FRDC FINAL REPORT

ESTABLISHING FINE-SCALE INDUSTRY BASED SPATIAL MANAGEMENT AND HARVEST STRATEGIES FOR THE COMMERCIAL SCALLOP IN SOUTH EAST AUSTRALIA

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Establishing fine-scale industry based spatial management and harvest strategies for the commercial scallop fishery in South East Australia.

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TABLE OF CONTENTS

List of figures

List of tables

2008/022: Establishing fine-scale industry based spatial management and harvest strategies for the commercial scallop fishery in South East Australia

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OBJECTIVES

1. Determine the broad- and fine-scale population linkages and stock status of commercial scallops (*P. fumatus*) in SE Australia.

2. Evaluate the effects of intensive rotational dredge fishing on scallop beds and scallop recruitment events.

3. Examine the importance of scallop density (spawner biomass) on synchronisation of spawning and recruitment success

1. NON-TECHNICAL SUMMARY

OUTCOMES ACHIEVED TO DATE

Objective 1:
Adoption of harvest strategies by all three jurisdictions of the commercial scallop fishery that sufficiently take in to account small- and large-scale population linkages and stock structure. If it is shown that there is only one stock in SE Australia, then a uniform harvest strategy across all three jurisdictions would be adopted.

Our findings demonstrated that the south east Australian commercial scallop population has a genetically homogeneous single population which largely allows for a uniform harvest strategy to be adopted across all three jurisdictions. However, there was some evidence of population structure within Bass Strait, which has implications for management of apparently genetically-linked populations in separate management jurisdictions. There has been some discussion at the jurisdiction level on how best to take in to account the genetic structuring within Bass Strait in order to increase the probability of recruitment. However, this has yet to be formally incorporated into any of the three harvest strategies and we are still not at the stage where there is a uniform harvest strategy across jurisdictions. In 2014 the Commonwealth moved to a 'little closed most open harvest strategy' for the Bass Strait Central Zone Scallop Fishery (BSCZSF), which sets it apart from Tasmania, but is more similar to Victoria.

Objectives 2 & 3:
Development and implementation of a risk-based assessment approach to the rotational fishing harvest strategy, which minimises the risks to adult spawner stock

and scallop communities.

With a view to development and implementation of a risk-based assessment approach to the rotational fishing harvest strategy, this study explored the effect of dredging activities on the benthic community within the fishing grounds of the BSCZSF. Abundance of all captured species (commercial scallop and all by catch) comprising the communities did not differ significantly between fished and non-fished areas in the regions examined. The total number of species and species richness did not differ significantly either. This suggests that the rotational fishing harvest strategy has a relatively low short- to medium-term impact on the benthic communities within the fishing grounds of the BSCZSF.

In accordance with research in other benthic molluscs we found a strong indication that the density of recruits is related to the density of adults in the previous year. In the areas studied, recruit density increased by between 2 and 10 times for every single unit of adult density prior to spawning. The density of adult spawners also has an impact on the level of synchronicity between spawning adults. This study showed a difference in spawning intensity and synchronisation between sites of high and low densities, and suggests that maintaining dense areas of adult scallops may increase the probability of recruitment, through increased spawning intensity. As such, development and implementation of a best-practice risk-based approach to the rotational fishing harvest strategy, which minimises the risks to adult spawner stock, would incorporate the protection of high density scallop beds in some manner. To this end, the protection of dense scallop beds has been incorporated into the 2014 Commonwealth Harvest Strategy, with at least part of the densest bed found during surveys closed to fishing during the season. Further work is needed to define optimal scallop densities required to maintain a range of biomass levels, but this is the ultimate aim.

Spatial management of the scallop fishery requires adequate information on the stock to ensure the implementation of appropriate management decisions. In addition to abundance and population data used for management decisions more information is needed to improve management of the commercial scallop (*Pecten fumatus*) resource.

The south east Australian commercial scallop fishery is divided into three jurisdictions, with spatial scale and specific rulings differing between them. Management decisions within one jurisdiction have the potential to affect the stock and stock recruitment in the other jurisdictions. Cross-jurisdictional interaction is more likely if the three fisheries are targeting a single biological stock.

Substantial recruitment events are the principal drivers of the fishery and a deeper understanding of the recruitment dynamics of scallops is essential. Variability in these recruitment events is due to a variety of interconnected factors that affect the density of adult spawner biomass. Both fishing and indirect effects of fishing activities such as modification of the benthic environment due to dredging can affect adult the spawner biomass. In addition the management strategies in the different jurisdictions may also play a part, especially if biological populations are not wholly contained in a single jurisdiction.

Delineation of biological stock requires information on population connectivity. This project focused on genetic stock structure as a useful proxy for a demographically cohesive unit because genetic differences between regions imply a limitation to dispersal.

Our findings showed the south east Australian commercial scallop population has a genetically homogeneous single population. There was however some evidence of population structure within Bass Strait. Significant, but slight differences in genetic structure between beds do occur in Bass Strait, which may have significant implications for management of apparently genetically-linked populations that occur in separate management jurisdictions.

Evidence from this study suggested that these differences may be due the effect of ocean gyres that exist in the Bass Strait and may force self-recruitment of certain beds and genetic separation from the general population of the scallops in the Strait. It is important to note that these differences may be due to genetic drift rather than spatial barriers to cross bed recruitment.

With a view to ensuring the ecological sustainability of the scallop fishery this study explored the effect of dredging activities on the benthic community within the fishing grounds of the Bass Strait Central Zone Scallop Fishery (BSCZSF). Industry-based dredge surveys were conducted in several areas of the BSCZSF before and after the areas were opened to fishing. Abundance of all species (commercial scallop and all by catch) comprising the communities did not differ significantly between fished and non-fished areas in the regions examined. The total number of species and species richness did not differ significantly either. This suggests that scallop dredging has a relatively low short- to medium-term impact on the benthic communities within the fishing grounds of the BSCZSF.

In accordance with research in other benthic molluscs we found a strong indication that the density of recruits is related to the density of adults in the previous year. In the areas studied recruit density increased by between 2 and 10 times for every single unit of adult density prior to spawning. However the patterns of recruit density did not equate to high levels of successful recruitment into adulthood. Numbers of recruits dropped significantly over the course of the year and most recruits did not survive to adulthood.

The density of adult spawners does have an impact on the level of synchronicity between spawning adults. This study showed a difference in spawning intensity and synchronisation between sites of high and low densities, and suggests that maintaining dense areas of adult scallops may increase the chances of recruitment, through increased spawning intensity.

Overall, the results of this study have significant implications for the sustainable management of south east Australian commercial scallop fisheries and greater continuity between jurisdictional harvest strategies.

