaken in October 2019 (Figure 2). This trip was undertaken in the area north-east of Fraser Island in 200 m water depth, where a large aggregation of Pearl Perch had been located during previous fieldwork. Under the supervision of project staff member, Richard Pillans, Mr Lunau implanted Vemco V13 acoustic tags in 14 Pearl Perch ranging in size between 34 and 65 cm TL (mean = 48.2 cm). After these fish were tagged-and-released, five Vemco VR2AR receivers were deployed in and around the aggregation.

The array was deployed around an isolated feature in ~200 m of water. Acoustic soundings around this feature indicated that fish were located in a confined area within 100 m of a distinct U-shaped feature that resembled a flooded riverbed close to the continental shelf. One receiver was placed within 100 m of the U-shaped feature (and close to the largest density of fish observed on the depth sounder) with four remaining receivers placed ~500 m north-east, north-west, south-east and south-west of the first receiver.

Figure 2: DAF veterinarian, Derek Lunau, implanting a Vemco V13 acoustic tag into the gut cavity of a Pearl Perch under the supervision of project staff member Dr Richard Pillans.

A second acoustic tagging trip was undertaken in the first half of 2022. Noosa charter operator, Mitch Bertacchini, has a history of targeting Pearl Perch at the northern end of the Sunshine Coast and was engaged by project staff to assist with locating fish for acoustic tagging. Again, Derek Lunau participated in this field work to perform the surgeries as stipulated by the DAF Animal Ethics committee.

Vessel Monitoring System (VMS) data

Fisheries Queensland were approached to supply VMS data with which to infer the location of Pearl Perch aggregations. Mandatory VMS was introduced in the line fishery in January 2019 and all commercial fishing vessels accessing the rocky reef fishery are required to have a VMS unit installed. The VMS polls the location of a line fishing vessel every five minutes, facilitating effort validation and compliance with spatial and temporal closures.

Project staff were aware that some commercial fishers were targeting Pearl Perch in the area north of Fraser Island, towards the Swain Reefs area (Figure 3). However, many of these fishers were unwilling to engage with this project and the FM routine monitoring program. As such, VMS data were used to infer the location of Pearl Perch aggregations by merging these data with mandatory logbook data supplied by fishers. Although logbook information can inform researchers about the general location of Pearl Perch aggregations, fishers are only required to supply location data at a spatial resolution of ~11 km by 11 km. Initially, project staff sought raw VMS data with which to determine the location of Pearl Perch aggregations: however, FQ were unwilling to supply raw data because of privacy concerns regarding the fisher's intellectual property. As such, FQ provided heat maps displaying the location of vessels that landed >100 kg of Pearl Perch in 2019 and 2020, combined, on days when Pearl Perch were caught.

3.4 Genetic stock structure

Sampling

NGS studies require high concentration, high molecular weight DNA from at least 15–20 animals per collection site. Samples were sourced from commercial fishers, recreational anglers, and researchers (Figure 4). Where possible, meta-data including fork length, sex, gonad stage and gonad weight were recorded, and otoliths collected. Small genetic tissue samples (~50 mg) of muscle were dissected from individual fish and preserved in 2mL vials containing, in the first instance, 200 proof molecular grade ethanol (EtOH) and later in DESS (20% DMSO, 0.25M EDTA and saturated salt).

Figure 3: A large commercial catch of Pearl Perch from the Swain Reefs area in central Queensland. The fish were landed in the Port of Bundaberg in October 2019.

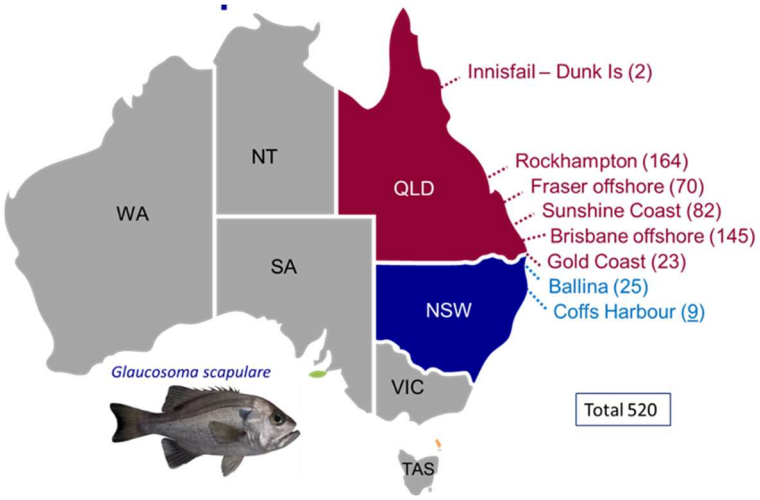


Figure 4: Number and origin of Pearl Perch tissue samples collected for genetic analysis.

DNA extraction

DNA was extracted from Pearl Perch tissue using several extraction protocols and kits including: 1) Salting out protocol (Miller *et al.* 1988), 2) Qiagen DNeasy blood and tissue kit (Qiagen Pty Ltd, Clayton, Victoria), 3) Qiagen MagAttract HMW DNA kit (Qiagen Pty Ltd, Clayton, Victoria), and 4) phenol:chloroform extraction (Sambrook and Russell 2006). The kit manufacturers guidelines or publication instructions were followed in the first instance with troubleshooting modifications generally being to the lysis temperature (lowered to 37°C) and lysis time (test range from 1 hour to overnight). A modified salting out protocol was optimised for Pearl Perch tissue to recover high molecular weight DNA (Box 1).

1. Transfer ~25 mg of finely diced tissue to a 2 ml tube and add 500 µl 1 x TE.
2. Heat inactivate nucleases @80C x 5 min in a heat block then remove liquid.
3. Add 500 µl Solution 2 (final [ ] 50 mM Tris-Cl, 5 mM EDTA, 2 % SDS).
4. Add 20 µl Prot K 20 mg/ml stock.
5. incubate @ 37°C until digested but no longer than 4 hrs.
6. Add 10 µl Rnase A (20 mg/ml) and invert mix.
7. Incubate for 15 min @ R/T.
9. Add 200ul NaCl (5M), invert mix.
10. Leave on ice x 20 min.
11. Centrifuge full speed x 10 min, fixed rotor.
12. Using wide a bore tip transfer super to new tube avoiding protein/tissue pellet – 700 µl.
13. Add 700 µl isopropanol and invert mix 6x.
14. Spin 10 min max speed, fixed rotor.
15. Remove and discard super.
16. Wash pellet with 1 ml 70% EtOH, stand for 10 min
17. Spin 5 min max speed, fixed rotor.
18. Remove and discard super.
19. Repeat 70% EtOH wash step (steps 16-18).
19. Air dry pellet.
20. Resuspend pellet in 100 µl 1xTE pH8.0.
21. Leave tube O/N in fridge for pellet to go into solution.
22. Quantify concentration on nanodrop (2 µl).
23. Run 2 µl on a 0.8% Agarose and TBE gel.
24. Store DNA @ -20C.

Box 1. Optimised salting out protocol for *G. scapulare*

NGS SNP genotyping and analysis

Reduced representation genotyping by sequencing enables an overlapping subset of the genome to be sequenced from a collection of samples (Peterson *et al.* 2012). Reduced representation libraries are size selected from genomic DNA digested with restriction enzymes, and regions adjacent to the cut sites are sequenced using Illumina Next Generation Sequencing (NGS) technology. Following DNA extraction of high molecular weight DNA, library construction and sequencing were to be outsourced to Diversity Arrays Technology Pty. Ltd. (DArT) in Canberra. They return a matrix of genotypes determined and preliminarily filtered through the DArTseq™ primary pipeline and the KDCompute framework (http://www.kddart.org/kdcompute.html).

The resulting SNPs would then have been analysed in the R package dartR (Gruber *et al.* 2018) for data quality control and marker selection using a range of functions that explore patterns in population genomic (SNP) datasets such as observed heterozygosity (Ho) and unbiased expected heterozygosity (He) (Nei 1978), inbreeding coefficient (FIS), and rarefied allelic richness (Ar). To determine genetic population structure within the species, two methods would be employed; discriminant analysis of principal components (DAPC) implemented in adegenet (Jombart *et al.* 2010) and FastStructure (Raj *et al.* 2014).

To construct reduced representation libraries for NGS, DArT requires 1 µg of high molecular weight DNA in a 20 µL volume (50ng/µL concentration).

Mitochondrial DNA sequencing and analysis

Based on the small amount of mitochondrial COI variation detected by Liu *et al.* (2010), a subset of 40 animals spanning the full geographic range were sequenced for this gene to determine if population structure might be detectable. Primers were designed off the published *G. scapulare* sequence (PPCO1F 5' TCAACTAATCACAAAGACATCGGTAC and PPCO1R 5' TATACTTCSGGGTGCCCAAAGAATCA) to amplify a 707-base product.

Amplification reactions were conducted in 10 µl volumes containing 1 µM of each primer pair, 10-50 ng of extracted DNA, 10x PCR buffer (Qiagen, Chadstone Victoria, containing 25 mM magnesium), 1 mM dNTP, and 1 unit of Taq DNA polymerase (Qiagen, Chadstone Victoria). Thermal cycling conditions consisted of an initial denaturation (95°C for 2 minutes) followed by 35 cycles of 95°C for 30 seconds, annealing at 50°C for 30 seconds and extension at 72°C for 1 minute 30 seconds, with a final extension step of 72°C for 7 minutes. Cycling was performed in a Biorad thermal cycler (DNA Engine Peltier, Biorad, Gladesville, NSW, Australia). PCR products were viewed on a 1% agarose TBE gel stained with GelRed (Biotium, USA). Prior to sequencing, PCR products were desalted using Exosap-it® (USB Corporation distributed by Thermo Fisher Scientific, Life Technologies Australia).

Approximately 20 ng of PCR product was used in standard ABI Dye Terminator sequencing reactions using Big Dye Vers 3.1 technology (Applied Biotechnology distributed by Thermo Fisher Scientific, Life Technologies Australia) and were run on an ABI 3130xl Genetic Analyser (Applied Biosystems, California, USA, now Thermo Fisher Scientific). Forward and reverse sequences amplified using the same primers as the initial PCR, were edited, and aligned using Sequencher (Vers 5.4.6 Gene Codes Corporation, Ann Arbor, MI, USA). A haplotype network of the COI sequences was constructed in TCS v1.21 (Clement *et al.* 2000) using a 95% connection limit.

3.5 Larval dispersion

Larval dispersal was simulated using a widely tested biophysical modelling approach based on a Lagrangian transport algorithm (Tracey *et al.* 2012). Ocean current velocities were incorporated into the model using the Bluelink ReANalysis (BRAN) product by the CSIRO (https://research.csiro.au/bluelink/bran2020-data-released/). BRAN2020 provides a 3D record of the

global ocean and incorporates a new two-step multiscale data assimilation process. The data used for this study included ocean observations covering 16 years from 2004–2020. To simulate dispersal events, larvae were released from known or assumed spawning locations (see Figure 5). From each of these locations, 100 larvae were released daily over the assumed peak spawning period from Nov-1 to Jan 31 (North of 24°S) and Mar-1 to May-31 (South of 24°S), which had been inferred from measurements of GSI (see Section 4.2). The combination of spawning sites, release dates and release years resulted in a total of 15.3 million larvae transport trajectories being calculated.

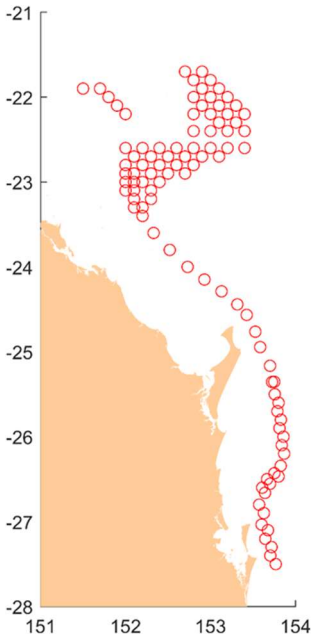
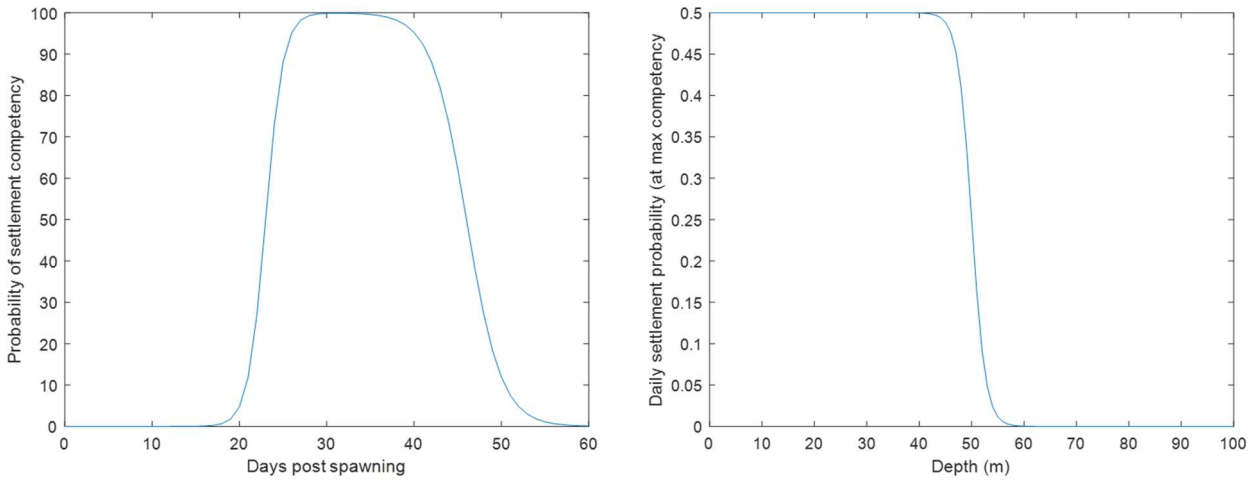


Figure 5: Map of the Queensland coast highlighting spawning locations used for dispersal modelling. The Swain Reefs area was represented by spawning locations North of 23°S.

Larvae were assumed to drift passively with surface currents. Settlement competency was assumed to have a peaked functional form, reaching 50% of the maximum level at 23 days and falling to 50% again by 46 days (see Figure 6a). This settlement profile was based on the assumption of a maximum larval dispersal period of 46 days, based on the larval duration of the congeneric West Australian dhufish (*G. herbraicum*) (Pironet and Neira 1998), and assuming that larvae would reach 50% competency halfway through this period. A daily larval mortality rate of 10% was applied (White *et al.* 2014).



(a) (b)

Figure 6: The probability of a larvae a) settling if present in suitable habitat, and b) settling each day as a function of its depth.

In the absence of robust spatial data on the distribution of reef habitat, settlement was assumed to occur once larvae encountered 50 m deep shelf regions, reaching a maximum settlement probability of 50% per larvae per day from about 40 m depth (see Figure 6b).

To understand the extent to which dispersal simulation outcomes were influenced by these assumptions about settlement competency, habitat depth and larval mortality rates, additional scenarios were run which simply tracked the position of larvae after 30 days of dispersal without further consideration of mortality, settlement competency or the availability of suitable settlement habitat (shallow shelf areas). Key outcomes from dispersal modelling were quantitative estimates of the probability of larval exchange among all release locations and final settlement destinations across the eastern Australian coastline. For clarity, these estimates of potential larval exchange probabilities were provided based on prior clustering of both spawning locations and settlement destinations into latitudinal bands that varied in spatial resolution from 1° to 0.1°.

4. Results

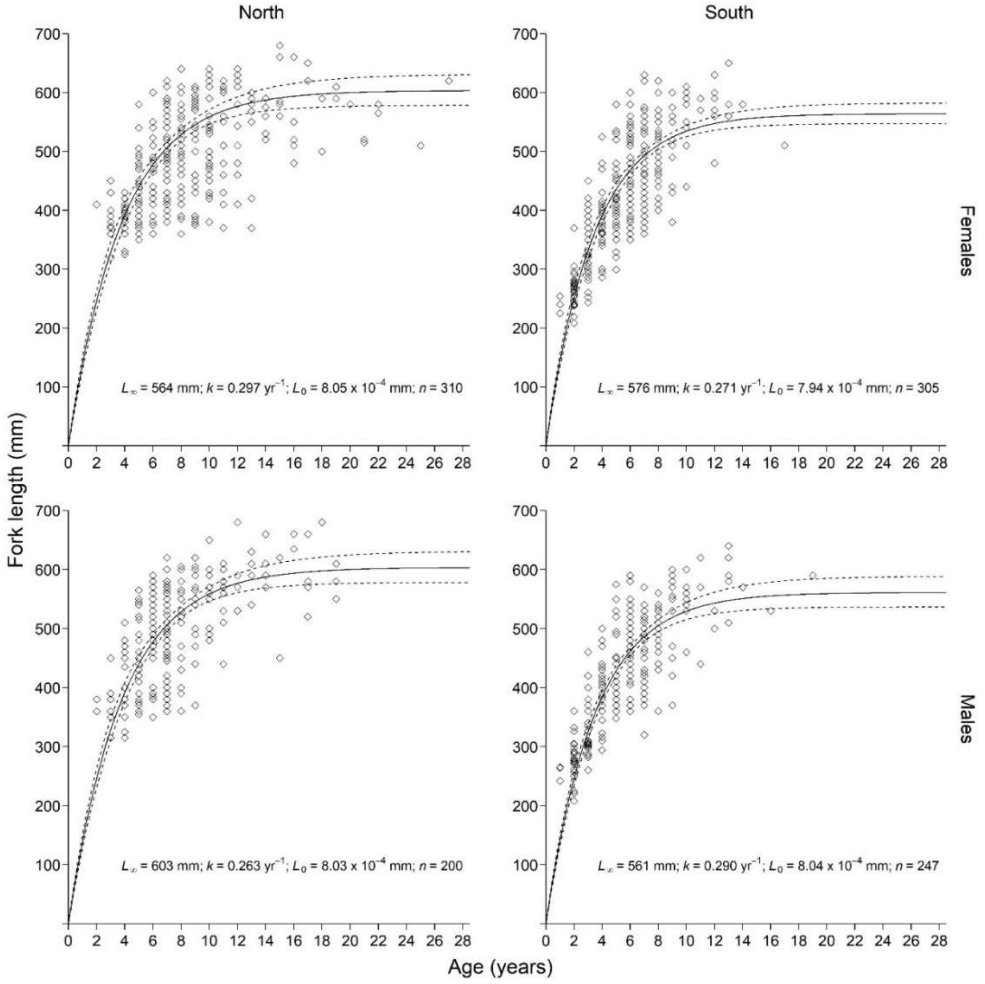


Figure 7: Mean length-at-age of Pearl Perch (*Glaucosoma scapulare*), derived using the von Bertalanffy growth function in a Bayesian framework, as a function of region and sex. The diamonds represent the observed lengths-at-age. Priors were set at $L_\infty \sim N(700, 35)$ and $L_0 \sim N(0, 0.001)$ for both sexes. A non-informative prior was used for the growth coefficient (k, Table 1) with a maximum value of 0.5 year^{-1}.

4.1 Growth

During the 2020 and 2021 calendar years, Fisheries Queensland collected 754 Pearl Perch with which to estimate growth and a further 399 individuals were collected as part of the current study, resulting

in a total of 1153 length-at-age observations. The mean length of the 551 fish collected from the northern region (Figure 1) was 491 mm FL (S.D. = 84.3 mm; range: 315–680 mm). Mean length of the 602 fish collected from the southern region was 423 mm FL (S.D. = 100.6 mm; range: 208–650 mm)(Figure 33). Two-sample *t*-tests indicated that this difference was statistically significant at the 99% level of confidence (t = 12.401, d.f. = 1142.1, $P < 0.001$). The mean age of the fish collected from the northern region was 8.13 years (S.D. = 3.77; range = 2–27 years) and 5.75 years (S.D. = 2.70; range = 1–19 years) in the south (Figure 34). Again, two-sample *t*-tests indicated that this difference was statistically significant at the 99% level of confidence (t = 12.217, d.f. = 988.7, $P <$ 0.001).

Generally, ageing between reads was consistent (n = 497, APE = 1.95), with the age bias plot showing little variation from the 1:1 line of equivalence (Figure 35). Further, Bowker's test of symmetry showed no between-reads bias (χ^2 = 41.82, d.f. = 29, P = 0.058) at the 95% level of confidence. The oldest individual collected was a 27 year old female with a length of 620 mm FL and the oldest male was 19 years old and 590 mm FL.

Marginal increment ratio was highest during the austral winter in both regions (Figure 36) and the Kruskal–Wallis test on ranks indicated that MIR varied significantly between months in each region (North: χ^2 = 29.30, d.f. = 10, $P < 0.001$; South: χ^2 = 134.03, d.f. = 11, $P < 0.001$). Mean MIR increased from January in each region, peaked in the winter, before decreasing through the spring. The lowest mean MIR occurred in January and November in the northern and southern regions, respectively. New edges were most likely to occur in summer in both regions (Figure 37) and the frequency of edge type differed significantly as a function of month in both regions (North: χ^2 = 18.57, d.f. = 10, P = 0.046; South: χ^2 = 132.04, d.f. = 11, $P < 0.001$).

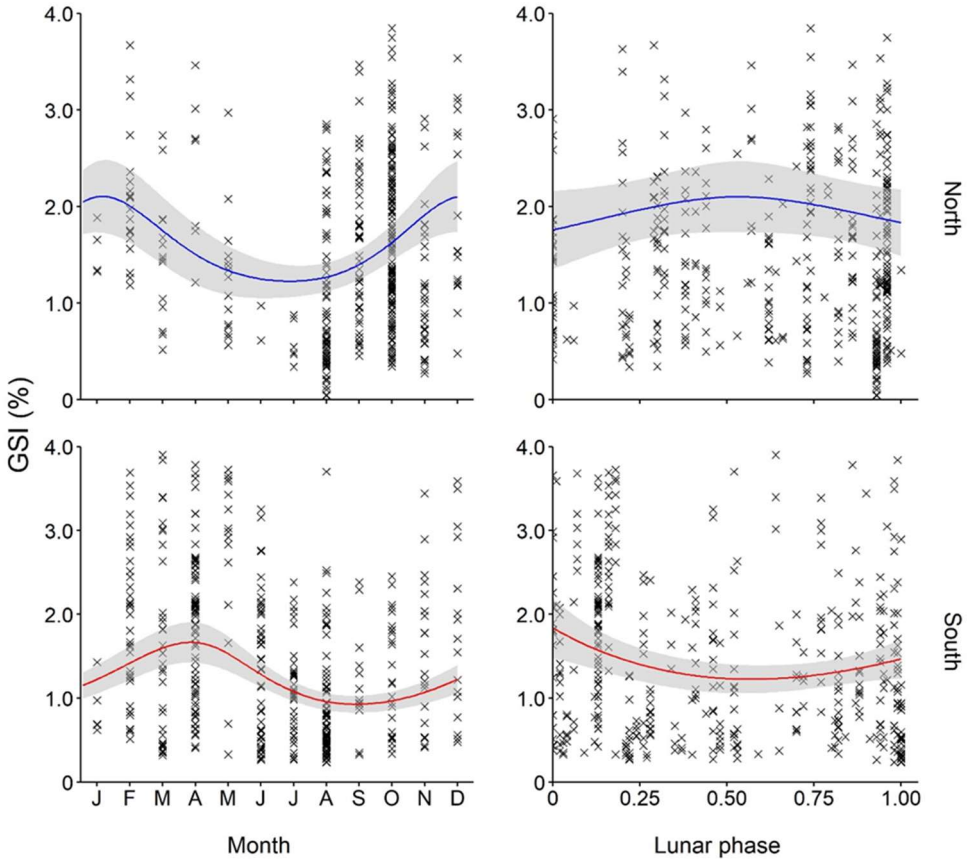


Figure 8: Mean monthly gonadosomatic index (GSI, %) for female Pearl Perch as a function of region, month and lunar phase quantified using generalised additive modelling (GAM). The solid lines represent mean GSI from the GAM from the best model identified in the analyses. The grey ribbons are 95% confidence intervals. Observed values are shown as crosses. Note: GSI was examined for mature females (> Stage 2, Table 2) only.