KEYWORDS: Commercial scallop; *Pecten fumatus*; fisheries management; spatial management; rotational harvest; microsatellites; fisheries stocks; population linkages; spawner biomass; recruitment; effects of fishing

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3. BACKGROUND

Spatial closures can be used as a management tool to provide: 1) increased protection from fishing and consequent increased abundance and mean size of exploited species; (2) enhanced local reproductive potential and therefore increased likelihood of larval export to the surrounding fishing grounds; and (3) protection of associated benthic communities and habitats (e.g. Ward *et al*. 2001; Gell and Roberts 2003; Halpern 2003; Beukers-Stewart *et al*. 2004). The major conclusion of FRDC 2003/017 "Juvenile scallop trashing rates and bed dynamics: testing the management rules for scallops in Bass Strait" was that spatial closures in the management of commercial scallop (*Pecten fumatus*) stocks, where the majority of the fishery is closed to fishing and only small discrete regions of the fishery are opened to harvesting, offers a real prospect for providing continuity and sustainability for the fishery (Haddon *et al*. 2006), especially when compared to conventional management (e.g. large area open and only a small area closed).

FRDC 2003/017 also identified the very extensive data/stock information requirements of closed area spatial management (see Haddon *et al* 2006; Harrington *et al*. 2008). Without credible up-to-date stock information, scallop beds cannot be opened to harvesting, within season contingency plans cannot be formulated, and longer term harvest strategies cannot be developed. This type of longer term information and planning is essential in creating a level of certainty within the catching sector (industry), which in turn allows the development of processing infrastructure and domestic and export markets. FRDC 2005/027 "Facilitating industry self-management for spatially managed stocks: a scallop case study" established the capacity for industry to contribute to the organisation and implementation of surveys at both the scale of the fishery, and the scale of individual scallop beds. The size structure and abundance data that is obtained during such surveys can be used by management to meet decision rules allowing the successful implementation of detailed spatial management strategies within the fishery.

FRDC 2003/017 and 2005/027 have provided a compelling argument for the spatial management of scallop fisheries in Australia using 'fishery closed areas' and industry-based voluntary rotational harvest strategies or 'paddock fishing'. Despite the obvious positives of spatial management for scallop fisheries, significant recruitment events are still the limiting factor in the commercial scallop fisheries, and we have no understanding of the impacts of this fishing method on the recruitment dynamics of scallops. There may be many reasons for this recruitment variability, such as differences in jurisdictional management strategies, particularly if it is one biological stock; the influence of the density of adult spawner biomass on recruitment; and the ecological effect of fishing on scallops and the benthic environment.

This study addresses a number of these fundamental questions, which are essential to the implementation of fine-scale spatial management of this resource, and which will contribute significantly to the understanding of sustainability. It will also assist with the development of the Commonwealth scallop harvest strategy and the rationalization study (see Sen 2011), which is examining options for improving management of the commercial scallop resource in south east Australia.

The south east Australian commercial scallop resource comprises three separate jurisdictions. The spatial scale of the harvest strategies, and specific decision rules applied within each jurisdiction are different (particularly between Victoria and the two other jurisdictions), and the application of rules and strategies on specific scallop beds depends purely on their location relative to the jurisdictional boundaries. Under this management arrangement, harvest decisions, strategies and rules applied within one jurisdiction have the potential to have either a negative or positive influence on the overall stock availability and recruitment success within other jurisdictions. The possibility of such cross-jurisdictional interaction is highly likely if the three fisheries target the one biological stock (i.e. there is a high level of mixing between the three jurisdictions).

Stocks represent demographically cohesive groups of conspecific individuals (Dizon *et al.*, 1992; Moritz, 1994; Begg and Waldman, 1999) and in the management of wild fisheries the accurate definition of a 'stock' is essential. By definition, changes to stock size are largely a function of recruitment, mortality rates (natural and fishing) and individual growth, not immigration and emigration. Thus, stocks represent natural management units because a relationship between productivity under various rates of harvest can be established.

Stock delineation requires an understanding of population connectivity to exclude the effect of immigration and emigration, which is inherently difficult to achieve in marine environments. Fisheries managers have utilized genetic approaches to stock definition for over fifty years (e.g. Ryman and Utter, 1987). Genetic differences among samples collected throughout the range of the putative stock are readily estimated through assays of genetic markers such as microsatellites. Genetic stock structure is a useful proxy for a demographically cohesive unit because genetic differences between regions imply a limitation to dispersal (e.g. Ovenden *et al.*, 2004; Dethmers *et al.*, 2006; Ward *et al.*, 2006; Ovenden *et al.*, 2009).

Counting progeny that have parents outside the target population (e.g. Christie *et al.*, 2010; Saenz-Agudelo *et al.*, 2011) can test limits to dispersal that are assumed from conventional genetic analyses of stock structure. This relatively new set of genetic methods can identify family groups in naturally occurring species and is possible due to the availability of large numbers of genetically variable loci (e.g. microsatellites and single nucleotide polymorphisms, SNP), the ability to cheaply assay large numbers of samples, and new statistical analysis frameworks. These methodologies can potentially also assess within-stock recruitment patterns, which is important because lack of knowledge about recruitment can be a major bottleneck to effective fisheries management.

Marine species with long larval periods like scallops (~ 30 days for *P. fumatus*, Young *et al.*, 1989) are typically assumed to have widespread dispersal and exist as spatially-extensive populations that exhibit minimal genetic population structure (Cowen, 2000). Using allozyme genetic techniques (Woodburn, 1988) appeared to confirm this assumption, demonstrating a low level of genetic divergence between populations of *P. fumatus* in south eastern Australia, particularly in Bass Strait. However, the assumption of widespread dispersal and random distribution of marine larvae has been challenged. There are many examples of genetic population structure in marine teleosts with pelagic larvae (e.g. Kovach *et al.*, 2010; Broderick *et al.*, 2011).

Southern Australian and Tasmanian abalone (*Haliotis rubra*) are an excellent example of an invertebrate species with pelagic larvae that have pronounced genetic stock structure (Miller *et al.*, 2009). Although recruitment from adjacent beds is assumed to be common in *P. fumatus* because larvae exist in the water column for approximately one month and can be passively advected over long distances by water currents during that time, self-recruitment is also thought to occur because beds occur within embayments (e.g. Port Phillip Bay, D'Entrecasteaux Channel – herein referred to as the 'DEC') that experience little water exchange.

Microsatellite DNA loci undergo relatively rapid mutation rates that lead to high levels of polymorphism. Consequently, microsatellite genetic techniques are a useful tool for fine-scale population discrimination in marine animals. Using microsatellite markers, Campanella *et al.* (2007) were able to demonstrate that bay scallops (*Argopecten irradians*) in Barnegat Bay, New Jersey, arose in 2004 from larvae transferred by currents down the Atlantic coast from Long Island, New York, instead of North Carolina. To date microsatellite loci have not been applied to identify family groups in wild populations of scallops. Li and Li (2011) used microsatellite markers to assess mating systems and reproductive success in bay scallops (*A. irradians irradians*). Microsatellite markers are regularly used for determining parentage in captive bred fish populations (e.g. Gold *et al.*, 2010), and have been used for defining families of lobsters in the wild (e.g. Bailie *et al.*, 2011).

Testing the assumption that commercial scallops within south eastern Australia constitute one stock has been a common topic of discussion at the level of the Tasmanian scallop FAC and Commonwealth scallop RAG/MAC for several years. Fishers and managers from all three jurisdictions (Victoria, Tasmania and the Commonwealth) expressed great interest in determining the population stock status of the species throughout its commercial fishery range. Such work is essential for any unification of harvest strategies across all jurisdictions and simplification of the jurisdictional arrangements for the scallop fishery under a rationalisation plan. If either a single stock or stock-structuring between beds in separate jurisdictions exists, management organisations will need to incorporate other jurisdictions in their decision-making processes. A greater level of communication and synchronisation of harvest strategies between jurisdictions will provide a better prospect for continuity and sustainability of the scallop resource and financial returns to fishers throughout southern Australia.

The allozyme study of Woodburn (1988) confirmed the species identity of Australian *P. fumatus*, but it lacked the power to elucidate population structure on a finer scale: a scale more relevant to fisheries managers. This study expands on this allozyme study by using more powerful genetic markers (microsatellite loci) applied to samples taken from major fishing grounds in Bass Strait, Victoria and Tasmania. We also take advantage of the power of the genetic markers to identify parent-offspring pairs to test the expectation that scallop beds in embayments (Port Phillip Bay, Victoria and DEC, Tasmania) experience self-recruitment. A preliminary examination of the potential influence of ocean currents on population connectivity was also undertaken using bio-physical modelling.

One of the most common types of reproduction in marine invertebrates is broadcast spawning: individuals release gametes (eggs and sperm) into the water column where

fertilization occurs. When any organism releases gametes into the sea the chances that a single spermatozoan finds and fertilizes an egg is very low. Dilution of gametes in the sea and the relatively short lifespan of sperm are among the factors that influence fertilization success (Levitan, 1995; Pennington, 1985). Fertilization success generally increases with higher densities of spawning individuals and greater synchronisation of spawning events as previous studies, mainly on corals, sea urchins and asteroids, have shown (Babcock *et al*., 1994; see Levitan, 1995 and references therein). Despite this evidence, little has been done to investigate the role of density in scallop recruitment success. For relatively sessile organisms such as the commercial scallop *P. fumatus*, high egg production (1.2 X $l0^6$ eggs per spawning event in wild scallops, Heasman *et al*., 1994) may not guarantee successful fertilization if densities are too low, proximities between individuals are too great or if spawning is not synchronous.

In spite of the lack of direct empirical studies, different research approaches have highlighted the association between scallop density and increased probabilities of recruitment. A review on the relationship between spawning stock and recruitment levels showed that, only with some exceptions, high densities of scallop spawning stocks are generally associated with higher recruitment levels (Orensanz *et al*., 2006). For example, a strong correlation between abundance of adult stock and following year recruits was found for the bay scallop fishery in North Carolina, with evidence of recruitment limitation at lower density areas (Peterson and Summerson, 1992). In addition, recent modelling approaches have shown that for marine free-spawners even mild fishing pressure can cause a strong reduction in larval production (Young *et al*., 1999). Maintaining high scallop density regions is therefore considered important for increasing the probability of recruitment occurring, partly due to the improved fertilization rates observed at greater densities (Smith and Rago, 2004).

Synchronous release of gametes of both sexes maximises the likelihood of successful fertilisation and production of larvae. It has been suggested that the degree of synchronisation over the spawning period may be more important to recruitment than actual reproductive production (Langton *et al*., 1987). Approximate synchronisation is achieved by maturation of gonads in response to environmental cues such as temperature and/or food (Cantillanez *et al*., 2005; Lundquist and Botsford, 2011; Simon and Levitan, 2011), while it is believed that precise synchrony relies upon chemical cues from neighbouring conspecifics (Beninger *et al*., 1995) that are detected by specific chemical receptors and communicated to the gonad to induce spawning (Barber and Blake, 2006). Consequently, areas with greater densities of mature, ready to spawn adults would have stronger chemical signals that could result in a higher synchronization of spawning. A study on fine scale distribution of the scallop *Placopecten magellanicus* (Stokesbury and Himmelman, 1993) showed that the majority of scallops were distributed within "clumps" of three or more scallops within beds as an adaptation to increase fertilization success. Even in hermaphrodite individuals, such as *P. fumatus*, inter-individual synchronisation is still very important as self-fertilization has been shown to be detrimental for larval growth and survival in other Pectinids (Beaumont and Budd, 1983; Ibarra *et al*., 1995).

Reducing populations of benthic spawners can lead to a reduction in the number of individuals contributing to the recruitment pool as well as lowering fertilization rates (Wolf, 1993). Young and Martin (1989) underlined a connection between periods of

commercial fishing and recruitment failure in *P. fumatus* scallop beds and suggested a minimum adult density to ensure subsequent recruitment. In this context, this study aimed to determine the importance of scallop density on recruitment success by 1) testing the potential relationship between adult scallop abundance and recruitment intensity 2) determining whether the spatial patterns detectable at the recruitment stage persist into adulthood and 3) testing whether the density of adult spawning stock influences the synchronisation of reproductive maturity and spawning. It is only with this information that detailed spatial and fine-scale management strategies can be refined such that they maximise the probability of recruitment at all scales. This in turn will provide industry with a greater probability for continuity and sustainability of the resource at the species range scale, as well as fishery, regional and bed level spatial scales.

The environmental impact of fisheries is under ever increasing scrutiny at both the government and community level for a number of social reasons. At the level of government, a fishery's impact on the target species, bycatch and associated biota is regularly measured, and fisheries are expected to make every effort to reduce their impact and meet an acceptable level of ecological sustainability. Without such assessment the fishery will not be granted Wildlife Trade Operation approval to export their product. At the level of the consumer, the Marine Conservation Society publish a 'good fish guide', which outlines good and bad fish choices when at the supermarket/fish mongers, which is based on sustainability and impacts of the various fisheries on the environment and ecosystems. Environmental considerations may also influence the sale of a product at the level of seafood suppliers, e.g. scallop processors in Canada are struggling to sell their product to large supermarket chains due to environmental concerns. Subsequently, industry, management and research must determine impacts of particular fisheries and fishing practices on the target species and the broader environment in order to ensure the sustainability of these fisheries and the continuation of local and export markets.