The VBGF was found to best fit all length-at-age datasets (Table 5, LOOICw = 1). There was no support for either the Logistic (LOOICw = 0) or the Gompertz (LOOICw = 0) growth functions. Significant differences in the L_∞ parameter were detected between males and females in the north region and between males from the north and south regions (Figure 38). As such, growth will be described as a function of both region and sex. The results are based on 1,062 length-at-age observations as sex was indeterminable for 91 animals either as a result of immature gonads or the absence of gonads from processed samples.

Males collected from the northern region grew larger than females (Figure 7, Figure 38, Table 6). Further, the males collected in the northern region grew larger than those in the southern region. No significant differences in the growth coefficient (k) or length-at-age-zero (L_0) were detected (Figure 38, Table 6). The estimated VBGF parameters for females and males collected from the northern region were L_∞ = 564 mm FL, L_0 = 8.05 x 10^{-4} mm FL and k = 0.297 $year^{-1}$, and L_∞ = 603 mm FL, L_0 = 8.03 x 10^{-4} mm FL and k = 0.263 $year^{-1}$, respectively. The estimated VBGF parameters for females and males collected from the southern region were L_∞ = 576 mm FL, L_0 = 7.94 x 10^{-4} mm FL and k = 0.271 $year^{-1}$, and L_∞ = 561 mm FL, L_0 = 8.04 x 10^{-4} mm FL and k = 0.290 $year^{-1}$, respectively.

4.2 Reproduction

Gonadosomatic index

During this study 897 female *G. scapulare* were assessed for GSI. The 442 individuals caught in the southern region had a mean FL of 480 mm (S.E. = 3.97, range = 265–670 mm), while the 455 individuals caught in the northern region had a mean fork length of 486 mm (S.E. = 3.60, range = 319–680 mm). Two-sample t-tests indicated that this difference was not significant at the 95% level of confidence (t = 0.99, d.f. = 883.84, P = 0.32, Figure 39). The GAM indicated that month, lunar phase and region affected GSI (Figure 8). The interaction between month and region was also found to have significantly affected GSI for both the northern (F = 10.04, e.d.f. = 1.76, P < 0.001) and southern (F = 32.26, e.d.f. = 1.94, P < 0.001) regions.

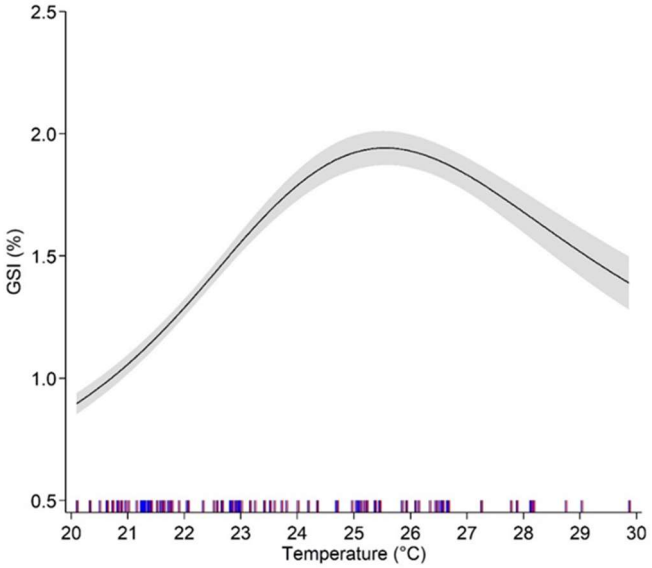


Figure 9: Mean gonadosomatic index (GSI, %) as a function of sea surface temperature quantified using a generalised additive model where GSI was the gamma-distributed response variable and daily sea surface temperature (SST) was added as a continuous explanatory variable with a cubic regression spline. The blue and red ticks along the x-axis represent the SST of GSI observations from the northern and southern regions, respectively, and the grey band represents the 95% confidence interval. Note: GSI was examined for mature females (> Stage 2, Table 1) only.

Gonosomatic Index was highest on the new moon in the southern region, while lunar phase had no effect on GSI in the northern region (Figure 8). Mean GSI was found to increase in spring in the northern region, reaching a peak in December and January. In contrast, mean GSI increased through summer in the southern region, with a peak in April.

Sea surface temperature was highest in the northern region (Figure 40). The mean daily SST at the northern point (Figure 1) over the study period was 25.0°C (S.D. = 2.36°C), compared to 23.6°C (S.D. = 2.22°C) at the southern point. Two-sample *t*-tests indicated that this difference was significant at the 95% level of confidence (t = 16.81, d.f. = 2927, $P < 0.001$). Throughout the sampling period, SST was lowest during August or September in both regions, and highest in February, March, or April. The reduced GAM indicated that SST significantly affected GSI (F = 52.04, e.d.f. = 1.97, $P <$ 0.001), with mean GSI >2% when SST was 25.26–26.32°C (Figure 9).

Peaks in mean GSI in each region coincided with a higher proportion of spawning and spent gonads (Stage 5 and 6) (Figure 41). Spawning fish were found in April, May, June, and December in the southern region, and in September, October, and November in the northern region. Developing gonads were observed in each month in the southern region, and in all months in the northern region apart from April, although sample size was low (n = 7, Figure 41).

Maturity

A total of 281 animals were used to assess length- and age-at-maturity, 200 of which were mature and 81 were immature. The logistic regressions indicated the length- and age-at-maturity of female *G. scapulare* was L_{50} = 353 mm FL (CI $_{\alpha=0.05}$ = 339–366 mm FL) (Figure 10a) and t_{50} = 4.42 years (CI $_{\alpha=0.05}$ = 4.04–4.77 years), respectively (Figure 10b). Further, the length and age at which 95% of females were mature was found to be L_{95} = 427 mm (CI$_{\alpha=0.05}$ = 408–457 mm FL) and t_{95} = 6.79 years (CI $_{\alpha=0.05}$ = 6.25–7.62 years), respectively.

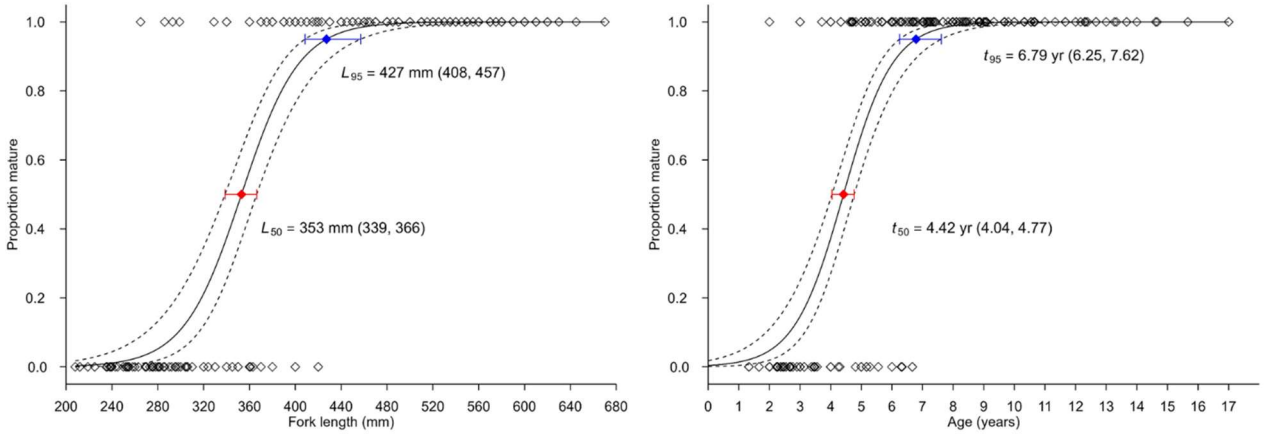


Figure 10: Maturity as a function of a) length (L_{50}, mm), and b) age (t_{50}, in years) for female Pearl Perch caught between July 2018 and June 2022 in Queensland. Dashed lines represent 95% confidence intervals. Hollow diamonds represent the observed data, where 0 = immature and 1 = mature. The red point represents the length and age at which 50% of females are mature and the blue diamond represents the length and age at which 95% of females are mature. Horizontal error bars represent the 95% confidence interval of the respective point estimates.

Batch fecundity

Fecundity was estimated from 41 females with a mean fork length of 506 mm (S.E. = 16.23, range = 283–640 mm). Fecundity estimates ranged from ~99,694 eggs for a 293 mm FL female to ~3,057,836 eggs for a 540 mm FL female, with a mean of 893,020 (S.E. = 98,360) eggs per female. Batch

fecundity was positively correlated ($t = 6.574$, d.f. = 39, $P < 0.001$) to fork length (Figure 11) and this relationship was estimated to be ln (F) = 2.4462 × ln (FL) – 1.7374 ($R^2 = 0.53$).

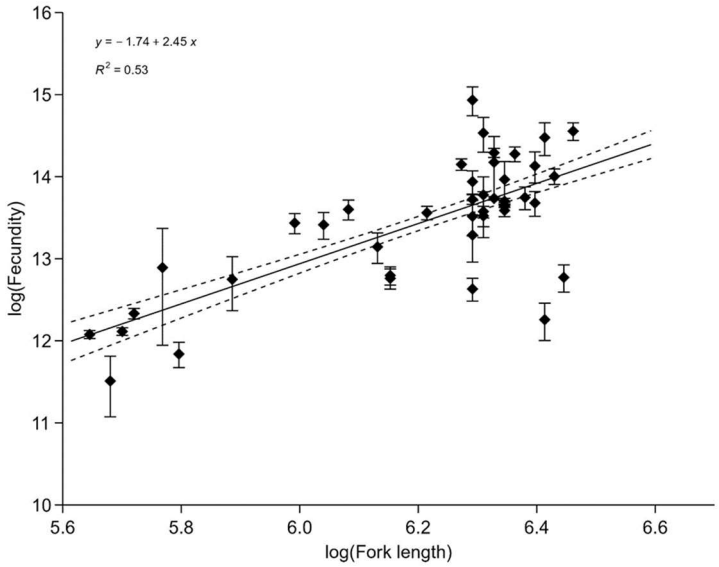


Figure 11: Batch fecundity as a function of fork length (in mm) for 41 Pearl Perch. The dashed lines represent 95% confidence intervals, and the error bars are the standard error around the mean of three measures of batch fecundity from each gonad pair.

4.3 Movement

Conventional tagging

Figure 12: Recreational fisher with a tagged Pearl Perch ready for release. This fish was tagged as part of the Suntag program administered by Infofish Services. Photo by Lachlan Baker used with permission.

A total of 3,110 Pearl Perch have been tagged as part of Suntag, and its predecessors, between September 1993 and January 2020. The mean fork length of these fish was 277 mm (S.D. = 38mm, range =170–390 mm) (Figure 42). A further 436 Pearl Perch were tagged as part of the current study, with a mean fork length of 315 mm (S.D. = 57 mm, range = 160–650 mm), resulting in a total of

3,546 tagged-and-released Pearl Perch. The fish caught as part of the current study were significantly larger than those caught as part of the Suntag program (t = -13.647, d.f. = 480.99, P < 0.001). Of the 3,546 tagged-and-released Pearl Perch, a total of 75 (2.1%) have been recaptured. Mean distance travelled between release and recapture was 2.2 km (S.D. = 4.5 km), with a range of 0–20 km (Figure 43a). Mean time-at-liberty was 108 days (S.D. = 223 days) and ranged between four and 1,550 days (Figure 43b). All but five individuals were at liberty for less than one year. Only ~11% of tagged Pearl Perch moved >10 km from the tagging location and ~79% were recaptured within two kilometres of the release site (Figure 13). Too few fish have been recaptured to facilitate robust analyses and, as such, only summary statistics are provided here.

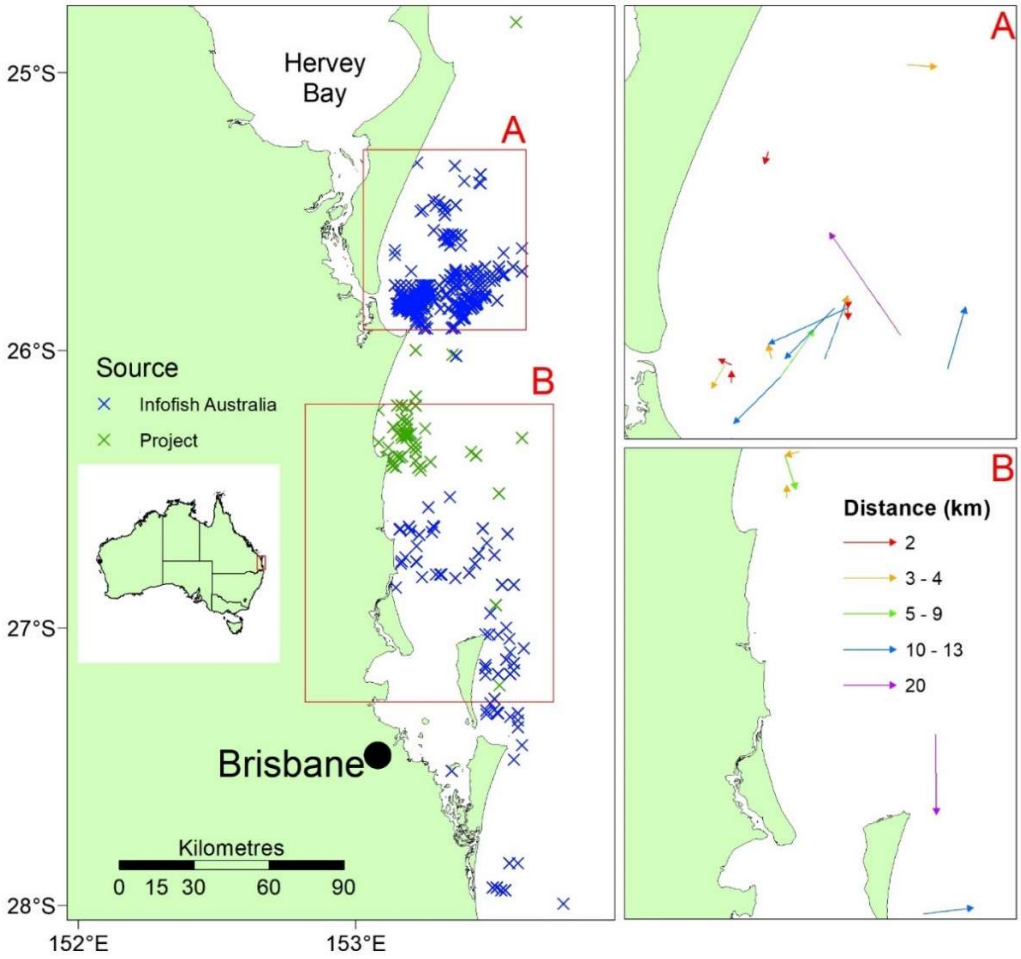


Figure 13: Release location of Pearl Perch, tagged between Hervey Bay and the Southport Seaway. Also shown are tag-recapture vectors for the 21 Pearl Perch where distance travelled was ≥2 km. The start of each line represents the release location, and the arrowhead point represents the recapture location of each individual.

Acoustic Tagging

On 22 May 2020, one of the five acoustic receivers deployed in October 2019 was caught by a prawn trawl vessel. Although the locations of the five receivers was outside previous trawling activity, as determined from trawl VMS data, the receiver closest to the trawling activity was removed by a trawl vessel. Fortunately, the trawl fisher contacted project staff to return the receiver which provided some interesting preliminary information regarding the movement around the aggregation.

The recovered VR2AR receiver (Serial no. 546827) recorded 2,495 detections from seven of the 14 Pearl Perch tagged (Figure 14). A 35 cm Pearl Perch, with tag number 59456, was detected on 1,764 occasions and remained in the area for the period the receiver was deployed.

A large (60 cm FL) Pearl Perch tagged, with tag number 59406, was detected on 638 occasions. This animal was detected by the receiver for two days after being released, before moving out of range (>~500 m) and returning a month later. The fish stayed in this area for a further 11 days before moving out of range for the remainder of the receiver's deployment.

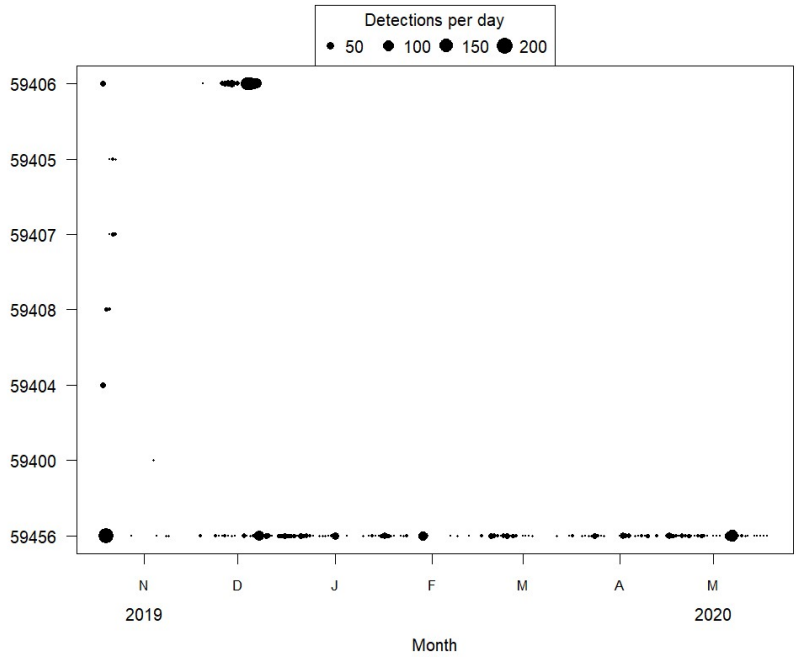


Figure 14: Detections of individual Pearl Perch from the receiver caught by a prawn trawler on 22 May 2020. Each number on the y-axis represents an individual tag number and are ordered from smallest (35 cm FL, 59456) to largest (60 cm FL, 59406).

The remaining four receivers were retrieved on 12 November 2020. The data from the receivers were downloaded with results shown in Table 3, Figure 15 and Figure 45.

Table 3: Size (FL, cm) of the 14 Pearl Perch tagged with acoustic tags in October 2019. Also shown are the number of receivers where each fish was detected and the number of detections.

Fork length	Tag_ID	Sites	Detections
47.0	59399	4	125
42.5	59400	3	17
42.5	59401	4	33
34.0	59402	1	9
59.5	59403		
43.0	59404	5	149
53.5	59405	5	53
60.0	59406	3	146746
48.0	59407	4	52
45.5	59408	5	53
43.0	59454		
65.0	59455		
35.0	59456	5	69098
56.0	59458	2	280799

Only four individuals remained within the receiver array for any significant period (Figure 45). Tag No. 59456 remained within the array for >12 months, indicating this individual remained with the

large aggregation located by project staff (Figure 15, Figure 44). Similarly, Tag No. 59406 stayed with the aggregation for 231 days before moving away (or being caught/dying). In contrast, three fish were not detected (Tag No. 59403, 59454 and 59455) after release and may have either departed the array immediately after release (prior to the receivers being deployed) or died as a result of capture, handling and release. The continual presence of the fish with tag number 59458 (Figure 15) indicates the fish died at the site of the aggregation in May 2020, and the tag continued to transmit until the receivers were recovered. All tagged fish were in good condition and swam off strongly following surgery and recovery, however predation and tagging-related mortality after release are possible.

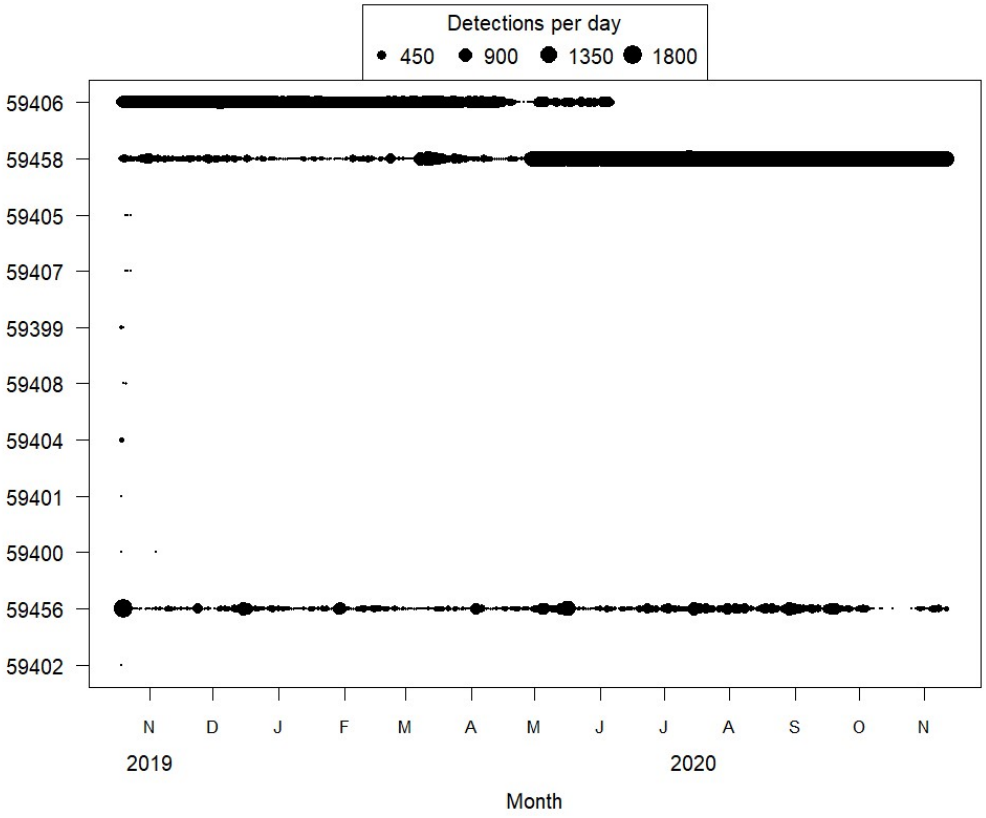


Figure 15: Detections of individual Pearl Perch from the four receivers not caught by a prawn trawler on 22 May 2020. Each number on the y-axis represents an individual tag number and are ordered from smallest (35 cm FL, 59456) to largest (60 cm FL, 59406).