Scallop dredging may impact the benthic community by reducing densities and shifting macrofaunal populations, removing colonial epifauna and reducing habitat complexity, and redistributing grain size of sediments and increasing silt in the water column (see Stokesbury and Harris 2006). Unfortunately studies assessing disturbances caused by scallop dredging against natural disturbance over time are not only difficult, but expensive, and as such they are either uncommon or inadequate (see Stokesbury and Harris 2006). However, FRDC 2005/027 has demonstrated that by using industry vessels and research quota, detailed before and after controlled scallop dredging impact studies can be adequately conducted, with such a study conducted within the White Rock region of the Tasmanian fishery during the 2006 season. Results of the study suggested that intensive fine-scale rotational fishing has an impact on species abundances, but does not remove species or effect sediment distribution and silting to a biologically significant level. This current study aimed to determine the effects of fishing on scallop and population recovery, as well as potential effects on the associated benthic community, within the open coastal waters of the Commonwealth managed BSCZSF commercial fisheries.

4. NEED

The spatial management of scallop fisheries elsewhere in the world has demonstrated the ability of this method to reduce recruitment variation, while increasing production. The implementation of detailed, spatially explicit management regimes in south east Australia offers a greater prospect for sustainability and continuity of the scallop fishery, but as yet there is insufficient information on the ability of the method to ensure adequate recruitment. The long-term continuity and sustainability of the commercial scallop resource is dependent on refining spatial management strategies, such that they are buffered against the impacts of recruitment variation.

Spatial harvest strategies applied within one jurisdiction may be influencing recruitment and harvesting ability within other jurisdictions. Such cross-jurisdictional effects are more probable if the scallop resource constitutes one stock, or if connected stocks are in separate jurisdictions. At finer spatial scales, there have been observations of localised recruitment, which implies regional/bed level self-recruitment. Therefore, detailed spatial management harvest strategies applied to a scallop bed/region may influence scallop recruitment processes. Additionally, research has identified the importance of maintaining high densities of spawner biomass for promoting recruitment over all spatial scales.

Broad- and fine-scale scallop stock structure, spawner biomass density/recruitment relationships, and an understanding of impacts of intensive fishing on scallop communities are needed to refine detailed spatial management/industry fine-scale management harvest strategies, such that they promote recruitment and minimise impacts on the broader environment. This will allow a move towards uniformity of sustainable spatial harvest strategies across the fishery, and simplification of the jurisdictional arrangements between Victoria, Tasmania and the Commonwealth (OCS).

5. OBJECTIVES

1. Determine the broad- and fine-scale population linkages and stock status of commercial scallops (*P. fumatus*) in SE Australia.

2. Evaluate the effects of intensive rotational dredge fishing on scallop beds and scallop recruitment events.

3. Examine the importance of scallop density (spawner biomass) on synchronisation of spawning and recruitment success.

6. METHODS

6.1 GENETIC POPULATION STRUCTURE OF SCALLOPS (*PECTEN FUMATUS*) IN SOUTHERN AUSTRALIA

6.1.1 Methods

Sample collection
Microsatellite genetic techniques were used to explore the population structure of commercial scallops in Bass Strait, and in particular to determine population linkages between and within the three commercial scallop jurisdictions of Tasmania, Victoria and the Commonwealth. *Pecten fumatus* were sampled from either commercial catches or scientific surveys from 18 locations throughout south eastern Australia from May 2008 to October 2009 (Fig. 6.1). To ensure contrast in the data, samples were taken from scallop beds at the extremes (Port Phillip Bay, adjacent to Melbourne in southern Victoria and the DEC, in south-eastern Tasmania) of the study area. We expected these locations to be genetically distinct not only because of the distance between them, but also because they occur within embayments and thus may be largely self-recruiting. Samples were also taken from scallop beds that were closely (e.g. 45km) and more distantly spaced (e.g. hundreds of kilometres). Biological information was also collected for the scallops sampled for genetics and included shell size.

For each scallop, approximately 200 mg of abductor muscle tissue was dissected and preserved in 1 ml of salt (NaCl) saturated solution containing 20% dimethyl-sulphoxide (DMSO). Sample vials were air freighted to the Molecular Fisheries Laboratory for DNA extraction and storage at -80°C.

Microsatellite locus discovery and primer design
New microsatellite loci for this study were discovered from the nuclear genome of *P. fumatus*. A large amount of high quality genomic DNA was extracted from two individuals and sent to the Savannah River Ecology Laboratory, Aiken, South Carolina, USA[1]. Extracted genomic DNA consisted of fragments greater than 12 kb in length and the concentration of the DNA in 200 µl of TE buffer was approximately 50 ng/µl. Microsatellite loci were isolated and primers were designed according to Peters *et al*. (2009). Loci were assessed for degree of polymorphism on a sub-sample of scallops and fifteen loci were selected for genotyping in the Molecular Fisheries Laboratory in Brisbane (Appendix 3A).

[1] http://www.srel.edu/microsat/Microsat_DNA_Development.html

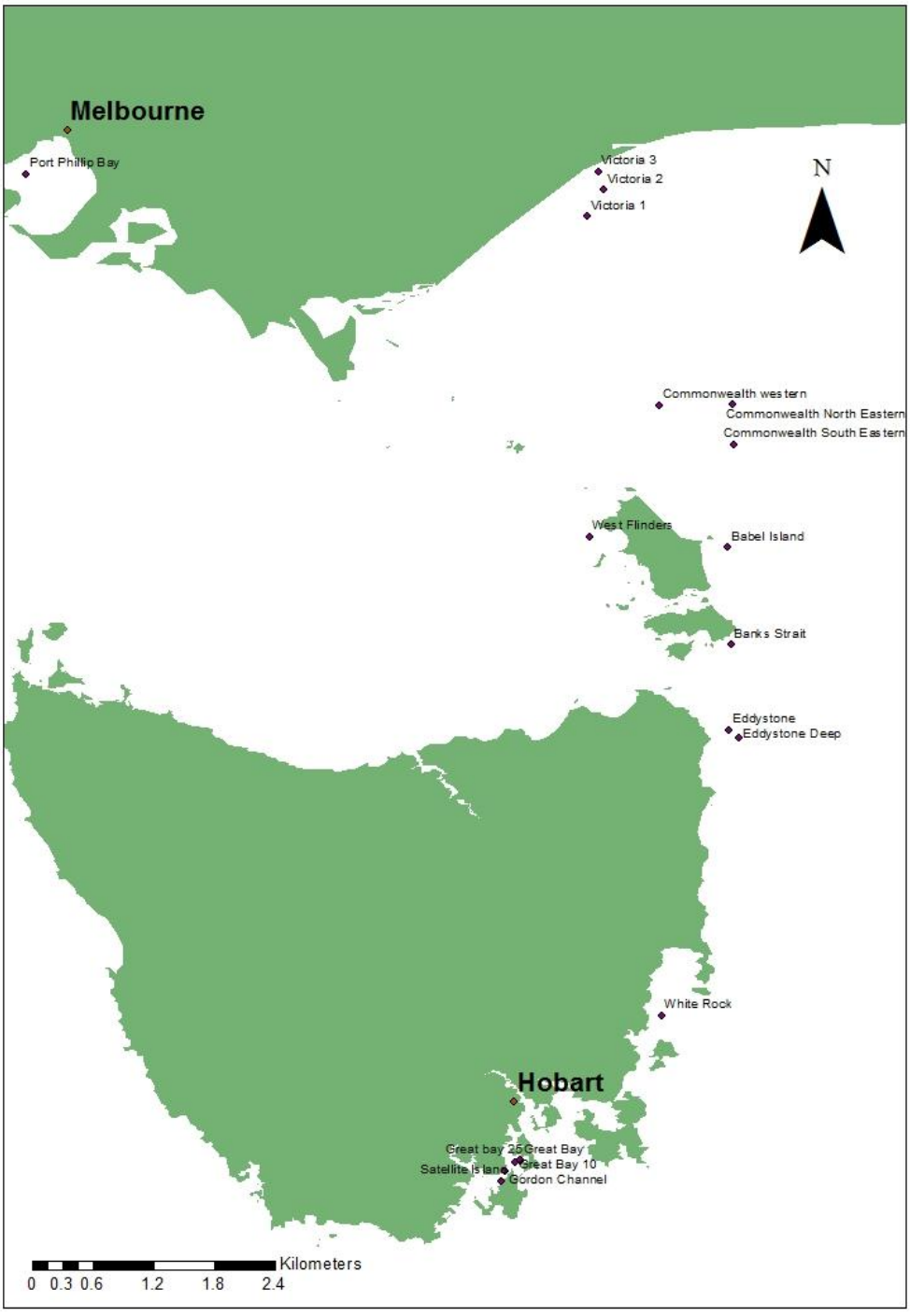


Figure 6.1. Map showing sampling locations of scallop beds surveyed for this study: Satellite Island (-43.3177, 147.2373), Gordon Channel (-43.2655, 147.2580), Great Bay 10 (-43.2204, 147.3113), Great Bay 25 (-43.2112, 147.3357), Great Bay (-43.2063, 147.3348), White Rock (-42.4478, 148.0732), Eddystone Deep (-40.9974, 148.4815), Eddystone (-40.9569, 148.4291), Banks Strait (-40.5095, 148.4376), Babel Island (-39.9996, 148.4197), West Flinders 2 (-39.9437, 147.6982), Commonwealth south eastern (-39.4608, 148.4506), Commonwealth western (-39.2584, 148.0644), Commonwealth north eastern (-39.2482, 148.4443), Victoria_1 (-38.2682, 147.6889), Victoria_2 (-38.1290, 147.7755), Victoria_3 (-38.0352, 147.7426) and Port Phillip Bay (-38.0479, 144.7542).

Genomic DNA extraction
For microsatellite genotyping, genomic DNA was extracted from 10 - 50 mg of the tissue from each individual scallop in deep 96-well plates. Samples were digested in 400 µl of a suspension of 20% Chelex-100 (w/v) in TE buffer (10 mM Tris, HCl pH 8.0, 1 mM EDTA) plus 400 µl Proteinase K (0.4 mg/ml) also in TE buffer. The tissue was digested to completion at 56ºC for three hours or overnight on a shaking platform. Plates were vortexed before centrifugation at 4000 rpm for 30 minutes to precipitate the Chelex resin and cellular debris. Two hundred µl of the supernatant was removed to fresh plates using a pipetting robot (Corbett Robotics). The plates were then heated in a Perkin Elmer (Waltham, MA, U.S.A.) 9600 or 9700 series thermocycler for three mins at 98ºC, bench cooled and stored at 4ºC for subsequent manipulation.

Microsatellite genotyping
Fifteen microsatellites developed specifically for *P. fumatus* were suitable for high throughput genotyping. An Eppendorf Motion 5075 platform was used to set up the microsatellite PCR amplifications, which were performed in 96-well plates using PerkinElmer (Waltham, MA, U.S.A.) 9600 & 9700 series thermocyclers. PCR reactions using a QIAGEN® (Hilden, Germany) Multiplex PCR Kit (6 µl) contained 3 µl of 2xMaster Mix, 0.6 µl of 5xQ solution, 0.2 µM tagged primer and 1 µM untagged primer, 1 µM fluoro-labelled CAG primer and approximately 10 ng of genomic DNA template. One primer from each pair was modified on the 5' end with an engineered sequence (CAG tag, 5'-CAGTCGGGCGTCATCA-3') to enable use of a third primer in the PCR that was fluorescently labelled (ABI) for detection (Schuelke, 2000). The DNA template and enzyme were denatured at 94^{o}C for 15 minutes, followed by 35 cycles consisting of 94^{o}C for 30 seconds, 57^{o}C for 45 seconds and 72^{o}C for 90 seconds. A final extension at 72^{o}C for 45 minutes was used to ensure complete addition of adenine to the PCR product, essential for consistent allele calling during genotyping. Compatible loci were amplified in multiplexed PCR reactions and all products were combined for gel separation on a Life Technologies™ (Carlsbad, CA, U.S.A.) ABI™ 3130*xl* Genetic Analyser located in the Molecular Fisheries Laboratory. Positive and negative extraction and PCR controls were used throughout and genotypes were scored and binned using Life Technologies™ Genemapper™ 3.7 software.

Data Analysis

Genetic population structure
Microsatellite data was used to test the expectation of the absence of population genetic structure within or between the sampled beds of scallops. GenAlEx 6 (Peakall and Smouse, 2006) was used to calculate a range of population genetic statistics including the number of samples genotyped, number of alleles per locus, number of effective alleles, information index, expected heterozygosity (H_E) and observed heterozygosity (H_O).

Tests for isolation by distance (IBD), Hardy Weinberg equilibrium, null alleles and linkage disequilibrium were computed using Genepop v 4.0.7 (Rousset, 2008). For linkage disequilibrium tests, the number of batches in the Markov chain was set to

1000 to achieve standard error of *p*-values of 0.01 or less. The tests were performed without separating genotypes into separate collection locations.

Population pairwise F_{ST} values (Weir and Cockerham, 1984) and their *p*-values were determined by Fstat v 1.9.3.2 (Goudet, 1995) by choosing options 'Fst per pair of samples' and 'pairwise tests of differentiation' with 1/1000 'nominal level for multiple tests'. Statistical significant levels on pairwise F_{ST} values was set by the Benjamin-Yekutieli false discovery rate (B-Y FDR) method described by Narum (2006), which is less conservative than the conventional Bonferroni correction.

Table 6.1. The datasets and software used for testing hypotheses about scallop population structure and self-recruitment.