A combination of significant weather events and staff availability hampered progression of the acoustic tagging component of the project. A second tagging trip was conducted off the Sunshine Coast in April 2022, and a receiver was deployed close to a shipwreck in 50 m water depth. Pearl Perch were caught at two locations during this trip: one where the receiver was deployed and another ~29 km to the west of the shipwreck. During this trip, 15 Pearl Perch were tagged with Vemco V13 acoustic tags. These fish had a mean size of 350 mm FL (S.D. = 21.4 mm, range = 31–38 cm).

The receiver was recovered on 29 November 2022. The five fish caught to the west of the shipwreck (tag numbers 59424, 59425, 59426, 59427, 59428) were not detected on the receiver. Of the ten fish released at the shipwreck, seven were detected by the receiver for more than two days (Figure 16). Generally, the number of detections was inversely correlated to fish size: those individuals close to the MLS of 38 cm TL on release were detected for a shorter period before leaving the range of the receiver. Two fish (tag numbers 59436 and 59438) caught at the shipwreck were detected for less than two days and one fish (tag number 59430) was not detected by the receiver.

Fisheries Queensland has committed to provide funding for acoustic tagging infrastructure in Queensland and is being used by the Integrated Marine Observing System (IMOS) to deploy receivers at various locations across the state. As part of this work, receivers have been deployed in areas where

Pearl Perch occur and, as such, any acoustic tags deployed during the current project may be detected throughout this network. The information from these receivers, if any, will be discussed in the final version of this report.

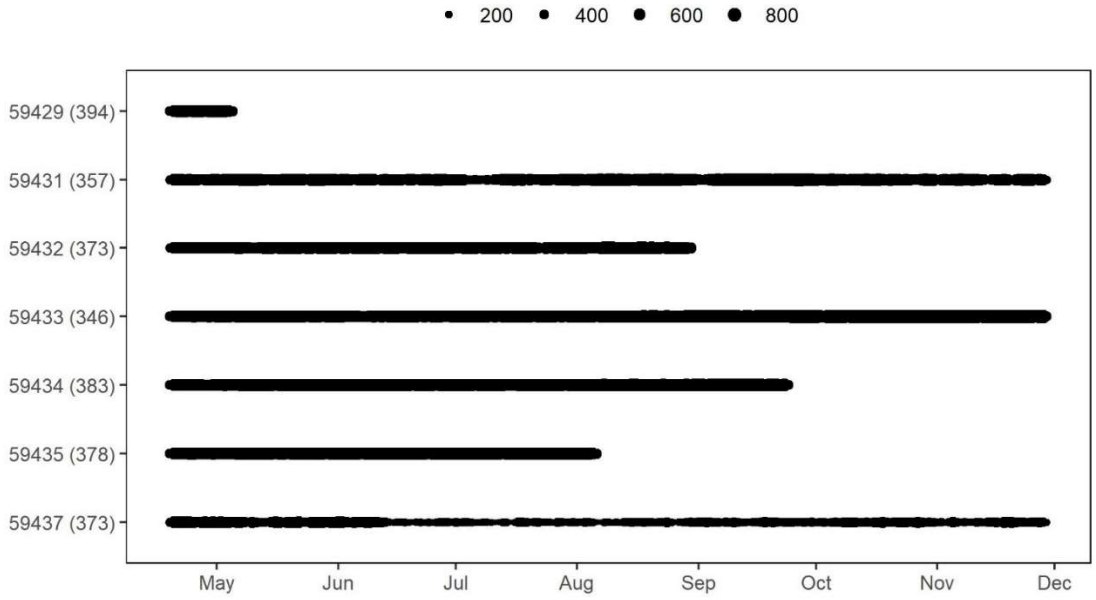


Figure 16: Number of daily detections of individual Pearl Perch from the receiver deployed off the Sunshine Coast in 2022. Each number on the y-axis represents an individual tag number and the number in parentheses is the total length of each animal in millimetres.

Vessel Monitoring System (VMS) data

In 2019 and 2020, logbook data indicated that a total of 18 and 16 vessels landed >100 kg of Pearl Perch in the northern and southern regions, respectively. These fishers targeted the area around the Swain Reefs complex, the area to the north-east of Fraser Island, and off the Sunshine Coast (Figure 17). The intense fishing effort of the Sunshine Coast corresponds to an area in which a single fisher operates, with whom project staff engaged at the start of the project. This fisher targeted large aggregations of Pearl Perch in deep water (~200 m), from which spawning fish were sampled by project and FM staff.

As expected, fishers concentrated fishing effort around the Swain Reefs complex at the southern end of the Great Barrier Reef. In 2019 and 2020, logbook data indicate a total of 12.1 t of Pearl Perch was landed by 29 fishers operating in this area. Some fishers also targeted Pearl Perch to the north-east of Fraser Island, where project staff located large aggregations of Pearl Perch during field work conducted in 2019. In this area, fishers harvested a total of ~4.3 t of Pearl Perch in 2019 and 2020, combined.

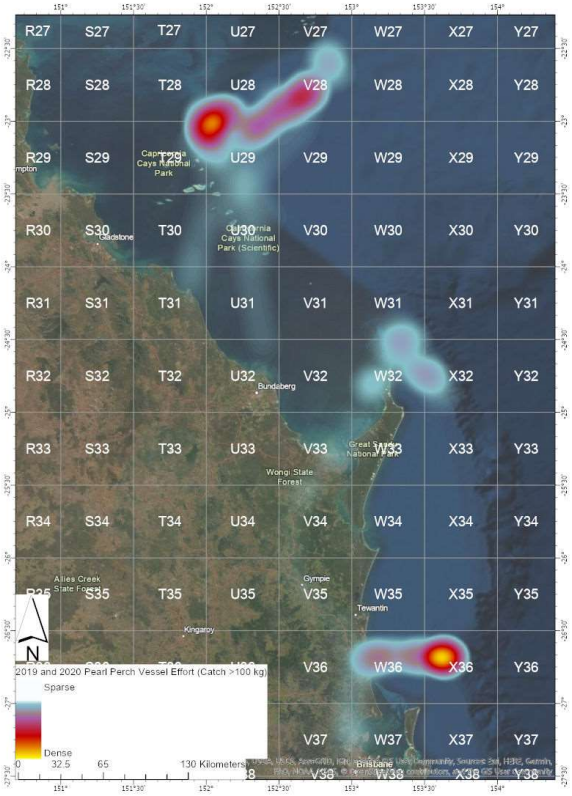


Figure 17: Heat map displaying the location of vessels that landed >100 kg of Pearl Perch in 2019 and 2020, combined.

4.4 Genetic stock structure

Tissue preservation

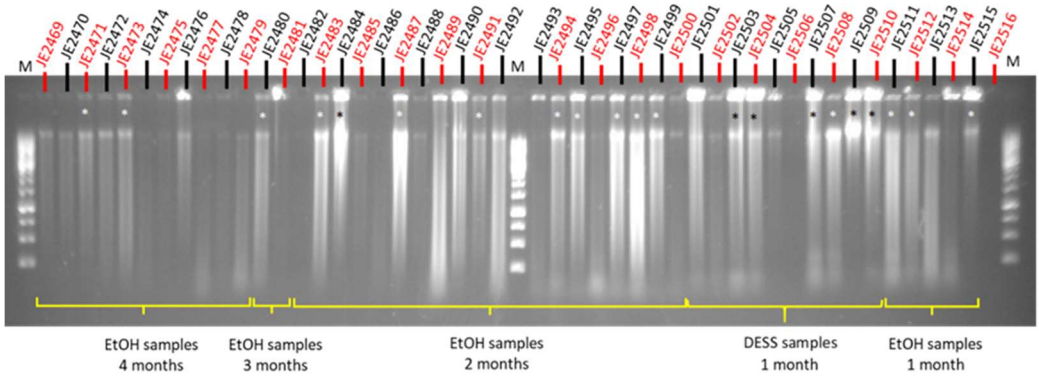


Figure 18: Time post preservation in ethanol was shown to affect DNA recovery from Pearl Perch tissue. Sufficient concentrations of DNA (marked with *) were recovered from only 14% of the older samples (4 months preserved in EtOH prior to extraction) compared to 60% of the 1 month preserved in DESS or EtOH samples. The outside marker lanes (M) are Generuler 1KB DNA ladder.

Tissue samples (~50 mg of muscle) were initially preserved in 200-proof molecular grade ethanol (EtOH) which were then stored at -20°C. This preservation method has been shown to facilitate the recovery of ultra-high molecular weight DNA for next-generation sequencing (Rodriguez-Ezpeleta *et al.* 2013; Dahn *et al.* 2022). In mid-2021, a problem was identified with the ethanol preservation and storage of Pearl Perch tissue. DNA recovery from ethanol preserved samples decreased rapidly within a few weeks of preservation, suggesting the presence of DNA nucleases (enzymes that cut DNA) that were not being inactivated by the ethanol (Figure 18). Following a literature search of alternative preservatives for fish DNA, DESS (DMSO, EDTA and saturated salt) was identified as

potentially a better storage medium (Oosting *et al.* 2020). In contrast to ethanol, which dehydrates cells and inhibits cellular processes that may breakdown DNA, the EDTA in DESS binds to metal ions deactivating metal-dependant enzymes. The salt in DESS stabilises the DNA and DMSO aids in the transfer of compounds across cell membranes (Oosting *et al.* 2020).

Results of the preservative test on Pearl Perch tissue extracted 24 days post capture and preservation in DESS or ethanol is shown in (Figure 19). DNA recovered from four out of five of the fish extracted, showed brighter high molecular weight bands from the DESS preserved tissue compared to tissue from the same fish stored in ethanol. In August 2021, the tissue preservative for storing the Pearl Perch samples was changed to DESS followed by storage at -20°C. At this time, the collection of new tissue samples for the genetics project was deemed necessary as not enough DNA could be recovered from the existing ethanol-stored specimens.

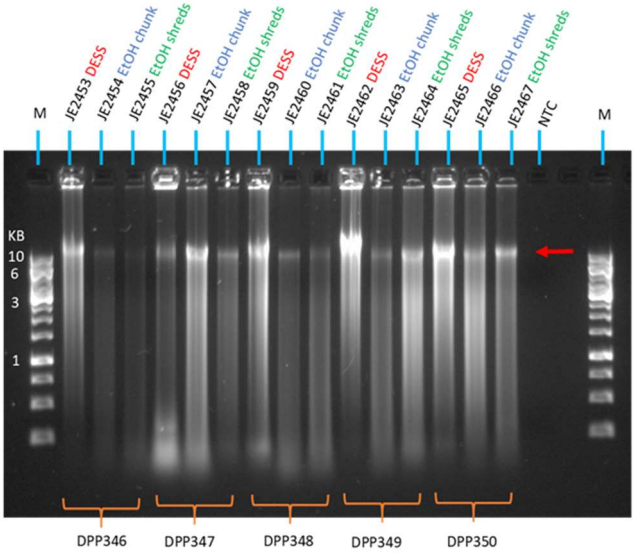


Figure 19: Salting out DNA extraction 24 days post capture of five Pearl Perch (with unique DPP numbers) comparing tissue preserved with either DESS or ethanol (as chunks of tissue or as smaller shredded pieces). The red arrow marks the desired band of high molecular weight DNA, smearing below this band is degraded DNA. The outside marker lanes (M) are Generuler 1KB DNA ladder.

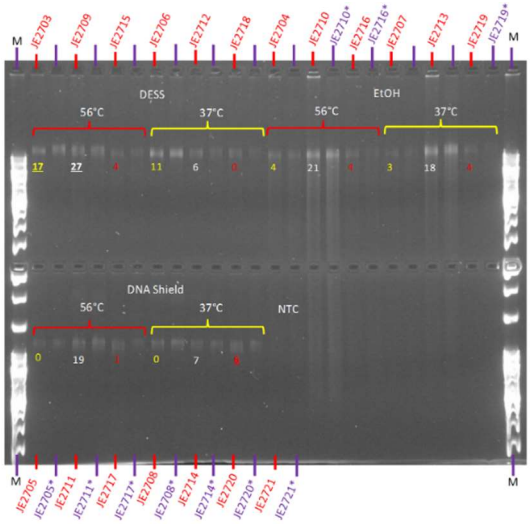


Figure 20: Qiagen MagAttract DNA extraction 35 days post capture of three G. scapulare fish comparing tissue preserved with either DESS, ethanol or DNA shield at two lysis temperatures (56°C or 37°C). Sample numbers marked with * represent a subsample of the DNA heated to 80°C for five minutes post extraction (test for post extraction nucleases). Numbers under DNA bands are DNA

concentrations in ng/µl. The extraction concentration that returned the highest DNA recovery for each of the three fish is underlined. The outside marker lanes (M) are Generuler 1KB DNA ladder.

Ongoing tissue degradation, even in DESS, was discovered in early 2022. Fresh fish were again collected, and a trial was conducted comparing DNA shield, a commercial tissue preservative, to DESS and ethanol. Better quality DNA was recovered from the tissue preserved in DNA shield and DESS compared to the ethanol preserved tissue. DNA recovery was slightly better for two of the three samples preserved in DESS than in DNA shield, although differences between the two preservatives were minimal (Figure 20).

DNA extraction

Initial troubleshooting of the Pearl Perch DNA extraction protocol identified that cell lysis temperature and cell lysis time were extremely important factors influencing how much high molecular weight DNA was recovered. Significantly more DNA was recovered from Pearl Perch tissue using a salting out protocol with a low temperature lysis, 37°C, and a short lysis time, less than 3 hours (Figure 21). This result is contrary to typical DNA extraction troubleshooting guidelines that recommend a 56°C lysis temperature to optimise cell rupture and protein digestion, and an extended lysis time to maximise DNA recovery.

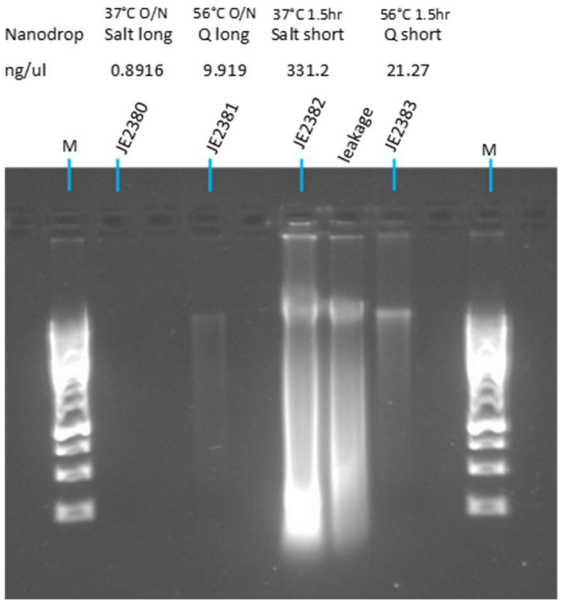


Figure 21: DNA extraction results testing extraction method (salting out protocol with 37°C lysis temperature versus a commercial Qiagen Dneasy blood and tissue kit with recommended 56°C lysis temperature) and digestion time (short, 1.5 hours versus long, overnight). The outside marker lanes (M) are Generuler 1KB DNA ladder.

Following advice from colleagues in New Zealand (authors of the Oosting *et al*., 2020 paper on problematic Snapper DNA) the extraction protocol was further optimised to remove salt, and an enzyme heat inactivation step of the Pearl Perch tissue prior to extraction was added. The optimised salting out protocol is detailed in Box 1 in the methods section. The protocol recovered good quality, high molecular weight DNA which appeared to be in high enough concentrations to progress to next-generation sequencing (Figure 22).

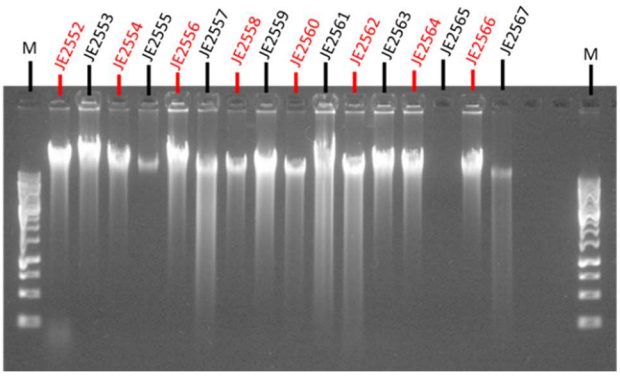


Figure 22: Example of DNA recovered from DESS preserved *G. scapulare* samples using the optimised salting out DNA extraction protocol (Box 1). The outside marker lanes (M) are Generuler 1KB DNA ladder.

Although preserving Pearl Perch tissue in DESS was shown to be an improvement over ethanol, DNA degradation in DESS was still apparent. For this reason, in late 2021, fresh samples were sourced, and their DNA extracted as soon as possible after preservation.

Extracted DNA integrity

To assess how effectively tissue stored in DESS was being preserved, DNA was extracted from two fish after they had been preserved for two weeks and again at six weeks after preservation. The results indicated that high molecular DNA could still be recovered from the DESS stored tissue six weeks after preservation, however, when the original 2-week extracted DNA was run alongside the 6-week extracted DNA, there was a 10-fold loss in DNA concentration from the original extraction (Figure 23). This indicates that the extracted DNA was continuing to degrade rapidly following the extraction, even when stored at -20°C.

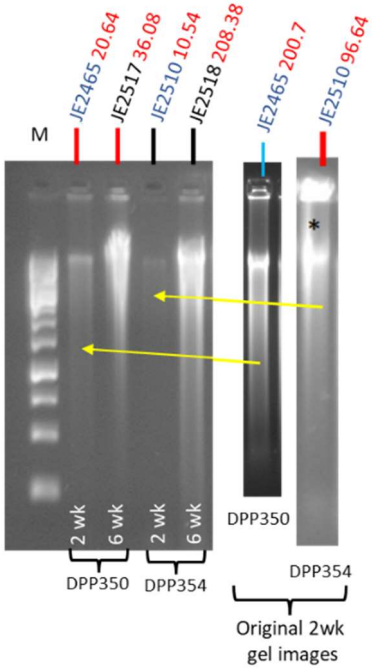


Figure 23: Results of a DNA extraction from two fish extracted twice, once at two weeks post preservation in DESS and once at six weeks post preservation. Gel images of the original two-week extractions are shown alongside to highlight that 90% of the DNA from the original extractions has been lost over the 4-week interval. The marker lane (M) is Generuler 1KB DNA ladder.

A spectrophotometer concentration reading of a further eight extractions that were sufficient for sequencing showed a 40 to 98% loss of DNA with only two of the eight samples retaining sufficient high molecular weight DNA to progress. All DNA samples were immediately transferred to a -80°C freezer in the hope of slowing down the rate of degradation.

It appears that the DNA nuclease is somehow being carried through the extraction. This may be due to the lowered extraction lysis temperature. Nucleases are typically disabled by heat-inactivation and proteinase K digestion during lysis in the DNA extraction.

A sample of extracted DNA was heated to 80°C for five minutes to determine if the nuclease could be inactivated following extraction (Figure 24). The answer was no. Although some degradation was expected, heating the DNA led to the complete loss of the high molecular weight band needed for next generation sequencing.

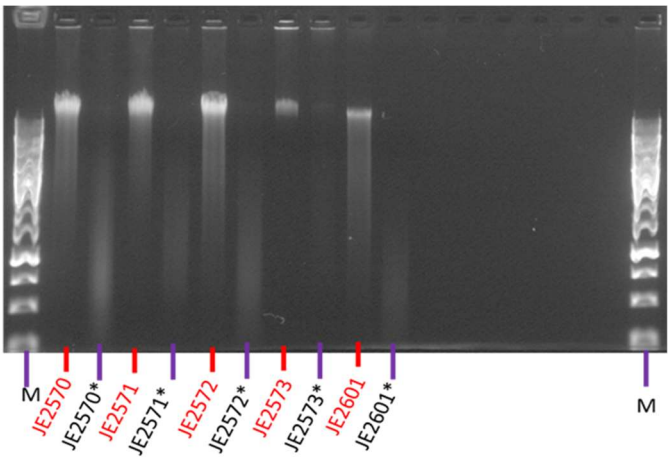


Figure 24: Nuclease heat inactivation at 80°C for five minutes (lanes marked with *) test on extracted high molecular weight *G. scapulare* DNA. The outside marker lanes (M) are Generuler 1KB DNA ladder.

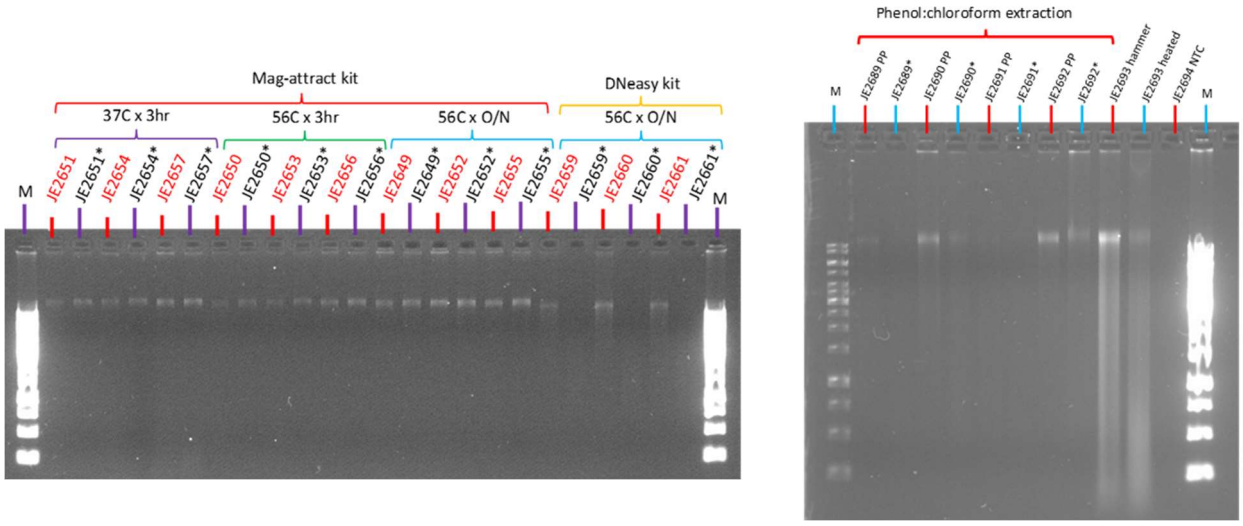
Examining the literature and communicating with other molecular experts identified some troubleshooting alternatives to try. Two new extraction protocols were tested, a Qiagen MagAttract kit which uses silica beads to separate the DNA from contaminants, and a phenol:chloroform extraction. Neither protocol was able to recover enough high molecular weight DNA for next generation sequencing (NGS). However, the magnetic bead protocol (Qiagen MagAttract) did appear to remove the nucleases, DNA heated post extraction was not degraded (Figure 25). In contrast the DNA extracted using a Qiagen Dneasy blood and tissue kit and the phenol:chloroform extracted DNA was degraded by heat. Unexpectedly, nether lysis temperature, nor lysis time appeared to affect DNA recovery through the Qiagen MagAttract kit (unfortunately recovery concentration was insufficient for NGS analysis for all treatments) (Figure 25).

Attempts to merge the salting-out lysis protocol with a bead-based purification failed. Technical specialists in NZ suggested it might be a chemistry problem with the silica beads and recommended switching to magnetic carboxy beads. Changing bead technology (Ampure carboxy beads and a home-made version was also tested) did not improve DNA recovery.