Data set	Loci number	Genotypes	Sampling locations	N	Analysed for	
					Population structure	Self-recruitment
D1.dat	15	Complete	17 locations	680	DAPC	MLRELATE
D1All.dat	15	Complete and partial	All	1124	-	-
D2.dat	11	Complete	17 locations	774	DAPC	MLRELATE
D2All.dat	11	Complete and partial	18 locations	1124	Pairwise Fst (fine and broad scale)	-
D3.dat	15	Complete	Five locations within the D'Entrecasteaux Channel (DEC)	214	-	MLRELATE

The sensitivity of DAPC to the presence of four loci out of Hardy-Weinberg equilibrium was tested by analysing datasets containing all loci (D1.dat) and 11 loci (D1All.dat). Pairwise F_{ST} analyses were performed on datasets containing all genotypes to maximise sample size, but only loci in Hardy-Weinberg equilibrium were used. There was one location represented by partial genotypes only; this accounts for the difference in sampling location numbers between D1.dat, D2.dat and D2All.dat.

In addition to the conventional method of detecting population structure using *F*-statistics, we used a multivariate method designed to identify and describe clusters of genetically related individuals (Jombart *et al.*, 2010). This method (discriminant analysis of principle components, DAPC) uses a sequential K-means approach to determine the number of clusters in the data, and then assigns individuals to clusters independently of their collection location. The overall approach was similar to commonly used methodology implemented in the software STRUCTURE (Pritchard *et al.*, 2000; Falush *et al.*, 2003). STRUCTURE uses a Bayesian clustering approach under an explicit population model. Using simulated data (e.g. 30 microsatellite loci, 50 allelic states), Jombart *et al.* (2010) demonstrated that DAPC performed more successfully than STRUCTURE in defining the number of groups and equalled the performance of STRUCTURE in assigning individuals to groups. STRUCTURE was less successful in determining the number of groups when the population model departed from an island model (i.e. towards a stepping stone model). Thus, we chose DAPC over STRUCTURE for analysing scallop microsatellite data where the type of population structure is unknown. DAPC also seemed appropriate as it assumes no

underlying genetic model, which may be more appropriate for mollusc data where microsatellite loci are known to depart from Hardy-Weinberg equilibrium. Discriminant analysis of principal components was performed using the methods of (Jombart *et al.*, 2010) as implemented in R (R-Development-Core-Team, 2011) using package *adegenet*. Subsamples from 1124 fifteen-locus scallop genotypes were created to form two datasets. The first dataset (D1.dat) included only samples that were fully (i.e. no missing allelic determinations) genotyped with all 15 loci (680 genotypes) from 17 locations. The second dataset (D2.dat) also only contained fully genotyped samples, except that genotypes from four loci (Loci A09, PeFu_P1_H11, PeFu_P2_D07, PeFu_P2_C07) shown to deviate from HWE were removed (774 genotypes amongst 17 locations with 11 loci). These two datasets were analysed by DAPC.

The pattern of DAPC clusters in random data was determined for comparison to DAPC analysis of D1.dat and D2.dat. The eleven locus dataset (D2.dat) was used to generate simulated random genotypes using program SHAZA (Macbeth *et al.*, 2011, http://www.dpi.qld.gov.au/28_6899.htm) using a command line:

shaza.exe -1 D2.dat –M 774 –Y 1.00 –p

The '-1' option defines the genotype data file, '-M' defines the number of genotypes to simulate,'-Y 1.00' defines the proportion of missing alleles in the data and the option '-p' is a command to print out the simulated data file. Datasets used for testing hypotheses about population structure are described in Table 6.1.

Recruitment analysis

The general approach taken to detect self-recruitment was to search for related individuals among samples from the same bed. Microsatellite genotypes were used to determine if a pair of scallops may represent a parent and an offspring (where the offspring would have at least one allele from the parent at each genetic locus) or may be siblings (where on average genotypes would share 50% of alleles). Self-recruitment would lead to more parent-offspring or sibling pairs within beds. We expected to find more related individuals in beds within an enclosed embayment (DEC) than in beds from Bass Strait or inshore waters.

The log-likelihood of relatedness was determined between all pairs of genotypes using the software MLRELATE (Kalinowski *et al.*, 2006). For each pair, a single parent-offspring (PO), or full-sibling (FS) or half-sibling (HS) or unrelated (U) relationship was designated based on which relationship gave the highest log-likelihood.

All sets of genetic markers have an upper limit on their power to be able to determine relationships based on genotypes. Even though a relationship may have a high likelihood, the relationships still could be false (Macbeth *et al.*, 2011). This is a common problem for studies of animals breeding in the wild. In this study, we addressed this problem by searching for related pairs in random, simulated datasets where pairwise relationships having higher likelihoods than unrelated likelihoods (if present) would be false. The magnitude of the likelihoods of the random relationships found was used as a guide to assess whether relationships in the empirical data were true or false. Simulated genotypes were generated based on empirical allele

frequencies. The likelihoods of different relationships were determined by MLRELATE among random genotypes from fifty simulated data sets. The simulated data was generated by the software SHAZA (Macbeth *et al.*, 2011) using the following settings:

```
shaza.exe -1 D2.dat –M 774 –Y 1.00 –p
```

for the 11 locus data file (D2.dat), and

```
shaza.exe -1 D3.dat –M 214 –Y 1.00 –p
```

for a 15 locus data file (D3.dat) containing samples from the DEC only with genotypes removed if missing alleles were present.

As a final check we wanted to determine if there was sufficient statistical power to find pairwise relationships in the data if they existed. To check this, we added known pairs of related genotypes to the D3.dat dataset. Two pairs of random genotypes from D3.dat were selected as parents and three genotypes were simulated to correspond to offspring from those parents. The three simulated genotypes represented three full-siblings. This simple design has twelve PO relationships and six FS relationships (Fig. 6.2). Datasets used for testing hypotheses about recruitment are described in Table 6.1.

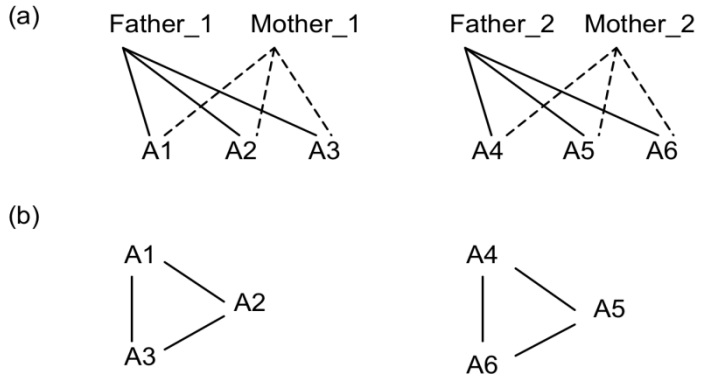


Figure 6.2. Control pedigree of six offspring (A1, A2, A3, A4, A5, A6) showing (a) 12 parent offspring (PO) relationships and (b) six full-sib (FS) relationships.

Preliminary bio-physical modelling to understand population connectivity
In order to better understand the population connectivity (as shown by the genetics) between the commercial scallop beds in the Commonwealth, Tasmanian and Victorian jurisdictions a bio-physical model of larval connectivity was constructed as described below.