An attempt to purify the extracted DNA obtained using the salting out protocol with magnetic beads lost 40-90% of the DNA with insufficient recovery to progress to NGS.

As such, the modified salting out protocol with low lysis temperature does recover sufficient, high molecular weight DNA, but nucleases prevent it from being NGS ready. The Qiagen MagAttract DNA kit appears to recover high molecular weight DNA that is free from nucleases, but the protocol recovered insufficient DNA to progress to NGS.

A solution could not be found to extract sufficient NGS-ready, high molecular weight DNA from Pearl Perch tissue.



a b

Figure 25: DNA recovery from Pearl Perch tissue using a) Qiagen MagAttract DNA extraction using silica magnetic beads at two different temperatures and two different lysis times (kit recommends 56°C and overnight lysis). DNA extracted suing a Qiagen Dneasy tissue kit was run alongside for comparison, and b) Combined tissue lysis from the salting out protocol followed by a phenol:chloroform DNA extraction. On both gels, sample numbers marked with * represents a subsample of the neighbouring DNA heated to 80°C for five minutes post extraction (test for post extraction nucleases). The outside marker lanes (M) are Generuler 1KB DNA ladder.

Mitochondrial DNA sequencing

Seven unique mitochondrial DNA COI haplotypes were sequenced from the 40 east-coast fish. The haplotypes differed from each other by up to five bases. One dominant haplotype (Haplotype 1, present in 80% of the samples) occurred across the entire sampled range, from Dunk Island to Coffs Harbour (Table 4, Figure 26). No evidence of geographic separation of similar haplotypes was observed. Although based on limited numbers, there may be a reduction in haplotype diversity south of Brisbane where only Haplotype 1 was found. A failure to find stock structure in mitochondrial DNA sequences is not indicative that stock structure does not exist. This marker is suitable for species level comparisons and has been used in other species for population studies, but it generally lacks sufficient resolving power to differentiate populations within a species.

Table 4: Summary of mitochondrial DNA samples and haplotypes

Location	Samples	Haplotype diversity	Haplotypes present (frequency)
Dunk Is	2	2	H1(1), H2(1)
Rockhampton Offshore	11	4	H1(7), H2(2), H3(1), H4(1)
Fraser Offshore	5	2	H1(4), H5(1)
Brisbane Offshore	15	4	H1(11), H3(2), H6(1), H7(1)
Gold Coast	2	1	H1(2)
Ballina	2	1	H1(2)
Coffs Harbour	3	1	H1(3)
Total	40		7 unique

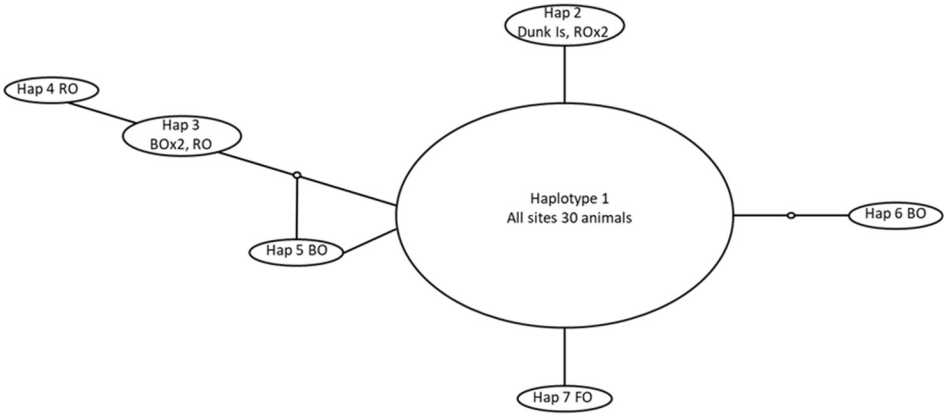


Figure 26: Mitochondrial COI haplotype network. Circles represent unique haplotypes and lines connecting the circles indicate single base mutations. Circle size indicates the relative frequency of the haplotype. RO=Rockhampton Offshore, BO=Brisbane Offshore, FO=Fraser Offshore.

4.5 Larval Dispersion

The simulated distribution of settlers following dispersal from known spawning locations along the Queensland coast approximated the assumed distribution of adult Pearl Perch by suggesting high levels of recruitment in shallow shelf areas extending from northern Queensland at approximately 21°S down to central New South Wales at approximately 31°S, which is close to Coffs Harbour (Stewart *et al*. 2013) (see Figure 27). Importantly, this general observation was not sensitive to assumptions about simulated larval mortality, the timing of settlement competency, or the distribution of putatively suitable settlement habitat (shallow shelf areas) (Figure 28).

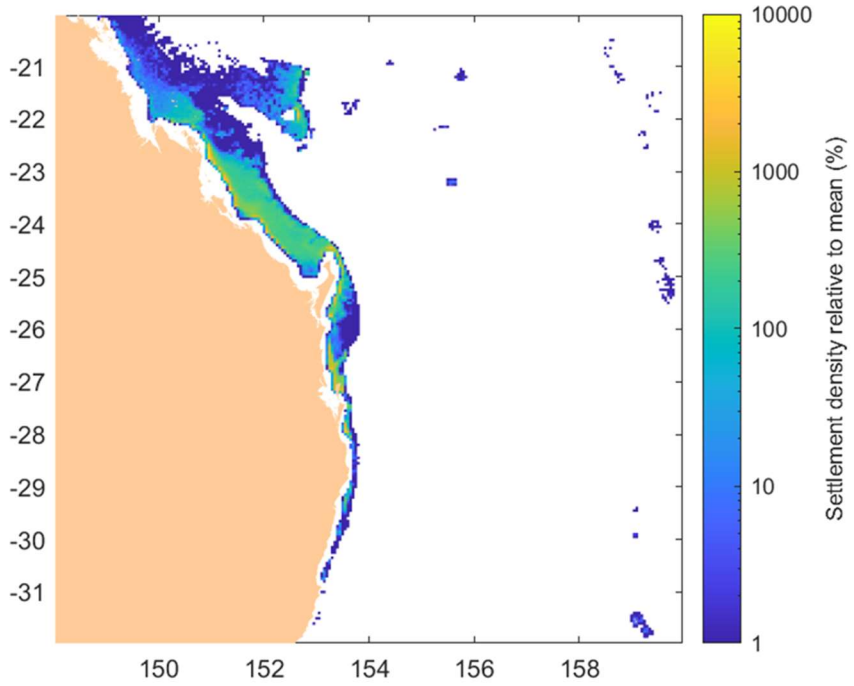


Figure 27: Relative density of settlers following dispersal from known spawning locations along the eastern Australian coastline. Data shown represent averages across all simulation years (2004–2020). Data were normalised using mean settlement across all settlement locations in the modelling domain as a baseline.

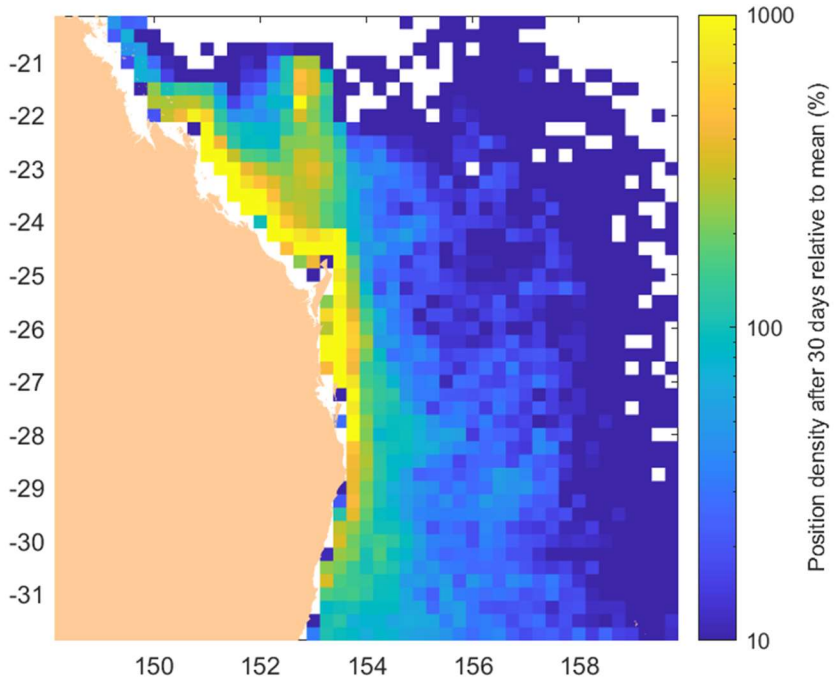


Figure 28: Relative density of larvae after 30 days of dispersal from known spawning locations along the eastern Australian coastline. In contrast to Figure 27, the data shown here ignore natural larval mortality and settlement.

As expected according to previous research, dispersal from simulated spawning locations appeared to be influenced by the prevailing southerly flow of the Eastern Australian Current during the spawning period (Ridgway and Dunn 2003; Stewart *et al.* 2013). That is, dispersal and settlement north of spawning locations appeared to be limited while dispersal and subsequent settlement south of spawning locations appeared to be more pronounced (Figure 27).

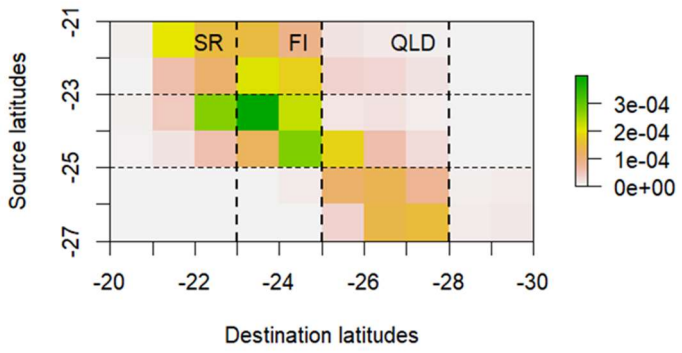


Figure 29: Dispersal probability matrix highlighting mean potential connectivity between 1-degree latitudinal bands across the east coast of Australia. Dashed lines indicate locations of the Swain Reefs area (SR, north of 23°S), Fraser Island (FR, approximately 25°S), and the QLD/NSW border (approximately 28°S).

Fraser Island appeared to represent a natural barrier to predicted dispersal, resulting in two largely disconnected clusters around 25°S between which larval exchange might be limited unless interannual variability in ocean currents results in maximum exchange (Figure 30). Multiple previous studies analysing population connectivity along the eastern Australian coastline have identified Fraser Island as a natural barrier (e.g. Krueck *et al.* 2020).

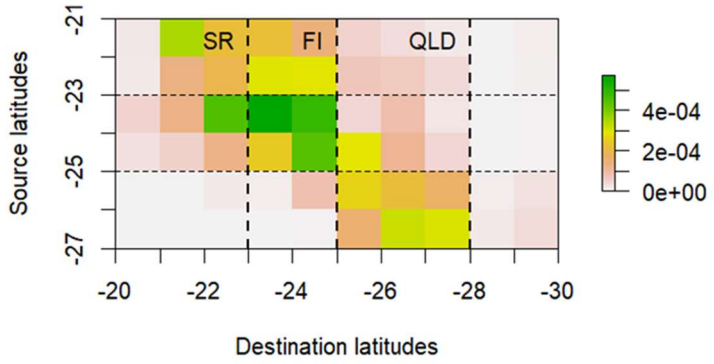


Figure 30: Settlement probability matrix highlighting maximum potential connectivity between latitudinal bands across the east coast of Australia. Dashed lines and abbreviations are as described in Figure 29.

Overall, the simulated concentration of settlers was highest on the extensive shelf region north of Fraser Island between 23° and 25°S. Connectivity between this region and the Swain Reefs area between roughly 21° and 23°S, which contained the highest number of simulated spawning locations (Figure 5), was likely to be high. However, the probability that larvae released from the Swain Reefs region dispersed and settled south of 23°S was comparatively higher than vice versa (Figure 29 and Figure 30).

Given the influence of Fraser Island as a natural dispersal barrier, the second connectivity hub was located between 25° and 28°S. Connectivity between this region in south-east Queensland and the northern connectivity hub between Fraser Island and Mackay (21° and 25°S) was largely unidirectional, with limited northward dispersal.

The general patterns of connectivity described above can be analysed in more detail based on matrices providing a higher spatial resolution (e.g., Figure 31). This includes regional contributions to settlement for individual spawning locations, which visualized that the Swain Reefs region seemed unlikely to be an important source region for regions south of Fraser Island (Figure 32).

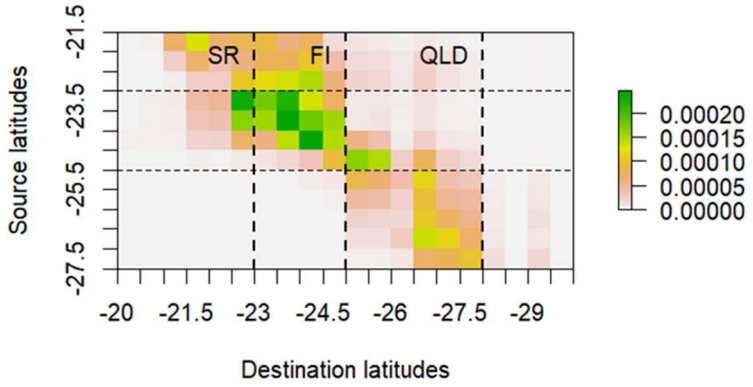
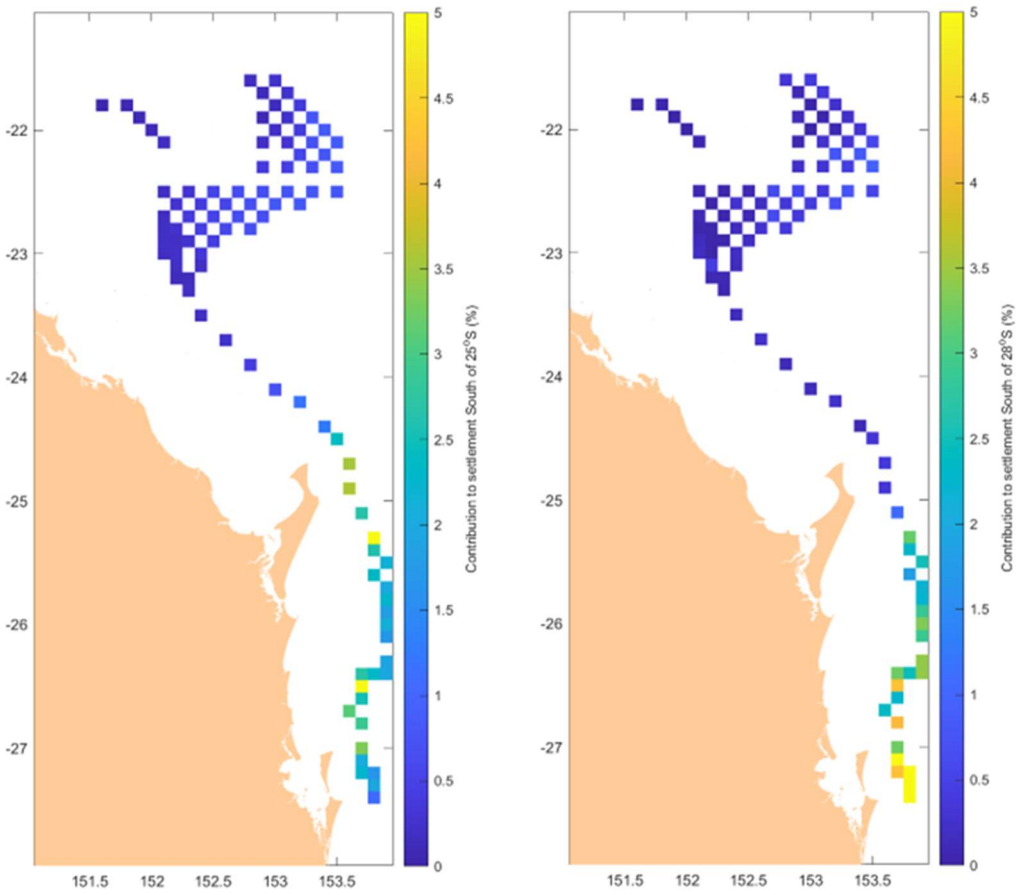


Figure 31: Settlement probability matrix highlighting mean potential connectivity between 0.5-degree latitudinal bands across the east coast of Australia. Dashed lines and abbreviations are as described in Figure 29.

Larval dispersal from known spawning locations in Queensland resulted in limited predicted settlement in New South Wales (Figure 31). If reproductive output from all simulated spawning locations was assumed to be uniform (e.g., 1000 larvae per destination), then settlement in New South Wales was predicted to amount to only 1% ± 0.7% of total settlement (mean ± SD across years). The maximum simulated settlement in New South Wales relative to mean total settlement following dispersal from simulated spawning locations was 2.7%.



(a) (b)

Figure 32: Relative contribution of all simulated spawning locations to total larval settlement a) south of Fraser Island, and b) south of the QLD/NSW border (at 28°S). This demonstrates that spawning sites North of Fraser Island make limited contribution to recruitment south of Fraser Island.

5. Discussion

Pearl Perch spawning varies temporally and spatially throughout their distribution in Queensland. Maximum mean GSI was found to coincide with SSTs of 25.26–26.32°C, which primarily occur between October and December in the northern region and between February and April in the southern region. The presence of female Pearl Perch with spawning ovaries in samples from the respective regions at these times is further evidence that SST influences spawning. This result is consistent with Lenanton *et al.* (2009) who reported similar observations for *G. hebraicum*, with GSI increasing as SST increased during the austral spring. A female Pearl Perch with spawning ovaries caught in December 2021 in the southern region (Figure 41) was caught on a day where SST was 25.4°C, and SST of 25.26–26.32°C occurred between December 2021 and May 2022 (Figure 40), indicating that spawning may have occurred over a protracted period.

While this study represents an important step in understanding the effects of SST on spawning periodicity in Pearl Perch, other environmental factors may also be influential (e.g., availability of spawning habitat). Further, social cues might influence the timing of spawning for Pearl Perch, as has been observed in *G. hebraicum* (Mackie *et al.* 2009). Thus, fish caught from a discrete Pearl Perch aggregation in any given month may not be representative of the spawning condition of fish in other aggregations located within that region. Considerable effort and expense would be required to test the presence of such complex interactions between environmental and behavioural factors affecting ovary development in Pearl Perch.

Similar to *G. hebraicum* (Hesp *et al.* 2002; Lenanton *et al.* 2009), female Pearl Perch with spawning (Stage 5) and spent (Stage 6) ovaries occured over several months in both regions, although the number of females with spawning ovaries was low (n = 13). The presence of both hydrated eggs and post-ovulatory follicles in reproductively active ovaries indicates Pearl Perch are serial spawners, which is also consistent with *G. hebraicum* (Hesp *et al.* 2002). Female Pearl Perch with spawning ovaries were caught when mean monthly GSI was either increasing or decreasing, indicating that some portion of the spawning biomass was able to spawn outside of the period when mean GSI was at a maximum. This is consistent with results reported for *G. hebraicum* by Hesp *et al.* (2002), who observed that some fish spawned in November despite the GSI of female fish being well below its maximum. Furthermore, a high proportion of female Pearl Perch had non-reproductive ovaries (Stages 2 and 3) throughout the spawning period in the respective regions, a life history strategy that is also employed by *G. hebraicum* (Lenanton *et al.* 2009).

The low number of females with spawning ovaries observed in the current study is potentially a result of the opportunistic nature of the sampling undertaken. Samples were provided by fishers who were constrained by weather and market forces, including targeting other species, which may have prevented fishers from accessing the fishing grounds during peak spawning periods. Low sample numbers in some areas could be in part due to increasingly stringent management interventions, prompting both commercial and recreational fishers to disengage with the FQ monitoring program, including some fishers who specialise in targeting Pearl Perch aggregations north of Fraser Island (A. Garland, pers. obs.). This, combined with the effects of the COVID-19 pandemic, significantly restricted the number of samples with which to assess reproductive activity throughout the current study. Additonally, the opportunistic nature of the fishery-dependent sampling throughout the current study likely introduced some sampling bias. For example, a fisher may have contributed a large number of Pearl Perch, caught from a single location, which would bias both GSI and gonad stage proportion for the month in which the sample was caught.

Female Pearl Perch with spawning ovaries were found in samples collected to the east and north of the traditional fishing grounds in southern Queensland and northern New South Wales. Prior to 2008, no female Pearl Perch with spawning ovaries were observed in fishery-dependent samples (Stewart *et al.* 2013) which led these authors to hypothesise that Pearl Perch migrate to spawn. However, the MLS in Queensland and New South Wales was 300 mm TL (286 mm FL) throughout the Stewart *et al.* (2013) study and, as a result, a high proportion of the fish sampled by these authors were smaller and younger than the of length- and age-at-maturity, respectively, estimated herein. Further, the Pearl Perch samples from Queensland in the study by Stewart *et al.* (2013) were caught primarily by fishers targeting Snapper on the heavily fished inshore (<100 m) grounds south of Fraser Island (Figure 1), during the Snapper spawning season (June–September, Sumpton and Jackson 2010), when Pearl Perch GSI is at its lowest and SST is ~19–21°C. As such, the results presented herein indicate that female Pearl Perch with spawning ovaries were very unlikely to occur in the samples obtained by Stewart *et al.* (2013).

Our results indicate that Pearl Perch mature at a larger size than previously assumed. Sumpton *et al.* (2013a) reported that L_{50} was 250–275 mm TL; however, their estimate was based primarily on fishery-dependent sampling that precluded the collection of smaller, immature Pearl Perch, resulting in a biased estimate of L_{50}. Similarly, (Hesp *et al.* 2002) estimated the L_{50} of *G. hebraicum* based primarily on samples provided by commercial and recreational fishers. These authors estimated a L_{50} for females and males of 301 mm TL and 320 mm TL, respectively, with only 16 of the 552 (3%) individuals <300 mm TL. Such bias was somewhat overcome in our study as we estimated L_{50} from the 281 individuals caught offshore from Brisbane and the Sunshine Coast, which included all 81 immature fish (~29%) caught throughout the current study under permit.

Batch fecundity of female Pearl Perch increases with fork length; larger individuals produce more eggs, which is consistent with *G. hebraicum* (Lenanton *et al.* 2009). Maximum estimates of batch fecundity derived herein exceed previously published estimates for any glaucosomatid. Maximum

batch fecundity for Pearl Perch was estimated at ~720,000 eggs (Sumpton *et al.* 1998) and at 533,900 eggs for *G. hebraicum* (Lenanton *et al.* 2009). The results presented herein indicate that larger females produce more eggs than do smaller fish, and protections for these larger animals during spawning may be beneficial to increasing egg production (Hixon *et al.* 2013). The imposition of a maximum legal size may benefit the Pearl Perch stock given the species' high post-release survival (Campbell *et al.* 2014). This strategy is currently used in Queensland for commercially and recreationally important species such as Dusky Flathead (*Platycephalus fuscus*) and Barramundi (*Lates calcarifer*). Previous research indicated that significant increases in the MLS would be required to increase the spawning biomass to appropriate levels (Campbell *et al.* 2021a), and the imposition of a maximum legal size may be more acceptable to stakeholders.