Bio-Physical model

To describe the oceanographic features of the model domain, the BRAN2p1 (Bluelink ReANalysis version 2.1) product was used (see http://www.cmar.csiro.au/staff/oke/BRAN.htm). BRAN2p1 is a three dimensional multi-year ensemble optimal interpolation reanalysis applied to a global ocean general circulation with a resolution grading from 2° in the North Atlantic to 1/10° in the Asian–Australian region from 90°E to 180°E, and from 16°N to 75°S (Oke *et al.*,

2008; Schiller *et al*., 2008). For this study we have focused on the 10-20 m two-dimensional layer of the BRAN product, based on the vertical distribution of *Placopecten magellanicus* larvae in the Bay of Fundy (Tremblay and Sinclair, 1988 in Tremblay and Sinclair, 1990) and Georges Bank (Tremblay and Sinclair, 1990). The model domain extends from 120°E to 180°E and from 30°S to 50°S, an area with 1/10° resolution in BRAN. The validity of the BRAN model in representing the regional ocean conditions has been demonstrated elsewhere (Oke *et al*., 2008; Schiller *et al*., 2008).

Each propagule, which represents a single scallop larva in the water column, was advanced through the model domain at six hourly time steps via a Runge-Kutta 4th order integration Lagrangian tracking algorithm applied to the current vectors of the BRAN circulation model and tracked for 30 days (approximate time scallop larvae are in the water column).

To evaluate hindcast scenarios the model was run for 4 annual spawning seasons, from 2004 – 2007. Propagules were released daily from the 1st of August (Julian day = 213) to the 31st of October (Julian day = 303). A total of 30 spawning locations (nodes) were randomly dispersed within a spawning box (Fig. 6.3). From each of these nodes 50 propagules were released on each day. Out of necessity, the spawning boxes were moved away from the coastal area where scallops were collected, as this was very close to the domain where there is no physical data for the model. This was necessary so as to avoid many propagules being excluded from the model, as they would get stuck in these areas with no data following release.

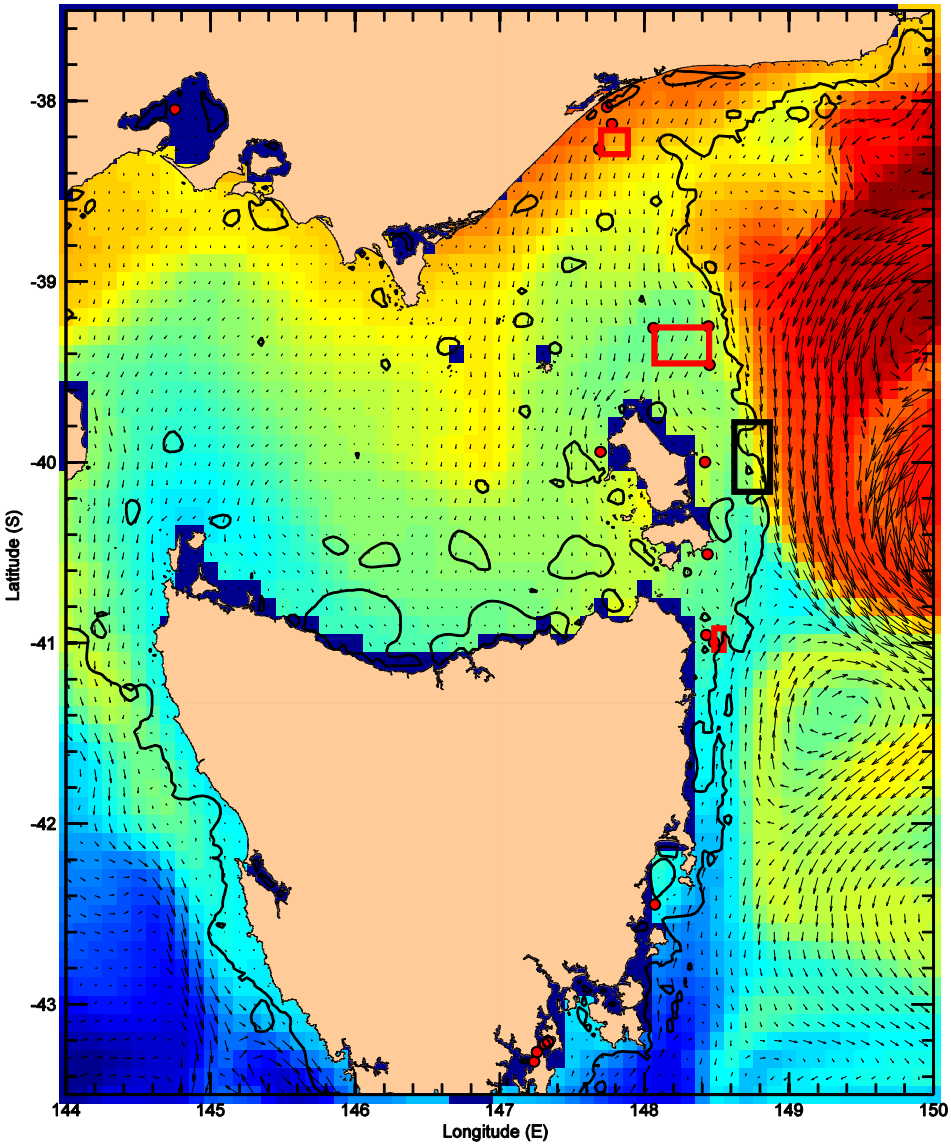


Figure 6.3. The current fields and water temperature (at 10-20 m depth) from the BRAN 2.1 model are shown. The dark blue areas close to the coast indicate areas outside the domain of the BRAN product i.e. no data. The black box east of Flinders Island represents the spawning box from which the 30 spawning nodes were randomly dispersed for the first run of the model. The red dots indicate where scallop samples were collected in 2008/09. The red spawning boxes indicate the position of other spawning boxes from which spawning nodes were randomly dispersed.

6.2 EVALUATE THE EFFECTS OF INTENSIVE ROTATIONAL DREDGE FISHING ON SCALLOP BEDS AND SCALLOP RECRUITMENT EVENTS.

6.2.1 Methods

Study site
A Before-After-Control-Impact (BACI) study was conducted within the eastern region of the (BSCZSF), between Victoria and Flinders Island. There had been no fishing in this region since 2006 due to the closure of the BSCZSF to commercial fishing from 2006 to 2008 by ministerial direction. Prior to 2006 only limited fishing activity had occurred within this region since 1998, due to the low availability of scallops.