Unlike previous research (Stewart 2011; Stewart *et al.* 2013; Sumpton *et al.* 2013a), larger, older fish were found in fishery-dependent and fishery-independent samples in the current study. The higher representation of ages ≥7 years in the current study is a direct result of the expansion of the fishery that occurred throughout the early 2000s. Until the early 1990s, fishers were mostly limited to fishing areas close to the coast, locating reefs via landmarks. At this time, Pearl Perch were caught incidentally by fishers targeting Snapper on inshore grounds (<100 m) south of Fraser Island (see Figure 1), the area from which Stewart *et al.* (2013) collected the Queensland samples during their study. Both Snapper and Pearl Perch have a long history of exploitation in this area such that the low spawning biomass of these species in the late 1990s (Sumpton *et al.* 2017; Wortmann *et al.* 2018) forced commercial fishers to move to offshore fishing areas to the east and north of the traditional fishing grounds. The expansion of the fishery was facilitated by the availability of modern electronic fishing aids including colour sounders and global positioning systems (GPS). These changes occurred concurrently with increases in vessel size and range, resulting from the uptake of four-stroke outboard engines, along with the use of electronic and hydraulic reels (Sumpton *et al.* 2013b). This increase in fishing power allows fishers to target Pearl Perch in deeper (>100–200 m) waters offshore from the Sunshine Coast and Fraser Island (see Figure 1), and in waters adjacent to the Swain Reefs. In these more remote areas, fishers have located substantial aggregations of large Pearl Perch, which are now regularly accessed by both commercial and recreational fishers.

The absence of older fish in age frequencies (termed 'age truncation') has been linked to over-exploitation (Siskey *et al.* 2016). The lack of older fish in the samples collected by Stewart *et al.* (2013), and those from the southern region in the current study, demonstrate the effect of fishing on Pearl Perch on grounds close to traditional ports. The age truncation observed has been shown to cause changes in fished populations that inhibit recovery (Hixon *et al.* 2013). In contrast, older fish are now found on remote offshore fishing grounds that have received relatively low levels of fishing effort, compared to areas closer to traditional ports.

The results from the current study demonstrate that Pearl Perch are a relatively long-lived species. The longevity of Pearl Perch (~27 years) is similar to that reported for the congeneric *G. buergeri* (Newman 2002) but shorter than the largest glaucosomatid, *G. hebraicum*, at 41 years (Hesp *et al.* 2002). The growth coefficient (k) derived herein is the highest reported for any glaucosomatid. Hesp *et al.* (2002) reported $k = 0.111$ year^{-1} for *G. hebraicum* caught in southern Western Australia and Newman (2002) reported $k = 0.139$ year^{-1} for *G. buergeri* from north-western Australia, based on samples collected in fish trawls. However, the growth curve reported by Newman (2002) resulted in a L_0 = ~60 mm, indicating a poor fit of the VBGF at younger ages. The under-sampling of younger fish is a common source of bias when assessing growth and has been shown to result in the under-estimation of k (Gwinn *et al.* 2010). Although younger fish were under-represented in the current study, using a prior for L_0 within a Bayesian framework minimises bias in the estimation of growth parameters despite the issues relating to the selectivity of the gear used to obtain samples (Smart and Grammer 2021).

Young (<1 year) Pearl Perch are typically associated with the sandy substrates utilised by penaeid prawns (Stewart *et al.* 2013) and are found in the discarded portion of penaeid-trawl discards in south-

east Queensland (Courtney *et al.* 2007). These young fish likely avoid habitats favoured by adults, which are characterised by rocky reef and gravel substrates (McKay 1997), to avoid predators such as Samsonfish (*Seriola hippos*) and Snapper , a strategy also observed in *G. hebraicum* (Hesp *et al.* 2002). In an effort to produce a more realistic mean length-at-age, in the absence of significant numbers of young fish, Stewart *et al.* (2013) constrained the age at zero length parameter to $t_0 = -0.02$ year. However, fixing one parameter of the VBGF is known to result in substantially biased growth estimates (Pardo *et al.* 2013) and this may have contributed to differences between the growth parameter estimates obtained by Stewart *et al.* (2013) and those from the current study. It should be noted that, while the growth parameter estimates derived by Stewart *et al.* (2013) for the Queensland portion of the stock ($L_\infty = 618$ mm, $k = 0.24$ year^{-1}) are similar to those derived for males from the northern region in the current study ($L_\infty = 603$ mm, $k = 0.26$ year^{-1}), the bias resulting from the absence of older fish in the study by Stewart *et al.* (2013) makes comparison of results between studies difficult.

Stewart *et al.* (2013) estimated the growth of Pearl Perch in Queensland and New South Wales from fish largely <10 years old (see Fig. 1 in that study). In the current study, growth was assessed from 1153 individuals, including 392 individuals aged ≥7 years (~34%), in contrast to the 34 (14%) fish sampled in Queensland and 11 (~5%) fish sampled from New South Wales at these ages by Stewart *et al.* (2013). There were no fish in the New South Wales samples >10 years, despite a lifespan of at least 19 years (Stewart 2011). The presence of these older animals in the current study enables improved model fitting at the upper end of the age range, reducing bias in the estimation of the VBGF parameters. Although the estimated L_∞ parameters presented here are lower than the maximum length (680 mm FL) of fish in the current study, the respective models produced reasonable fits to the observed length-at-age data for older fish.

A significant difference in the L_∞ parameter between sexes was apparent for fish collected from the northern region. This is consistent with results reported for *G. hebraicum* by Hesp *et al.* (2002): however, in contrast to the current study, these authors found that females had a higher L_∞ and lower k than did males. No significant difference in growth between the sexes was detected for fish collected from the southern region which is consistent with the results reported by Stewart *et al.* (2013) and by Newman (2002) for *G. buergeri*. A significant difference in L_∞ was also detected between regions for male Pearl Perch, with larger fish caught in the northern region. This contradicts the results presented by Stewart *et al.* (2013), who derived a higher L_∞ in the southernmost part of the species' range and attributed this difference to higher water temperatures to the north facilitating the faster growth in the fish sampled from Queensland.

The tag-recapture information generated during this study provides no evidence of spawning migrations. A total of ~3,500 Pearl Perch have been tagged with dart tags, none of which moved more than 20 kilometres. The low recapture rate (~2%) implies: 1) a high levels of tag loss, 2) emigration to areas outside of the fishery, 3) high incidence of non-reporting of recaptures, 4) low post-release survival (PRS), and 5) high levels of biomass. Of these options, low PRS is the least likely, given the species' high PRS (Campbell *et al.* 2014), and a recent stock assessment that demonstrated biomass is at historically low levels (Sumpton *et al.* 2017). A more likely explanation for the low recapture rates is tag loss: several of the Pearl Perch recaptured during the current study exhibited significant infection around the tag site which would have likely led to tag loss. The lack of tag returns from areas where Pearl Perch are known to spawn does not necessarily preclude spawning migrations. For example, the size of the fish tagged was such that a high proportion of these were not yet mature and migrations to spawning areas would not be expected. Further, the levels of fishing effort in the areas where spawning occurs is low, compared to areas closer to the coast, and tag returns are less likely from these areas. Lastly, commercial fishers are more likely to access spawning locations and, given the high number of fish caught, tags can be easily overlooked.

The second tagging trip, undertaken off the Sunshine Coast, provided an interesting observation. Those fish that were well under the MLS of 38 cm TL were detected for long periods post-capture,

while those close to, or over, the MLS were no longer detected and most likely caught soon after the tagged fish reached the MLS. The shipwreck is well-known among local anglers, and it is likely that the fishing pressure at the site is high, resulting in the presence of very few legal-sized fish.

The larval distribution model presented herein indicates that larvae are carried southward from spawning locations by the East Australian Current (EAC, Stewart *et al.* 2013), a western boundary current in the southwest Pacific Ocean (Ridgway and Dunn 2003). However, Fraser Island represents a barrier between spawning fish in the north and settlement grounds to the south. The model suggested that, while a relatively small proportion of the larvae from the Swain Reefs area will move southward, the majority settle north of Fraser Island. Conversely, all larvae spawned south of Fraser Island move southwards. These results are consistent with those reported by Schilling *et al.* (2022), who found the majority of spanner crab larvae settling in southern Queensland and northern New South Wales originated from the area south of Fraser Island. The model indicated that ~1% of the larvae spawned in Queensland settle in New South Wales: however, this result is contingent on the number and location of spawning sites used in the model.

The number and location of spawning sites used in the larval dispersion model were inferred from information provided directly and indirectly by commercial fishers. Firstly, commercial fishers provided the general locations of Pearl Perch aggregations. Project staff were able to engage with several commercial fishers that target Pearl Perch, who provided information on fishing areas and depths from which project staff were able to infer likely spawning locations. Additionally, social media posts from recreational fishers indicate that large Pearl Perch are caught in the deeper waters (>100 m) offshore from Brisbane and the Gold Coast[1]. Secondly, project staff were able to infer the locations of spawning sites from the heat maps supplied by Fisheries Queensland. These maps confirmed the information provided directly from commercial fishers, with large catches taken from deep water offshore from the Sunshine Coast and Fraser Island, and from the Swain Reefs area (Figure 17). Lastly, commercial logbook data provided catch size and location data at a resolution of 6 nm^2. Again, the locations of large catches reported by fishers in mandatory logbooks occurred in the same areas as those described by commercial fishers. Logbook data indicated that, in the 2019 and 2020 calendar years, observed commercial catch rates were 26.5 kg day^{-1} in the northern region (Figure 1) and 15.7 kg day^{-1} in the southern region. This demonstrates that the Pearl Perch biomass in the northern region is likely to be higher, compared to the southern region. These lines of evidence informed the number and location of spawning sites provided in Figure 5. However, without absolute knowledge of spawning biomass and locations, there is uncertainty around the estimates of larval dispersal and settlement. Furthermore, exact settlement locations are not well known and are inferred from penaeid-trawl and crab bycatch (Sumpton *et al.* 2003; Courtney *et al.* 2007). Although the hydrodynamic model used provides excellent long term temporal coverage and good results for transport across broad spatial scales, it is limited in its accuracy and coverage close to the coast and in shallow water. Aspects such as larval retention in eddies behind headlands are not captured by this model.

Sea surface temperature (SST) increased at ~1°C $decade^{-1}$ in the period 1993–2016 in south-eastern Australia (Pattiaratchi 2020). Climate-driven increases in SST have been shown to cause poleward shifts in species distributions (Champion *et al.* 2021; Hu *et al.* 2022) and anecdotal reports suggest Pearl Perch have been caught by recreational fishers as far south as Montague Island in southern New South Wales (36°15'S) in recent years. This poleward shift is a result of the EAC strengthening and penetrating further south (Ridgway 2007) and these changes are likely to influence the dispersal of Pearl Perch larvae. Along with the poleward movement commonly associated with climate-driven increases in SST, there is also evidence that some species respond to increasing temperatures by moving into deeper waters (Perry *et al.* 2005). Pearl Perch are now primarily caught in commercial quantities in deeper (>150 m) offshore waters in southern Queensland. However, the increasing catch of these fish is more likely a result of increased fishing power in recent years rather than a

[1] e.g., https://www.youtube.com/watch?v=T1q8C75yFNg and https://www.youtube.com/watch?v=FxuySJAeAb4&t=1s

distributional shift: significant numbers of Pearl Perch are still caught in shallower waters (80–100 m) north of Fraser Island where fishing effort is low, compared to areas of similar depths close to southern Queensland ports such as Mooloolaba (Figure 1). Further research is required to determine the effects of climate-driven changes to SST and other environmental variables on the biology of Pearl Perch across its distribution.

The inability to determine the stock structure using genetic techniques is a significant impediment to achieving the objectives of the current study. The third objective of this study was to determine the contribution made to the Pearl Perch stock by spawning fish north of Fraser Island using genetic analysis. With this information, FQ would be able to make evidence-based management changes to protect these spawning fish to ensure the long-term sustainability of the stock. However, the poor quality of the DNA extracted from Pearl Perch tissue prevented robust genetic analysis. Although project staff used various methods to increase the quality of the DNA extracted, all attempts failed to produce DNA of sufficient quality for Next Generation Sequencing (NGS). Further, on occasions when sufficient DNA of sufficient quality was extracted from Pearl Perch samples, the extracted DNA continued to degrade rapidly following the extraction, even when stored at -20°C. To avoid this problem, DAF researchers studying the stock structure and connectivity of black jewfish in Queensland (*Protonibea diacanthus*, FRDC Project Number 2019/056) sent tissue samples to Diversity Arrays Technology (DArT) for DNA extraction. Initially, the extractions resulted in DNA concentrations unsuitable for NGS: however, DArT's optimization process facilitated DNA extraction of a quality suitable for sequencing. As such, should genetics be used to determine the stock structure of Pearl Perch in future studies, tissue samples should be sent to DArT for DNA extraction to ensure enough high-quality DNA is extracted for NGS.

While surgeries to insert acoustic tags in fish were performed by DAF staff during previous research projects, clarification of the Veterinary Surgeons Act (1936) means that invasive procedures such as these can now only be performed by registered veterinarians or their students. Further, the DAF Animal Ethics Committee advised that DAF vessels could not be used as a platform for performing surgeries, even for those researchers who had been granted Animal Ethics approvals from their own institutions. As a result of this situation, a DAF veterinarian was recruited to perform surgeries, with instruction from a project staff member. Although the DAF veterinarian was willing to participate, it was often difficult to organise acoustic tagging fieldwork around their schedule. This, combined with Covid-related restrictions throughout 2020 and 2021, delayed acoustic tagging field work. As a result of the issues raised around performing surgeries during the current study, DAF scientists developed a submission to the review of the *Animal Care and Protection Act 2001*. At the end of 2022, this review resulted in amendments to the Act that included clarification of the scientific use of animals, allowing DAF staff to insert acoustic tags, provided appropriate training has been undertaken.

The Integrated Marine Observing System (IMOS) has increased the coverage of acoustic receivers in Queensland, funded by the Queensland Government, to determine the movement of important marine species. Although none of the Pearl Perch tagged with acoustic tags during the current project have been detected by IMOS receivers, project staff will continue to monitor IMOS detection data after the completion of the project.

The Pearl Perch spawning biomass is currently estimated to be 22% of pre-fishing levels (Lovett *et al.* 2022). In response to declining spawning biomass, Fisheries Queensland introduced management changes in 2019, designed to prevent further declines and decrease fishing mortality. These changes included an annual total allowable commercial catch (TACC) of 15 t, a small increase in the MLS from 350 mm TL to 380 mm TL, a decrease in the recreational in-possession limit from five to four, and the imposition of an annual spawning closure for all sectors between July 15 and August 15. Our results indicate the current spawning closure is unlikely to protect spawning Pearl Perch. This closure was primarily implemented to reduce the fishing mortality of Snapper during its peak spawning period of July and August (Sumpton and Jackson 2010), when aggregations of spawning fish are targeted due to increased catchability, and large catches are possible (Mackie *et al.* 2009; Crisafulli

et al. 2019). The retention of Pearl Perch during this period was prohibited to minimise the incidental capture of Snapper by fishers targeting Pearl Perch on grounds where both species occur. Most stakeholders understand the need for the protection during spawning and, in Queensland, species such as Tailor (*Pomatomus saltatrix*), Barramundi (*Lates calcarifer*) and Coral Trout (*Plectropomus* spp.) have spatial and/or temporal spawning closures in place as protection from overexploitation during spawning periods. However, fishers are likely to question the benefits of a spawning closure if the species spawns at times outside the temporal closure as is the case currently for Pearl Perch. Our results indicate that an effective spawning closure for Pearl Perch would need to vary in both time and space.

6. Conclusion

Pearl Perch is endemic to the east coast of Australia and has been subject to a long history of exploitation in the southern part of its distribution. In the early 2000s, increasing fishing power allowed fishers to access offshore areas to the east and north of the traditional fishing grounds in southern Queensland and northern New South Wales. Fishers located aggregations of large (>60 cm TL), older (>10 years) fish, not previously observed during fishery-dependent sampling, in the areas between Fraser Island and the Swain Reefs, and in deeper water (>150 m) offshore from the Sunshine Coast. Importantly, spawning fish were also found in catches from these areas.

Fishery-dependent and fishery-independent sampling undertaken during the current study revealed spawning varied spatially and temporally. Spawning female Pearl Perch were found in March, April, May, and December in southern Queensland and in September, October and November north of Fraser Island. Gonosomatic Index was highest on the new moon in the southern region, while lunar phase had no effect on GSI in the northern region. Mean GSI was found to increase in spring in the northern region, reaching a peak in December and January. In contrast, mean GSI increased through summer in the southern region, with a peak in April. Peaks in mean GSI coincided with SSTs between 25.26 and 26.32°C. Age- and length-at-maturity were found to be 4.42 years and 353 mm FL, respectively. Batch fecundity was positively correlated with fish size and ranged between 99,694 eggs for a 293 mm FL female to ~3,057,836 eggs for a 540 mm FL female, with a mean of 893,020 (S.D. = 98,360) eggs.

Pearl Perch were found to live at least 27 years and reach asymptotic length faster than previously described. The presence of older fish in samples reduced bias in the growth parameter estimates, compared to previous estimates. Growth was found to differ as a function of sex and region with males growing larger than females at the northern end of the species' range and males were larger in the north compared to those from the south.

The lack of spawning fish in fishery-dependent sampling undertaken prior to 2000 prompted the hypothesis that Pearl Perch migrated northwards to spawn. The tag-recapture data reported herein does not support this hypothesis and shorter, cross-shelf movements are more likely. Too few large, mature fish were tagged to determine the movement of pre-spawn Pearl Perch and no tagged fish were captured in areas where spawning is known to occur. Further, too few fish were tagged with acoustic tags to provide any evidence of large-scale movements.

The larval dispersion model developed herein indicated that most of the larvae spawned north of Fraser Island, settled in the same area, with only a small proportion settling south of Fraser Island. Conversely, all larvae spawned south of Fraser Island were carried southward on the East Australian Current to southern Queensland and northern New South Wales. Given the spawning locations used by the model, only ~1% of the larvae spawned in Queensland settled in New South Wales, all of which originated in the area south of Fraser Island.

Acoustic tagging was only used to estimate movement adjacent to a suspected spawning aggregation and a limited number of receivers were deployed around an isolated feature. This was a pilot study to evaluate movement around, and potentially away from, an aggregation. The limited number of receivers and tags deployed in only two locations has provided useful information to plan future research. In the future, more receivers would need to be deployed over a larger area and preferably not on such isolated habitat. Water depth, strong current and possible post-release predation by sharks contributed to the lack of adequate data for analysis.

The increasing access to offshore fishing grounds is of concern: the lack of spawning animals found on traditional grounds indicates that the Pearl Perch stock is heavily reliant on spawning animals inhabiting these remote areas. The one-month spawning closure introduced in 2019, occurring annually between July 15 and August 15, provides very little protection for spawning Pearl Perch. However, prior to the introduction of the spawning closure, commercial catch was high in July and August, coinciding with high Snapper catch rates during its spawning season and, as such, the current closure does reduce fishing mortality.

The lack of access to offshore grounds prior to 2000 provided refugia for spawning Pearl Perch as evidenced by the lack of spawning fish in fishery-dependent samples collected at this time. The aggregating behaviour of Pearl Perch makes them an easy target for commercial fishers, and large catches are possible in a short time. As such, it would be prudent to provide these aggregations with some level of protection during spawning periods. However, should temporal closures be employed to protect spawning fish, two separate temporal closures would be required given spawning varies spatially and temporally.

7. Implications

Knowledge of spawning times and locations provides fishery managers with the ability to develop harvest strategies that minimise impacts on spawning fish and increase egg production. The current temporal spawning closure that occurs between July 15 and August 15, annually, provides no protection for spawning fish. Lunar phase had a variable effect on GSI and, as such, implementing spawning closures like those used to protect spawning coral trout in Queensland, would be inappropriate for Pearl Perch.

The correlation between sea surface temperature and ovary development implies that spawning will likely occur earlier each year due to climate-induced warming. Should temporal spawning closures be implemented to protect spawning fish, the starting date of the closure will need to be reassessed if water temperatures rise as expected.

The estimate of length-at-maturity of L_{50} = 353 mm FL (~372 mm TL) implies that 50% of the fish at this size are mature. Generally, minimum legal sizes (MLSs) allow a fish to spawn at least once before recruiting to the fishery. This is currently the case for Pearl Perch and has been since 2019, when the MLS was increased from 350 mm TL to 380 mm TL. Prior to 2019, however, the MLS was below L_{50}.

The imposition of a maximum legal size may be beneficial for Pearl Perch given the higher fecundity of larger individuals and the species' resilience to catch-and-release. Prohibiting the retention of large Pearl Perch may deter fishers from accessing large aggregations during the spawning period.

The tag-recapture information generated during this study provides no evidence of spawning migrations. However, the lack of tag returns from areas where Pearl Perch spawn is not evidence that spawning migrations do not occur. Most of the fish tagged to date were immature and spawning migrations are, therefore, not expected. Further, tag loss and non-reporting of recaptures are likely explanations for the low tag recovery rates.

The inability to recover DNA of sufficient quality for Next Generation Sequencing necessitates further genetic sampling. While genetic analysis failed to determine stock structure, the larval dispersion models provide information on the likely source of larval settlement throughout the fishery. The results indicate fish settling on traditional grounds in southern Queensland and northern New South Wales are spawned south of Fraser Island. The increasing strength of the EAC is likely to transport Pearl Perch larvae further south.

Any future management changes imposed to protect spawning Pearl Perch will necessarily result in the release of captured individuals. Given the number of fish released, significant efforts will be required to educate fishers on methods that maximise the survival of released fish, particularly in the deeper offshore waters where fish caught during the current study exhibited barotrauma symptoms such as exophthalmia. Similarly, sharks were present at offshore grounds and methods that mitigate both depredation and post-release predation should be extended to stakeholders.

8. Recommendations

1. The results of this study should be used to inform the future harvest strategies such as spatial spawning closures and the imposition of a maximum legal size. Given the increasing fishing effort in areas where spawning aggregations are found, protections should be implemented for spawning Pearl Perch.

2. Estimates of age- and length-at-maturity derived herein should be used in future stock assessments to improve the accuracy of, and confidence in, stock assessment outputs. Given the differences in spawning and growth, consideration should be given to dividing the Queensland portion of the stock into two separate sub-stocks for future stock assessments.

3. Fishery monitoring with aims of collecting reproductive biology information should continue. The current study has significantly improved the knowledge of the Pearl Perch's reproductive biology: however, further sample collection will improve estimates of spawning times. Specifically, samples collected during full and new moon periods may lead to improvements in the GAM model developed to assess GSI. This monitoring should also include New South Wales to determine if spawning Pearl Perch are present in deeper, offshore waters.

4. The larval dispersion model outputs would benefit from the identification of settlement locations. In the current study, settlement locations were inferred from data collected during trawl and crab bycatch research. Additionally, knowledge of true spawning aggregation areas is currently incomplete and could not be represented accurately in the model. Efforts should be made to quantify these potential inputs to improve larval dispersion models.

5. Genetic sampling should be undertaken, and samples be sent to DArT to ensure DNA of sufficient quality can be extracted for Next Generation Sequencing (NGS).

6. Future research should concentrate tagging effort at large Pearl Perch. Commercial fishers should be engaged to catch large Pearl Perch at likely spawning locations to ensure enough are tagged-and-released to enable robust analyses of tag-recapture data. Further acoustic tagging should be undertaken to determine movement to or from aggregations.

7. Efforts should also be made to determine the effect of climate-driven increases in sea surface temperatures and the strength of the EAC on the transportation of larvae. The effect of these and other environmental factors are currently unknown. The effect of increasing ocean temperature on the distribution of Pearl Perch in Queensland is currently unknown.

8. Should management changes be introduced, such as a maximum legal size, that result in increased rates of release, resources should be dedicated to educating fishers about maximising

the survival of released fish. The Rocky Reef Working Group should be engaged to discuss the most efficient methods of extending information to fishers. The mandatory use of tools that mitigate the effects of barotrauma, such as release weights, venting tools or Coucum's Cages, should be considered by fishery managers and the working group. Further, methods to reduce depredation and post-release predation by sharks should be extended to fishers to maximise the survival of released fish.

9. Fishing power has clearly increased in the rocky reef fishery. Current estimates of fishing power are based on subjective estimates of the effects of a range of technological changes on catches between 1982 and 2012 provided by fishers. The effects of recent advances, such as spot-lock electric motors, digital steering for outboard motors and the use of electric reels with multiple hooks, remain unquantified. Further research is required to empirically derive estimates in fishing power increases.

9. Extension and Adoption

The primary method of extending the outputs of this project was through Fisheries Queensland's RRWG. The extension of results at the RRWG meeting, convened on 13–14 July 2021, enabled engagement with a variety of stakeholders. The RRWG was comprised of commercial fishers, recreational anglers, charter operators, a representative of the Great Barrier Reef Marine Park Authority, a representative of New South Fisheries and fishery managers. The Principal Investigator of the current project is also a member of the RRWG. It is expected that the RRWG members engage with their networks to extend results broadly. The minutes from the appropriate discussion are presented in Appendix 4 (page 57) and a communique of meeting outcomes can be found at https://www.daf.qld.gov.au/business-priorities/fisheries/sustainable/fishery-working-groups/rocky-reef-working-group/communiques/communique-13-14-july-2021.

A media release, authorised by FRDC on 12 July 2019, was distributed to news outlets on 30 July 2019 (Appendix 5, page 59). The media release generated some interest from Grant Broadcasting and the PI was interviewed by Michelle Widdicombe from this organisation. The interview was aired on 31 July 20196 across the Grant network of radio stations including:

- Zinc 96.1FM, Sunshine Coast;
- Hitz 93.9FM, Bundaberg;
- 4RO, Rockhampton;
- 4MK and Star 101.9 FM, Mackay;
- Star 106.3 FM, Townsville; and
- Star 102.7 FM and 4CA, Cairns.

The media release was also highlighted on the website of Fishing World magazine, shown in Figure 47 (https://www.fishingworld.com.au/news/where-do-pearl-perch-spawn).

Along with the media release, a Facebook post was developed for this project. During project development, Facebook was seen as a method of extending results. However, the Facebook post (**Error! Reference source not found.**) received an overwhelming negative response. This was likely due to the imminent implementation of the fishery reforms (introduced on September 2019), designed to reduce the harvest of Pearl Perch and also included the imposition of vessel monitoring system (VMS) tracking for line vessels. These changes attracted significant criticism from fishers and resulted in the disengagement of some stakeholders from the research and management of the rocky reef fishery.

At the start of the project, a pamphlet was produced with the objective of generating interest in the project (Appendix 6, page 62). The pamphlets were placed on the counters of fishing tackle shops in

the hope that recreational anglers would donate Pearl Perch frames. Unfortunately, interest was minimal. Again, the management changes that occurred at the time the project commenced adversely affected engagement with fishers throughout the project.

The ageing work conducted as part of this project was published in the journal Aquaculture, Fish and Fisheries and was available online on 22 December 2022. The citation for the article is as follows:

Campbell, M. J., McLennan, M. F., Nicolson, J. R., Garland, A., Prosser, R. M. & Midgley, R. F. (2022). Improving estimates of growth for pearl perch (*Glaucosoma scapulare*) in Queensland, Australia. *Aquaculture, Fish and Fisheries,* https://doi.org/10.1002/aff2.90.

A manuscript detailing the reproductive biology of Pearl Perch submitted to the Journal of Applied Ichthyology for publication on 27 January 2023.

10. References

Beamish, R., and Fournier, D. (1981) A method for comparing the precision of a set of age determinations. *Canadian Journal of Fisheries and Aquatic Sciences* **38** (8), 982–983.

Cailliet, G.M., Smith, W.D., Mollet, H.F., and Goldman, K.J. (2006) Age and growth studies of chondrichthyan fishes: the need for consistency in terminology, verification, validation, and growth function fitting. *Environmental Biology of Fishes* **77** (3), 211–228.

Campbell, M., O'Neill, M., Taggart, K., Khorsandian, A., Krueck, N., Dijkstra, B., Brady, P., and Hussain, S. (2021a) Development of a user-friendly MSE framework for Queensland's rocky reef fishery. FRDC Project No. 2019/020. Queensland Department of Agriculture and Fisheries, Brisbane, Queensland. pp. 39. URL: https://www.frdc.com.au/project/2019-020

Campbell, M.J., McLennan, M.F., Courtney, A.J., and Simpfendorfer, C.A. (2021b) Life-history characteristics of the eastern shovelnose ray, *Aptychotrema rostrata* (Shaw, 1794), from southern Queensland, Australia. *Marine and Freshwater Research* **72** (9), 1280-1289.

Campbell, M.J., McLennan, M.F., and Sumpton, W.D. (2014) Short-term survival of discarded pearl perch (*Glaucosoma scapulare* Ramsay, 1881) caught by hook-and-line in Queensland, Australia. *Fisheries Research* **151**, 206–212.

Campbell, M.J., and Rigby, C.L. (2022) A re-examination of the growth of the gummy shark (*Mustelus antarcticus*) from Queensland, Australia. *Marine and Freshwater Research*, -.

Champion, C., Brodie, S., and Coleman, M.A. (2021) Climate-Driven Range Shifts Are Rapid Yet Variable Among Recreationally Important Coastal-Pelagic Fishes. *Frontiers in Marine Science* **8**

Clement, M., Posada, D., and Crandall, K.A. (2000) TCS: a computer program to estimate gene genealogies. *Molecular ecology* **9** (10), 1657-1659.

Courtney, A.J., Haddy, J.A., Campbell, M.J., Roy, D.P., Tonks, M.L., Gaddes, S.W., Chilcott, K.E., O'Neill, M.F., Brown, I.W., McLennan, M., Jebreen, J.E., van der Geest, C., Rose, C., Kistle, S., Turnbull, C.T., Kyne, P.M., Bennett, M.B., and Taylor, J. (2007) Bycatch weight, composition and preliminary estimates of the impact of bycatch reduction devices in Queensland's trawl fishery. Queensland Department of Primary Industries and Fisheries, No. Fisheries Research and Development Corporation (FRDC) Final Report 2000/170, Brisbane, Queensland. pp. 307. URL: https://www.daf.qld.gov.au/__data/assets/pdf_file/0007/75769/BycatchFinalReport2007-FullReport.pdf

Crisafulli, B.M., Fairclough, D.V., Keay, I.S., Lewis, P., How, J.R., Ryan, K.L., Taylor, S.M., and Wakefield, C.B. (2019) Does a spatiotemporal closure to fishing *Chrysophrys auratus* (Sparidae) spawning aggregations also protect individuals during migration? *Canadian Journal of Fisheries and Aquatic Sciences* **76** (7), 1171-1185.

Dahn, H.A., Mountcastle, J., Balacco, J., Winkler, S., Bista, I., Schmitt, A.D., Pettersson, O.V., Formenti, G., Oliver, K., Smith, M., Tan, W., Kraus, A., Mac, S., Komoroske, L.M., Lama, T., Crawford, A.J., Murphy, R.W., Brown, S., Scott, A.F., Morin, P.A., Jarvis, E.D., and Fedrigo, O. (2022) Benchmarking ultra-high molecular weight DNA preservation methods for long-read and long-range sequencing. *GigaScience* **11**

Fisher, B. (2020) FSSgam: Code for full subsets model fitting using GA(M)M, https://github.com/beckyfisher/FSSgam.

Fisher, R., Wilson, S.K., Sin, T.M., Lee, A.C., and Langlois, T.J. (2018) A simple function for full-subsets multiple regression in ecology with R. *Ecology and Evolution* **8** (12), 6104-6113.

Gabry, J.T.M. (2020) bayesplot: Plotting for Bayesian Models. R package version 1.7.2, https://mc-stan.org/bayesplot.

Grant, E. (2004) 'Grant's guide to fishes, 10th edition.' (E. M. Grant Pty Limited: Scarborough, Queensland) 880

Gruber, B., Unmack, P.J., Berry, O.F., and Georges, A. (2018) dartr: An r package to facilitate analysis of SNP data generated from reduced representation genome sequencing. *Molecular Ecology Resources* **18** (3), 691-699.

Gwinn, D.C., Allen, M.S., and Rogers, M.W. (2010) Evaluation of procedures to reduce bias in fish growth parameter estimates resulting from size-selective sampling. *Fisheries Research* **105** (2), 75-79.

Hesp, S.A., Potter, I.C., and Hall, N.G. (2002) Age and size composition, growth rate, reproductive biology, and habitats of the West Australian dhufish (*Glaucosoma hebraicum*) and their relevance to the management of this species. *Fishery Bulletin* **100** (2), 214-227.

Hixon, M.A., Johnson, D.W., and Sogard, S.M. (2013) BOFFFFs: on the importance of conserving old-growth age structure in fishery populations. *ICES Journal of Marine Science* **71** (8), 2171-2185.

Hu, W., Du, J., Su, S., Tan, H., Yang, W., Ding, L., Dong, P., Yu, W., Zheng, X., and Chen, B. (2022) Effects of climate change in the seas of China: Predicted changes in the distribution of fish species and diversity. *Ecological Indicators* **134**, 108489.

Jombart, T., Devillard, S., and Balloux, F. (2010) Discriminant analysis of principal components: a new method for the analysis of genetically structured populations. *BMC Genetics* **11** (1), 94.

Krueck, N.C., Treml, E.A., Innes, D.J., and Ovenden, J.R. (2020) Ocean currents and the population genetic signature of fish migrations. *Ecology* **101** (3), e02967.

Lenanton, R., St. John, J., Keay, I., Wakefield, C., Jackson, G., Wise, B., and Gaughan, D. (2009) Spatial scales of exploitation among populations of demersal scalefish: implications for management. Part 2: Stock structure and biology of two indicator species, West Australian dhufish (*Glaucosoma hebraicum*) and pink snapper (*Pagrus auratus*), in the West Coast Bioregion. Final report to Fisheries Research and Development Corporation on Project No. 2003/052. Fisheries Research Report No. 174. Department of Fisheries, North Beach, Western Australia. pp. 187.

Liu, S.-H., Yeh, W.-B., and Mok, H.-K. (2010) Phylogeny of Glaucosomatidae inferred from molecular evidence. *Journal of Fish Biology* **76** (2), 348-356.

Lovett, R., Northrop, A., and Stewart, J. (2022) Stock assessment of Australian pearl perch (*Glaucosoma scapulare*) with data to December 2019. Department of Agriculture and Fisheries, Brisbane, Queensland. pp. 52. URL: https://era.daf.qld.gov.au/id/eprint/8871/1/Stock_assessment_of_Australian_pearl_perch_with_data_to_December_2019.pdf

Mackie, M.C., McCauley, R.D., Gill, H.S., and Gaughan, D.J. (2009) Management and Monitoring of Fish Spawning Aggregations within the West Coast Bioregion of Western Australia. Final report to Fisheries Research and Development Corporation on Project No. 2004/051. Fisheries Research Report No. 187. Department of Fisheries, North Beach, Western Australia. pp. 244.

McKay, R.J. (1997) 'Pearl perches of the world (Family Glaucosomatidae). An annotated and illustrated catalogue of the pearl perches known to date. FAO Fisheries Synopsis No. 125/17.' (FAO Rome, Italy) 19

Miller, S., Dykes, D., and Polesky, H. (1988) A simple salting out procedure for extracting DNA from human nucleated cells. *Nucleic acids res* **16** (3), 1215.

Natanson, L.J., Casey, J.G., and Kohler, N.E. (1995) Age and growth estimates for the dusky shark, *Carcharhinus obscurus*, in the western North Atlantic Ocean. *Fishery Bulletin* **93** (1), 116–126.

Newman, S.J. (2002) Age, growth, mortality and population characteristics of the pearl perch, *Glaucosoma buergeri* Richardson 1845, from deeper continental shelf waters off the Pilbara coast of north-western Australia. *Journal of Applied Ichthyology* **18** (2), 95-101.

Officer, R.A., Gason, A.S., Walker, T.I., and Clement, J.G. (1996) Sources of variation in counts of growth increments in vertebrae from gummy shark, *Mustelus antarcticus*, and school shark, *Galeorhinus galeus*): implications for age determination. *Canadian Journal of Fisheries and Aquatic Sciences* **53** (8), 1765–1777.

Oosting, T., Hilario, E., Wellenreuther, M., and Ritchie, P.A. (2020) DNA degradation in fish: Practical solutions and guidelines to improve DNA preservation for genomic research. *Ecology and Evolution* **10** (16), 8643-8651.

Pardo, S.A., Cooper, A.B., and Dulvy, N.K. (2013) Avoiding fishy growth curves. *Methods in Ecology and Evolution* **4** (4), 353–360.

Pattiaratchi, C., Hetzel, Y (2020) Sea Surface Temperature Variability. In 'State and Trends of Australia's Ocean Report'. (Eds. AJ Richardson, R Eriksen, T Moltmann, I Hodgson-Johnston and JR Wallis). (Integrated Marine Observing System (IMOS))

Perry, A.L., Low, P.J., Ellis, J.R., and Reynolds, J.D. (2005) Climate Change and Distribution Shifts in Marine Fishes. *Science* **308** (5730), 1912–1915.

Peterson, B.K., Weber, J.N., Kay, E.H., Fisher, H.S., and Hoekstra, H.E. (2012) Double Digest RADseq: An Inexpensive Method for De Novo SNP Discovery and Genotyping in Model and Non-Model Species. *PLOS ONE* **7** (5), e37135.

Pironet, F.N., and Neira, F.J. (1998) Hormone-induced spawning and development of artificially reared larvae of the West Australian dhufish, *Glaucosoma hebraicum* (Glaucosomatidae). *Marine and Freshwater Research* **49** (2), 133-142.

Raj, A., Stephens, M., and Pritchard, J.K. (2014) fastSTRUCTURE: Variational Inference of Population Structure in Large SNP Data Sets. *Genetics* **197** (2), 573-589.

Rasband, W. (2022) ImageJ: Java-based image processing. U.S. National Institutes of Health. Bethesda, Maryland, USA https://imagej.nih.gov/ij/download.html

Ridgway, K.R. (2007) Long-term trend and decadal variability of the southward penetration of the East Australian Current. *Geophysical Research Letters* **34** (13)

Ridgway, K.R., and Dunn, J.R. (2003) Mesoscale structure of the mean East Australian Current System and its relationship with topography. *Progress in Oceanography* **56** (2), 189-222.

Rodriguez-Ezpeleta, N., Mendibil, I., Álvarez, P., and Cotano, U. (2013) Effect of fish sampling and tissue storage conditions in DNA quality: considerations for genomic studies. *Revista de Investigaciones Marinas* **20**, 77-87.

Rowsell, N., and Davies, J. (2012) At-sea observation of the stout whiting fishery 2009–10. Technical Report. Department of Agriculture, Fisheries and Forestry, Brisbane, Queensland. URL: http://era.daf.qld.gov.au/id/eprint/6552/1/FOP%20Stout%20Whiting%20Report%202012%20final.pdf

Sambrook, J., and Russell, D.W. (2006) Purification of Nucleic Acids by Extraction with Phenol:Chloroform. *Cold Spring Harbor Protocols* **2006** (1), pdb.prot4455.

Schilling, H.T., Hewitt, D.E., Malan, N., Taylor, M.D., and Johnson, D.D. (2022) Cross-jurisdictional larval supply essential for eastern Australian spanner crabs (Ranina ranina). *Marine and Freshwater Research*, -.

Simpfendorfer, C.A., Chidlow, J., McAuley, R., and Unsworth, P. (2000) Age and growth of the whiskery shark, *Furgaleus macki*, from southwestern Australia. *Environmental Biology of Fishes* **58** (3), 335–343.

Siskey, M.R., Wilberg, M.J., Allman, R.J., Barnett, B.K., and Secor, D.H. (2016) Forty years of fishing: changes in age structure and stock mixing in northwestern Atlantic bluefin tuna (Thunnus thynnus) associated with size-selective and long-term exploitation. *ICES Journal of Marine Science* **73** (10), 2518-2528.

Smart, J.J. (2020) BayesGrowth: Estimate fish growth using MCMC analysis. R package version 0.3.0. https://github.com/jonathansmart/BayesGrowth.

Smart, J.J., Chin, A., Tobin, A.J., and Simpfendorfer, C.A. (2016) Multimodel approaches in shark and ray growth studies: strengths, weaknesses and the future. *Fish and Fisheries* **17**, 955–971.

Smart, J.J., and Grammer, G.L. (2021) Modernising fish and shark growth curves with Bayesian length-at-age models. *PLOS ONE* **16** (2), e0246734.

St. John, J., and Syers, C.J. (2005) Mortality of the demersal West Australian dhufish, *Glaucosoma hebraicum* (Richardson 1845) following catch and release: The influence of capture depth, venting and hook type. *Fisheries Research* **76** (1), 106-116.

Stenekes, N., and Sahlqvist, P. (2011) Community involvement in recreational fisheries data collection: Opportunities and challenges, ABARES Technical report 11.5. Australian Bureau of Agricultural and Resource Economics and Sciences, Canberra. pp. 67. URL: https://www.agriculture.gov.au/sites/default/files/sitecollectiondocuments/abares/publications/TR11.5_RecFisheries.pdf

Stewart, J. (2011) Evidence of age-class truncation in some exploited marine fish populations in New South Wales, Australia. *Fisheries Research* **108** (1), 209-213.

Stewart, J., Sumpton, W., Lockett, M., and Hughes, M. (2013) Age-based demographics of the pearl perch *Glaucosoma scapulare* across it distribution and implications for management of its fisheries. *Journal of Applied Ichthyology* **29** (4), 801-807.

Sumpton, W., Campbell, M., McLennan, M., Brown, I., Fraser, K., Wesche, S., and Kerrigan, B. (2013a) Addressing knowledge gaps for the sustainable management of rocky reef fisheries in southern Queensland (FRDC Final Report 2008/015). Queensland Department of Agriculture,

Fisheries and Forestry, Brisbane, Queensland. pp. 248. URL: https://frdc.com.au/Archived-Reports/FRDC%20Projects/2008-015-DLD.pdf

Sumpton, W., Gaddes, S., McLennan, M., Campbell, M., Tonks, M., Good, N., Hagedoorn, W., and Skilleter, G. (2003) Fisheries biology and assessment of the blue swimmer crab (*Portunus pelagicus*) in Queensland. Final report to FRDC on Project No. 98/117. Department of Primary Industries and Fisheries, No. QO03002, Brisbane, Australia. pp. 156.

Sumpton, W., McLennan, M., Campbell, M., and Kerrigan, B. (2013b) Assessing technology changes and risks to the sustainable management of deepwater line fisheries in southern Queensland. FRDC Final Report (Project No. 2010/053). Department of Agriculture, Fisheries and Forestry, Brisbane, Queensland. pp. 71. URL: https://era.daf.qld.gov.au/id/eprint/4686/1/FRDC_2010-053-DLD.pdf

Sumpton, W., Yeates, M., Joyce, R., McLennan, M., and Jackson, S. (1998) Offshore Rocky Reef Fisheries in south-east Queensland: Report to the Queensland Fisheries Management Authority. Queensland Department of Primary Industries, Brisbane, Queensland. pp. 104.

Sumpton, W.D., and Jackson, S. (2010) Reproductive biology of snapper (*Pagrus auratus*) in subtropical areas of its range and management implications of reproductive differences with temperate populations. *Asian Fisheries Science* **23** (2), 194-207.

Sumpton, W.D., O'Neill, M.F., Campbell, M.J., McLennan, M.F., Campbell, A.B., and Stewart, J. (2017) Stock assessment of the Queensland and New South Wales pearl perch (*Glaucosoma scapulare*) fishery. Queensland Department of Agriculture and Fisheries,, Brisbane, Queensland. pp. 87. URL: https://era.daf.qld.gov.au/id/eprint/5676/1/Stock%20Assessment%20of%20Pearl%20Perch%20Fishery.pdf

Thurstan, R.H., Campbell, A.B., and Pandolfi, J.M. (2016) Nineteenth century narratives reveal historic catch rates for Australian snapper (*Pagrus auratus*). *Fish and Fisheries* **17** (1), 210-225.

Tracey, S.R., Hartmann, K., and Hobday, A.J. (2012) The effect of dispersal and temperature on the early life history of a temperate marine fish. *Fisheries Oceanography* **21** (5), 336-347.

Vehtari, A., Gabry, J., Magnusson, M., Yao, Y., Bürkner, P.C., Paananen, T., and Gelman, A. (2020) loo: Efficient leave-one-out cross-validation and WAIC for Bayesian models.R package version 2.4.1.

White, J.W., Morgan, S.G., and Fisher, J.L. (2014) Planktonic larval mortality rates are lower than widely expected. *Ecology* **95** (12), 3344-3353.

Wood, S.N. (2017) 'Generalized Additive Models: An Introduction with R (2nd edition).' (Chapman and Hall/CRC: New York, NY) 496

Wortmann, J. (2020) Queensland rocky reef finfish harvest and catch rates. Queensland Department of Agriculture and Fisheries, Brisbane, Queensland. pp. 19. URL: https://era.daf.qld.gov.au/id/eprint/7486/1/Rocky%20reef%20catch%20rates%202020.pdf

Wortmann, J., O'Neill, M.F., Sumpton, W.D., Campbell, M.J., and Stewart, J. (2018) Stock assessment of Australian east coast snapper, *Chrysophrys auratus*: predictions of stock status and reference points for 2016. Department of Agriculture and Fisheries, Brisbane, Queensland. pp. 122. URL: https://era.daf.qld.gov.au/id/eprint/6341/1/SnapperStockAssessment2018V3.pdf

Appendices

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Appendix 2 – Intellectual Property

No intellectual property has been generated from this project. UTAS retain the intellectual property of the larval dispersion modelling.

Appendix 3 – Supplementary results

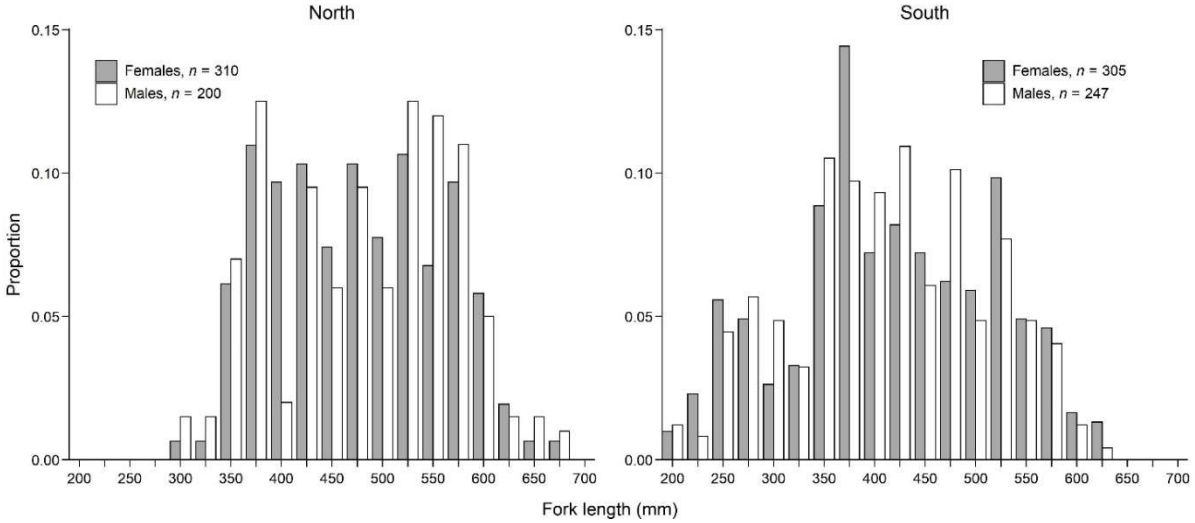

Figure 33: Length frequency distributions for Pearl Perch (*Glaucosoma scapulare*) caught in Queensland between January 2020 and December 2021. Note: sex was indeterminable for 91 animals either as a result of immature gonads or the absence of gonads from processed samples.

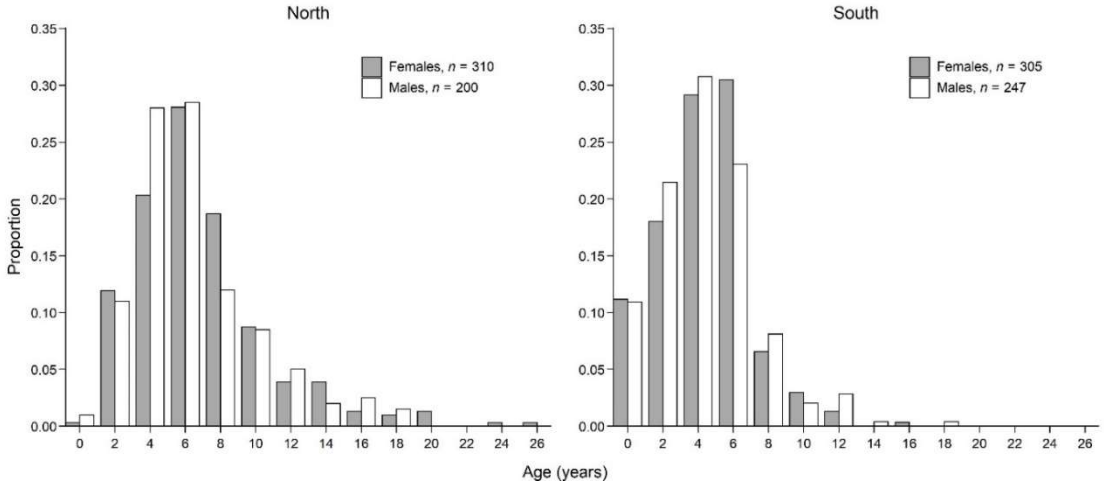

Figure 34: Age frequency distributions for Pearl Perch (*Glaucosoma scapulare*) caught in Queensland between January 2020 and December 2021. Note: sex was indeterminable for 91 animals either as a result of immature gonads or the absence of gonads from processed samples.

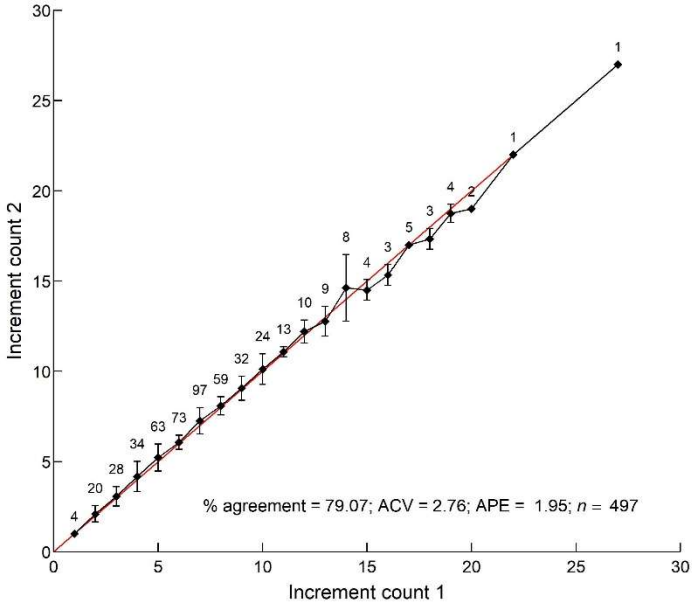

Figure 35: Age bias plot for 497 *Glaucosoma scapulare*. Error bars represent one standard deviation from the mean. Also shown are relevant indices of agreement between the two reads. The red line represents the line of equivalence. Numbers atop each point are the number of animals assigned the respective increment counts.

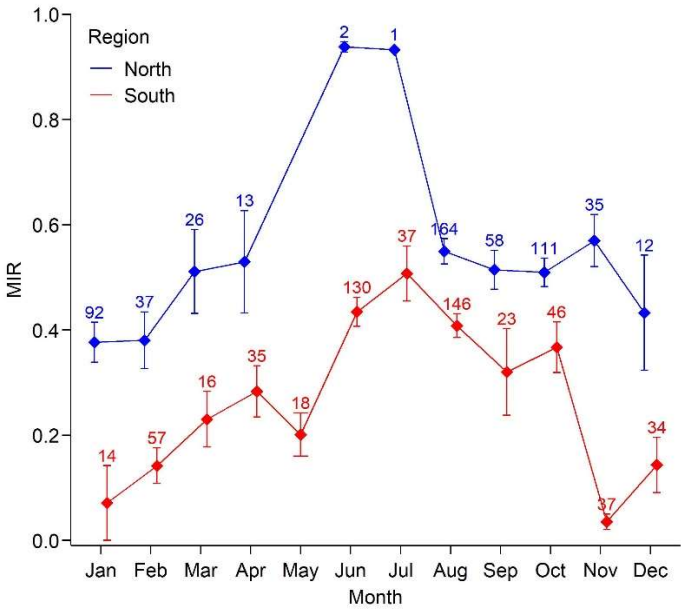

Figure 36: Variation in mean marginal increment ratio (MIR, ± S.E.) as a function of month and region for the 1,144 *Glaucosoma scapulare* ≥2 years caught between January 2020 and December 2021 in Queensland, Australia.

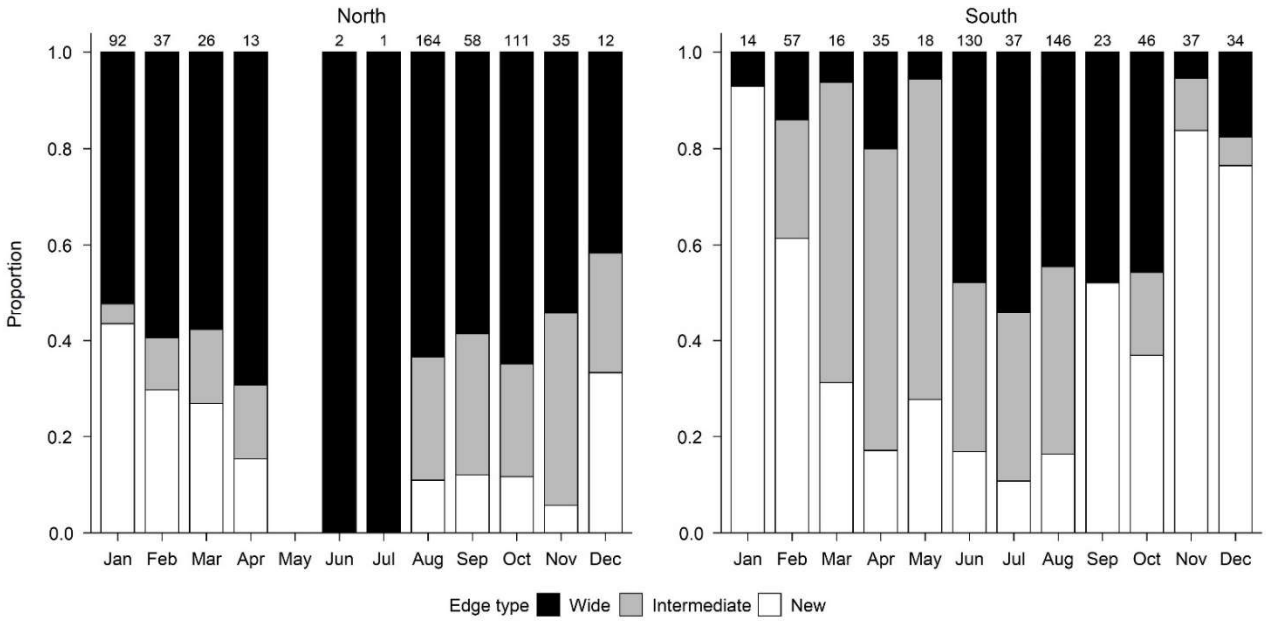

Figure 37: Variation in edge type as a function of month and region for *Glaucosoma scapulare* caught in Queensland, Australia, between January 2020 and December 2021. The number above each bar is the sample size.

Table 5: Relative performance of the three candidate growth functions used to assess the growth of 1,062 *Glaucosoma scapulare* caught in Queensland, Australia, between January 2020 and December 2021. In all cases, the length-at-age data were best described by the von Bertalanffy Growth Function (VBGF), given the priors used. Note: LOOIC is the leave-one-out-information-criterion and LOOICw is the LOOIC weights.

Region and sex	Growth function	LOOIC (S.E.)	LOOICw
North			
Sexes combined	VBGF	6197 (28)	1
	Gompertz	7270 (75)	0
	Logistic	19629 (192)	0
Males	VBGF	2253 (17)	1
	Gompertz	2669 (50)	0
	Logistic	7281 (118)	0
Females	VBGF	3472 (17)	1
	Gompertz	4285 (88)	0
	Logistic	10716 (140)	0
South			
Sexes combined	VBGF	6658 (30)	1
	Gompertz	10172 (94)	0
	Logistic	18024 (210)	0
Males	VBGF	2710 (21)	1
	Gompertz	4921 (79)	0
	Logistic	7461 (128)	0
Females	VBGF	3396 (20)	1
	Gompertz	5873 (88)	0
	Logistic	9365 (152)	0

Table 6: Growth parameter estimates for Pearl Perch (*Glaucosoma scapulare*) representing the mean values of the posterior distributions of the respective parameters and numbers in parentheses are the 95% credible intervals from their posterior distributions generated by the 'BayesGrowth' package via R statistical software. Note: L_∞ is the asymptotic length; L_0 is the length at $t = 0$; k is the growth coefficient of the von Bertalanffy Growth Function; and σ is the estimated residual error.

Region and sex	L_∞ (mm)	k (year^{-1})	L_0 (mm)	σ
North				
Sexes combined	567	0.300	4.11×10^{-3}	66.92
	(553–581)	(0.275–0.328)	(3.03×10^{-5}–2.23×10^{-3})	(63.17–71.02)
Males	603	0.263	8.03×10^{-4}	67.87
	(578–631)	(0.229–0.300)	(3.14×10^{-5}–2.26×10^{-3})	(61.39–75.20)
Females	564	0.297	8.05×10^{-4}	65.48
	(547–582)	(0.264–0.332)	(2.95×10^{-5}–2.24×10^{-3})	(60.50–70.93)
South				
Sexes combined	549	0.303	3.97×10^{-3}	60.96
	(534–566)	(0.280–0.328)	(3.53×10^{-3}–2.21×10^{-3})	(57.61–64.54)
Males	561	0.290	8.04×10^{-4}	58.47
	(537–588)	(0.256–0.327)	(2.89×10^{-5}–2.24×10^{-3})	(53.47–63.81)
Females	576	0.271	7.94×10^{-4}	63.56
	(550–605)	(0.239–0.306)	(3.11×10^{-5}–2.23×10^{-3})	(58.63–69.06)

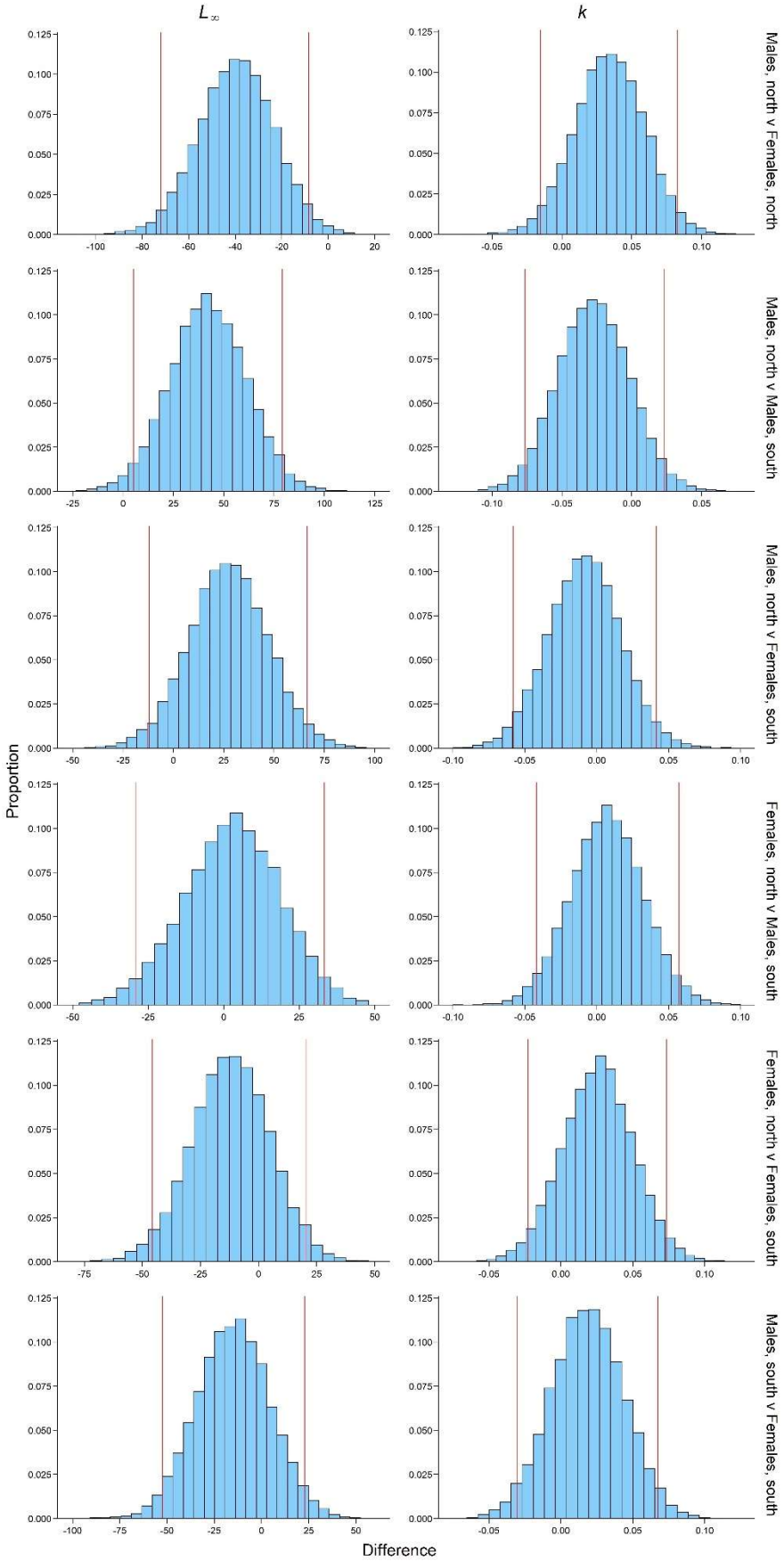

Figure 38: Frequency histograms of vectors representing the difference between the parameter estimates, L_∞ and k, for the respective regions and sexes for Pearl Perch (*Glaucosoma scapulare*). Differences in growth parameters between sexes and regions were assessed by comparing 10,000 posterior estimates of L_∞ and k. Red vertical lines represent the 95% confidence interval of the distribution.

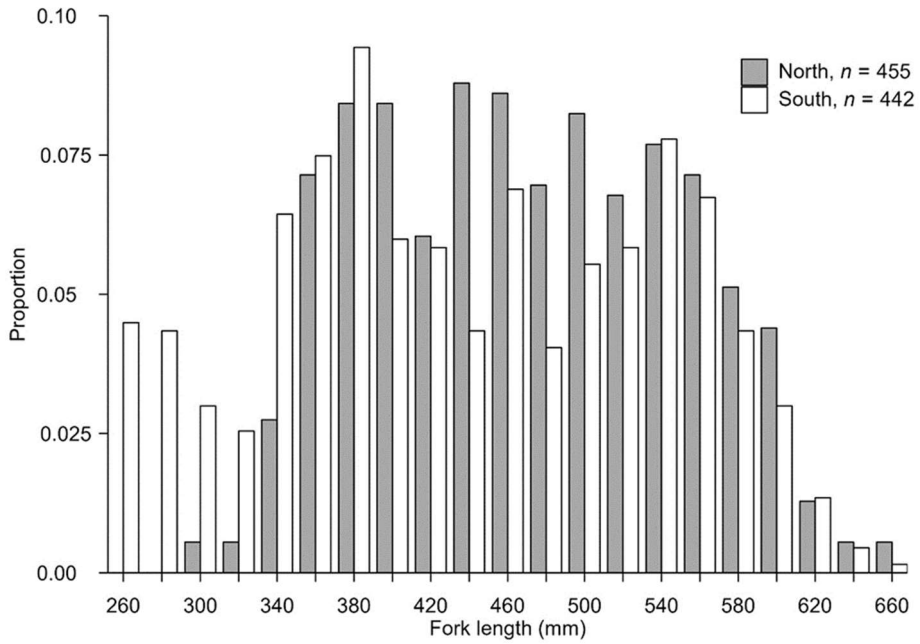

Figure 39: Length frequency (FL, mm) distribution of 897 female Pearl Perch assessed for gonosomatic index as a function of region (Figure 1) in Queensland, Australia.

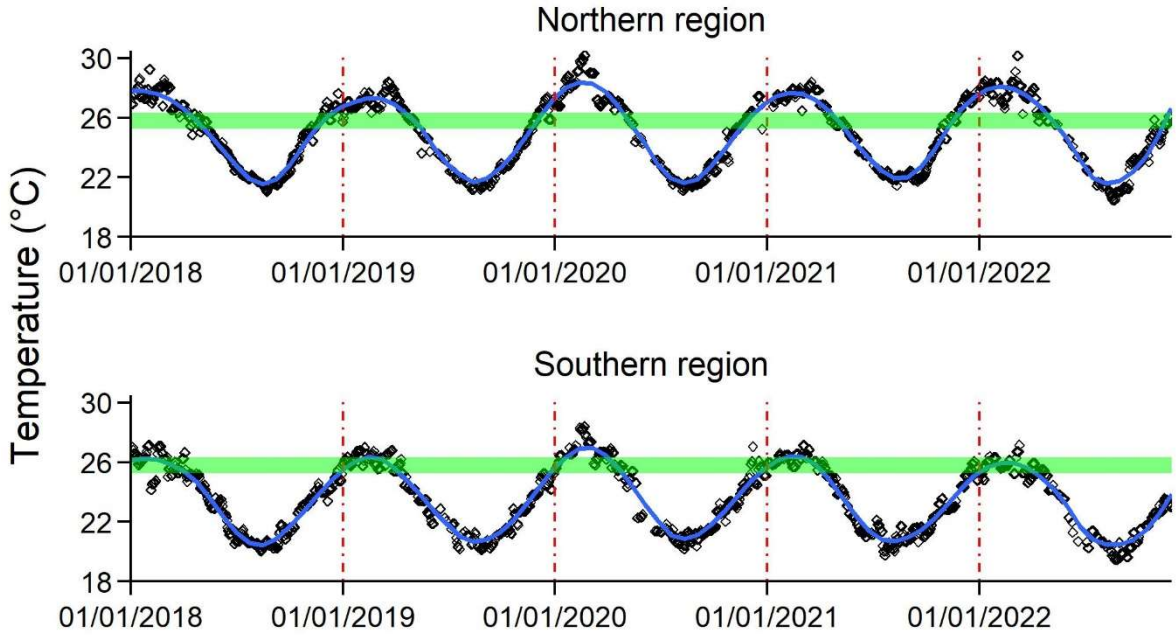

Figure 40: Daily sea surface temperature (SST) at two sites, representing the approximate midpoint of locations from which Pearl Perch were sampled in the current study from the northern (22.4°S, 152°E) and southern (26.8°S, 153.6°E) regions (Figure 1) for the period 1 January 2018 to 29 November 2022. The semi-transparent green bands represent the SST range 25.26–26.32°C, when GSI was >2%. The blue lines are loess smoothing curves, and the red vertical lines represent the first day of each year

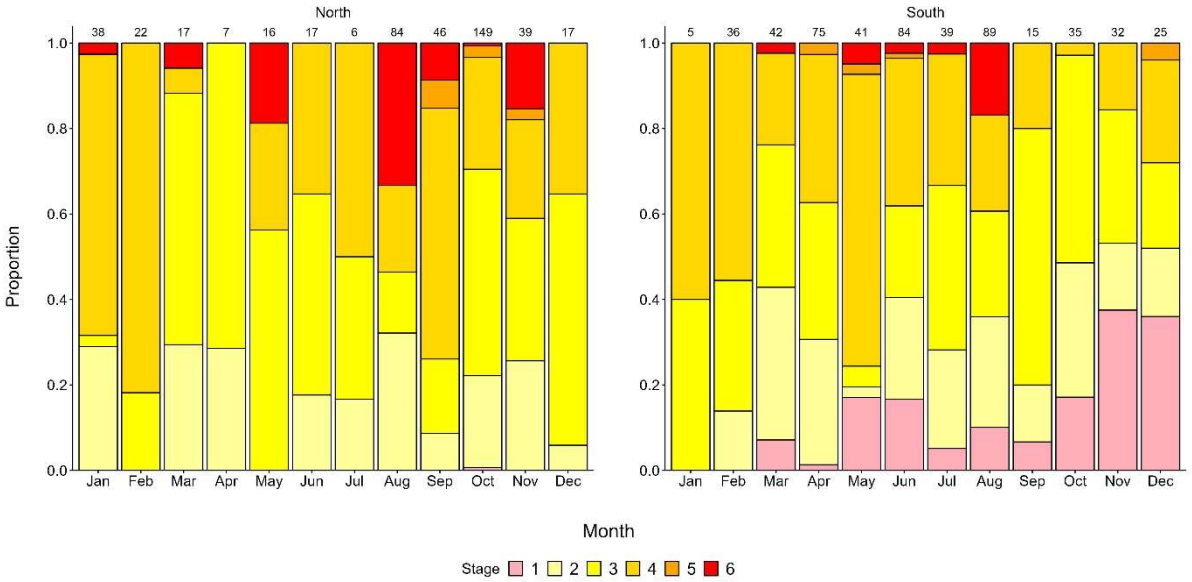

Figure 41: Gonad stage of female Pearl Perch *Glaucosoma scapulare* as a function of month and region. Numbers atop each bar represent the number of animals in each month.

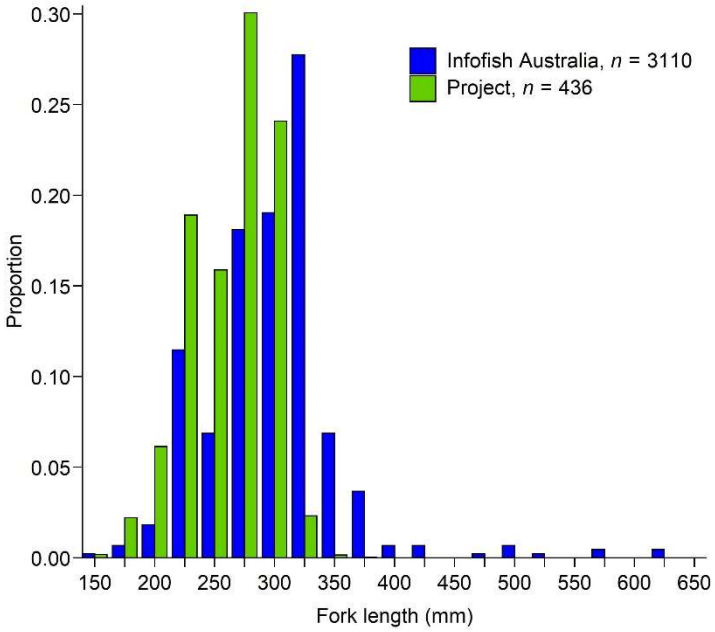

Figure 42: Length frequency of Pearl Perch (fork length, mm) tagged with conventional dart tags. A total of 3,110 fish were tagged by recreational anglers as part of the Suntag program administered by Infofish Australia and 436 were tagged as part of the current project.

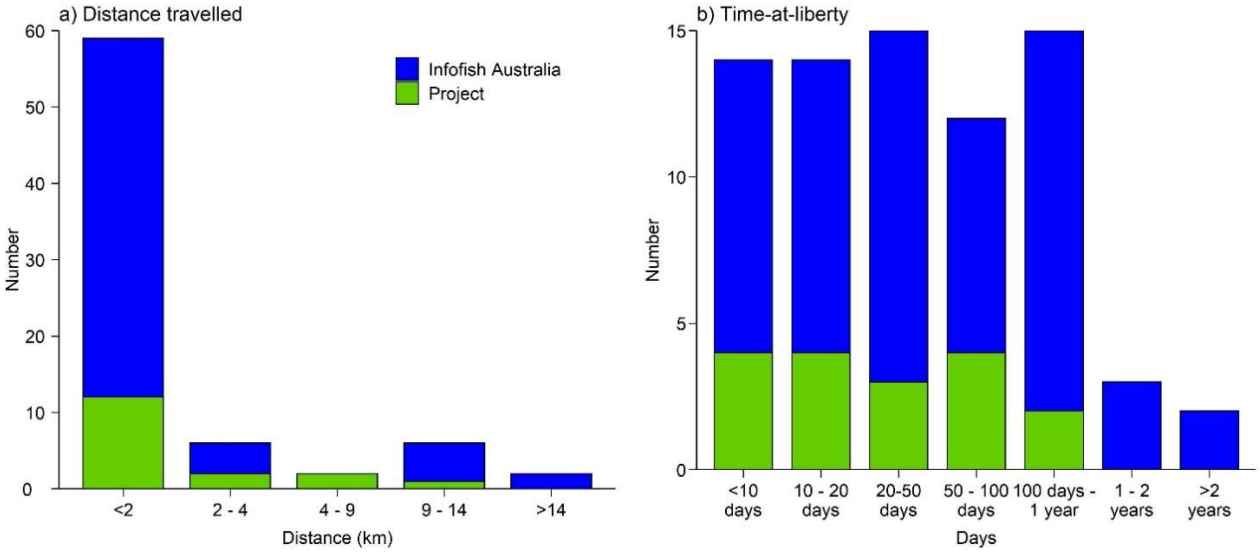

Figure 43: Frequency distribution of the (a) distances between tagging and recapture and (b) time-at-liberty for 75 Pearl Perch caught by recreational fishers as part of the Suntag program (blue) and as part of the current study (green).

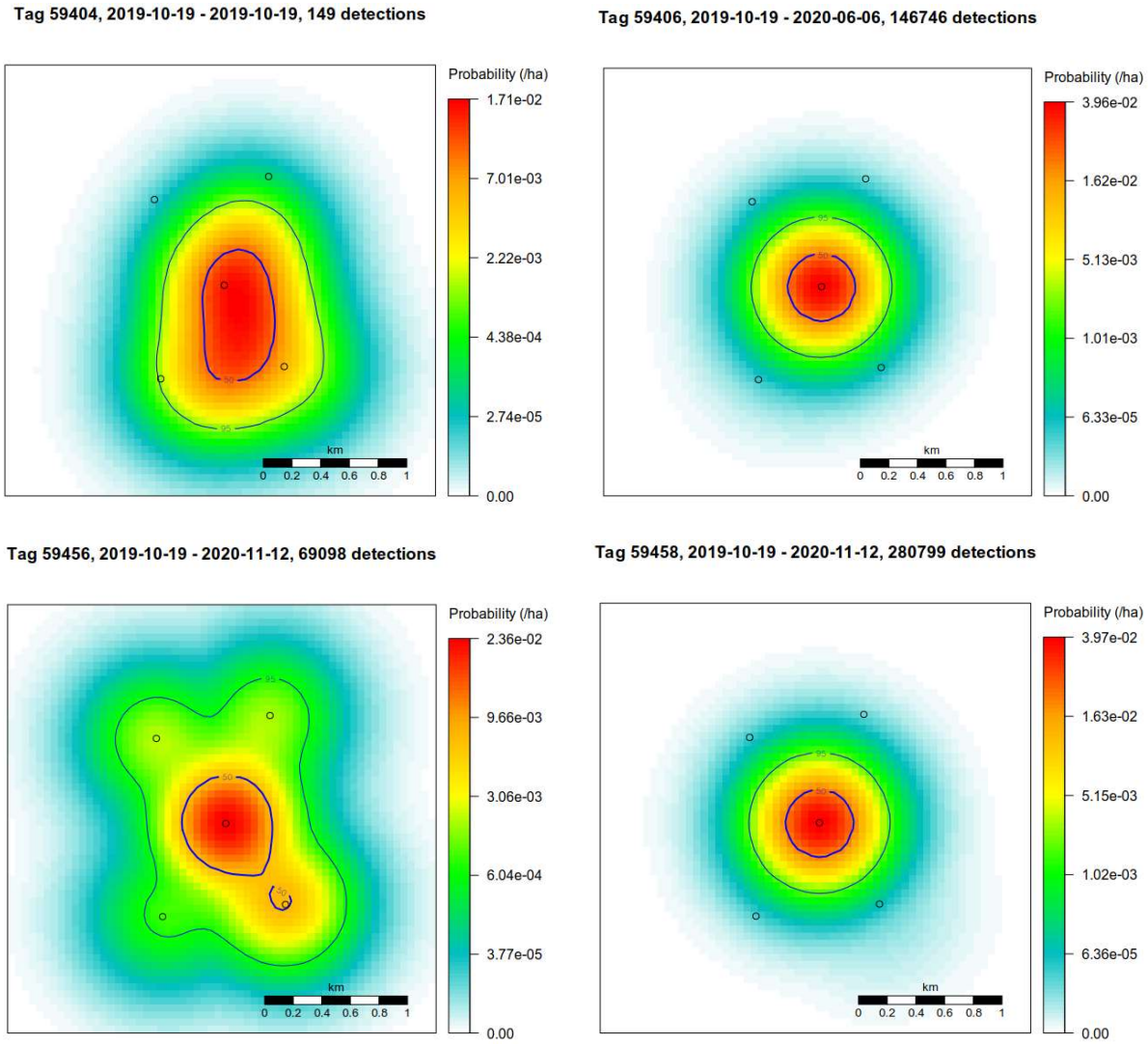

Figure 44: Activity space estimates from fixed kernel utilisation distributions (KUD) for four of the Pearl Perch tagged with Vemco V13 tags on 19 October 2019. The five small hollow circles represent the locations of the five receivers. The middle receiver was deployed in the middle of the aggregation. The thick blue line and thin blue line represent the 50% and 95% contour areas, respectively. The detection span and number of detections are shown above each plot.

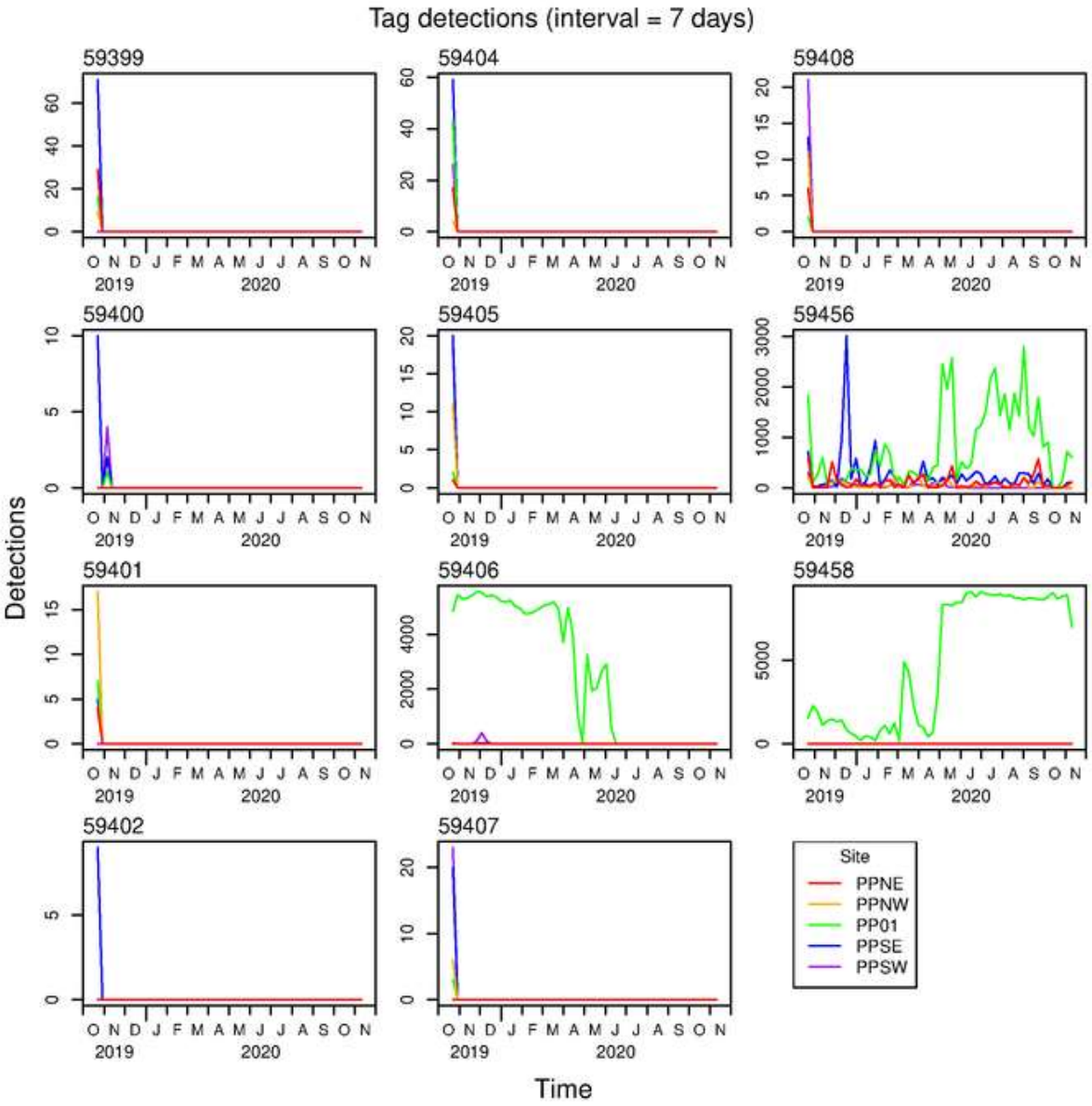

Figure 45: Tag detections for 11 Pearl Perch tagged in October 2019. Each panel represents a fish tag number and the lines on each graph correspond to a receiver in the array which detected each fish: north-eastern, north-western, middle, south-eastern, and south-western (see Figure 44 for locations of each receiver within the array).

Appendix 4 – Rocky Reef Working Group minutes

The minutes from Rocky Reef Working Group, convened on the 13 and 14 of July 2021 are presented below and a communique of meeting outcomes can be found at https://www.daf.qld.gov.au/business-priorities/fisheries/sustainable/fishery-working-groups/rocky-reef-working-group/communiques/communique-13-14-july-2021.

The following minutes were Animal Science Queensland provided an update on a research project assessing the spawning characteristics and reproductive biology of pearl perch in Queensland. Gonad samples were obtained through the fishery monitoring program and fishery independent samples collected under research permit. The project assessed GSI data and gonad stage. This project provided the first evidence of a "ripe" gonad while noting stage 4 gonads were prevalent through the year. Fish in stage 4 condition were found to the north and east (Swains' region) as well as in the south. Spawning may be peaking between 1st quarter and the full moon which aligns with high catch rates in the fishery.

Results suggest that pearl perch are likely to be serial spawners and have a prolonged spawning period across several months (North between Aug–Mar peaking in Oct - Nov; South between Mar–Aug). Further work is being undertaken on spawning locations and larval dispersion, but preliminary results suggest that pearl perch do not move much between sites, particularly as larger or older fish.

Fish were tagged using conventional and acoustic tags and monitored using an acoustic array and through recaptures. Of 3129 tagging records, only 2% have been recaptured. This is a low rate of recapture which is normally around 8-10%. Most recaptures indicate movement of less than 2km with 6 or 7 having moved more than 10km. 275 genetic samples have also been collected from fish between Innisfail and Coffs Harbour to help refine our understanding of the species east coast stock.

The working group identified and discussed the need for a separate spawning closure for pearl perch noting the northern population does not spawn during the current closure period. The working group discussed the value of having separate pearl perch closures (north and south) noting the population in the south was more depleted than the north. However, sampling in the north has already indicated a lower average size of fish being caught from that spawning aggregation.

Concern was raised that there are three closures already for commercial fishers north of Frazer with the Snapper spawning closure, and two coral reef fin fish closures. Consideration needs to be given to the cumulative impact of these closures on business operation and continuity.

Appendix 5 – Media release

Queensland Government

Department of Agriculture and Fisheries

Media Release

30 July 2019

Where do Pearl Perch spawn?

Recreational, charter and commercial fishers are invited to donate Pearl Perch fish frames as part of a study into better understanding the species' spawning habits.

Project leader and Department of Agriculture and Fisheries (DAF) scientist, Matthew Campbell said the Department was working to find out more about the reproductive biology of Pearl Perch with very few spawning fish caught in traditional fishing grounds.

"We do know that spawning occurs at the northern end of their range near the Swain Reefs area and in the deeper waters off Fraser Island," he said.

"Fish in spawning condition have also recently been caught in deep water offshore from the Sunshine Coast.

"As part of our research, we want to collect Pearl Perch from these and other areas to better understand the location and timing of spawning.

"We'll be doing our own field trips to collect Pearl Perch, but we encourage fishers to help us out by donating their own fish frames.

"The frames allow us to assess important information such as maturity, spawning activity and growth.

"We'll also be tagging spawning Pearl Perch to determine movement to and from spawning locations.

"Previous research suggests Pearl Perch may migrate to spawning areas and by using tagging and acoustic tracking we can test this theory."

To donate a Pearl Perch fish frame, please record a general location and water depth of capture and contact (DAF) on 13 25 23 to arrange collection.

Results of this research will help improve our knowledge of Pearl Perch which is currently classified as depleted.

The project is a partnership between DAF and CSIRO, and is co-funded by the Federal Government's Fisheries Research and Development Corporation.

Figure 46: Project-related post that appeared on the Fisheries Queensland Facebook page on 30 July 2019.

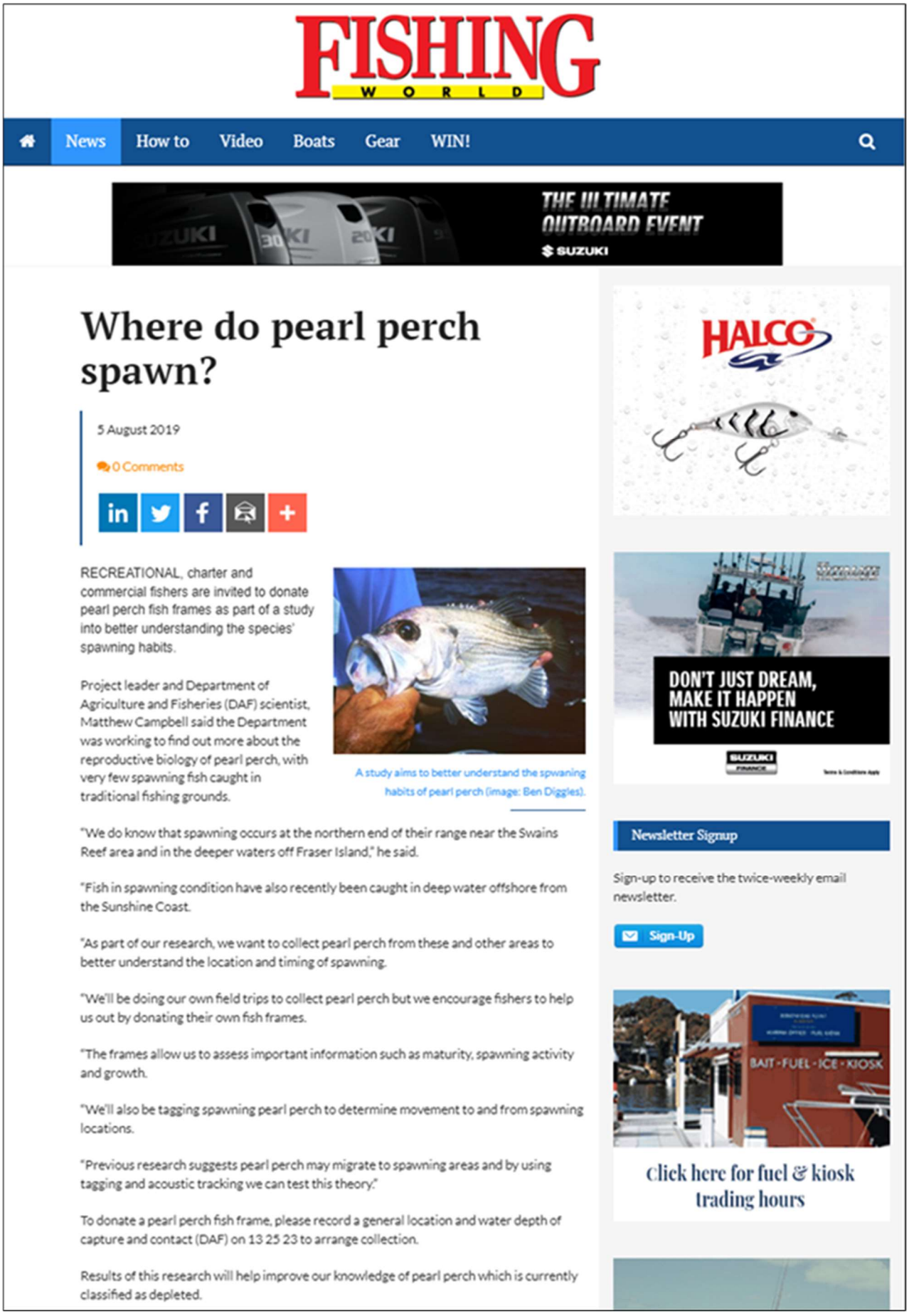

Figure 47: Screenshot of the article, based on the media release, posted on the Fishing World website on 5 August 2019.

Appendix 6 – Project pamphlet

The pamphlet below was placed in fishing tackle shops to generate interest in the project.

Appendix 7 – Keen Angler Program newsletter

Project staff contributed to the Keen Angler Program newsletter in November 2020, to promote the project's objectives and some preliminary results. Below is an excerpt from the newsletter.

Target species

Inshore and estuarine species:

- yellowfin bream (*Acanthopagrus australis*)
- sand/summer whiting (*Sillago ciliata*)
- dusky flathead (*Platycephalus fuscus*)
- tailor (*Pomatomus saltatrix*)
- mulloway (*Argyrosomus japonicas*)
- king threadfin(*Polydactylus macrochir*)

Rocky reef:

- snapper (*Chrysophrys auratus*)
- pearl perch (*Glaucosoma scapulare*)

Coral reef:

- red emperor (*Lutjanus sebae*)
- largemouth nannygai/ saddletail snapper (*Lutjanus malabaricus)*
- smallmouth nannygai/ crimson snapper *(Lutjanus erythropterus)*
- spangled emperor (*Lethrinus nebulosus*)

Mackerel:

- spotted mackerel (*Scomberomorus munroi*)
- Spanish mackerel (*S. commerson*)
- school mackerel (*S. queenslandicus*)

Research snippets

School mackerel monitoring

Andrew holds up a school mackerel

Fisheries Queensland has been collecting biological information from school mackerel harvested by the recreational sector via boat ramp survey since 2013. A 2019 stock assessment found the southern stock was sustainable, and recommended biological monitoring be expanded to the commercial fishery. In January 2020, Fishery Monitoring staff began collection biological information from commercial fishers and seafood processors, to combine that with frames collected from KAP program. If you catch and keep school mackerel (even if it is one) we want your frames!

Pearl perch project

DAF research scientists are part-way through a research project to investigate aspects of the spawning biology of pearl perch in Queensland.

The project, a collaboration between DAF and the Commonwealth Scientific and Industrial Research Organisation (CSIRO), is co-funded by the Federal Government's Fisheries Research and Development Corporation (FRDC).

DAF researcher, Mark McLennan, with a large pearl perch caught off Fraser Island.

Previous research revealed that very few spawning fish occur on the traditional fishing grounds offshore of Brisbane and the Sunshine Coast. Spawning fish are more likely to be found offshore from Fraser Island and in the Swains Reef area. DAF research staff have been collecting pearl perch from recreational and commercial fishers fishing these and other areas to determine the location and timing of spawning.

Results to date indicate that pearl perch are spawning in deep water (~200 m) offshore from the Sunshine Coast/Fraser Island area September and October. Spawning aggregations of pearl perch have been located in these areas by DAF research staff.

Interestingly, spawning appears to occur later in October and November around the Swains Reef, indicating that fish in this area may be part of a sub-population. DAF research scientists will examine this using modern genetic techniques. Keen anglers can participate in this research by providing frames with the gut intact, allowing researchers to examine the gonads and assess reproductive activity.