The dredge surveys were undertaken in a 1428 km^2 area of the BSCZSF, which consisted of distinct western and eastern zones (Fig. 6.4), herein referred to as WZ and EZ respectively. The WZ scallops were not exposed to commercial fishing pressure in either of the two years examined and provided control sites. The EZ, however, had at least one impacted area exposed to fishing and two undisturbed control areas in each of the two years. The initial 'before' survey (survey 1) was conducted between 19th and 20th May 2009 and surveys were conducted at sites in both the EZ and WZ. Following this, the fishery was opened between 1st June and 31st December 2009, and beds within the southern section of the EZ were fished. All commercial fishing operations within the impacted area had ceased by early October 2009. The second survey, an after dredge impact survey, was conducted within all impacted and control areas over the 16th and 17th October 2009 (Table 6.2). Similarly the surveys in the second year took place before, and after the fishing season (Table 6.2), however the impacted (commercially fished) region was primarily in the northern section of the EZ.

Table 6.2: Dates of the Dredge surveys conducted before and after the scallop fishing seasons in 2009 and 2010.

	Before fishing season	After fishing season	Before limited fishing season	After limited fishing season
Survey	**1**	**2**	**3**	**4**
Dates	19, 20 May 2009	16. October 2009	20, 21 June 2010	19. October 2010

The BACI design assumes that control and impacted areas have similar communities and environmental conditions, and that these communities will change over time in the same fashion, except for any disturbances caused by scallop dredging in the impacted areas. Previous dredge and video surveys suggest that all strata contained similar habitats, dominated by commercial scallops (Haddon *et al*, 2006). Water depths ranged from 39 to 51 meters, with a gradual increase in depth from southern to northern regions. Previous work near the current study site classified sediments as medium to coarse sand (0.25 mm to 1 mm size range) (Haddon *et al*, 2006) and the sediments within the current study area are believed to also fall within this range. Given the relatively close proximity of all sampling sites, each site was believed to be similarly affected by swell and tidal currents.

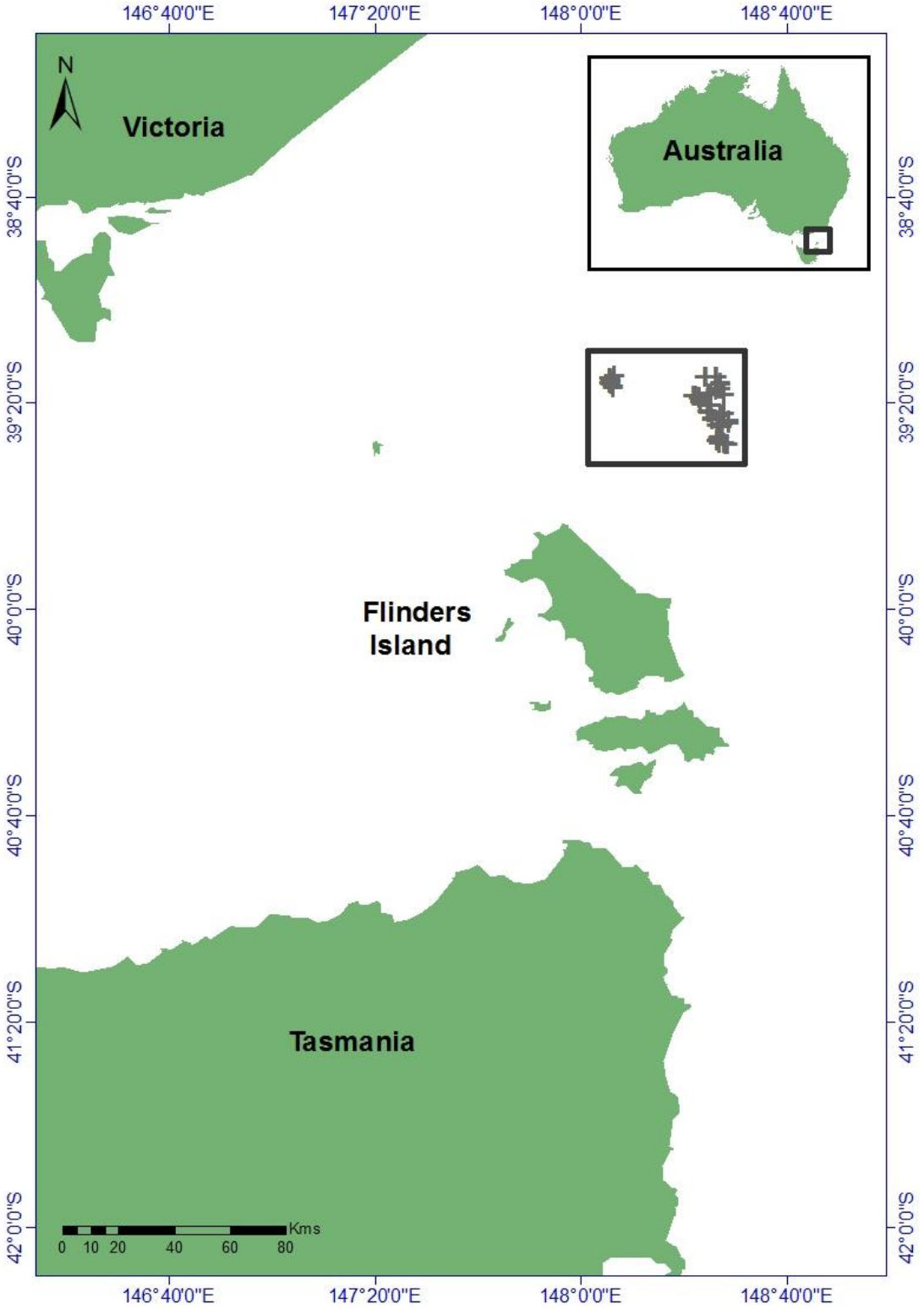


Figure 6.4. Location of the study area and dredge tow locations (+) within the BSCZSF.

Benthic Dredge Surveys

All benthic dredge surveys were conducted on board the FV 'Brid Voyager' using a commercial box dredge (Cover and Stirling, 1994) with a width of 4.2 m and mesh dimensions of 46 x 70 mm. Randomly selected sample sites were undertaken within both the WZ and EZ. A sample dredge tow of approximately 5 minutes duration covering between 450 and 700 meters in length (determined by GPS), was conducted at each sample site at depths of between 39 and 51 metres. All sample tows were conducted on relatively calm days, and sample tow transects were repeated as closely as possible during each survey.

Upon completion of each sample tow, the dredge contents were sorted and all macrofauna identified to the lowest identifiable taxon. Where the abundance of the dredge contents was low all individual taxa were counted. Where abundances of the catch were high a total count was estimated by counting all individuals within a randomly selected subsample and then scaling counts to 100%. To account for variations in the exact tow distance of each sample tow, all abundance estimates were standardised to the relative number caught per $1m^{-2}$ sampled area.

Fishing effort in the number of hours fished obtained from commercial fishing logs was used to give an estimate of the effort for each sample tow (Fig. 6.5) and these levels of fishing effort were expanded from starting tow locations to a circular area with a 1 km diameter (Fig. 6.6).

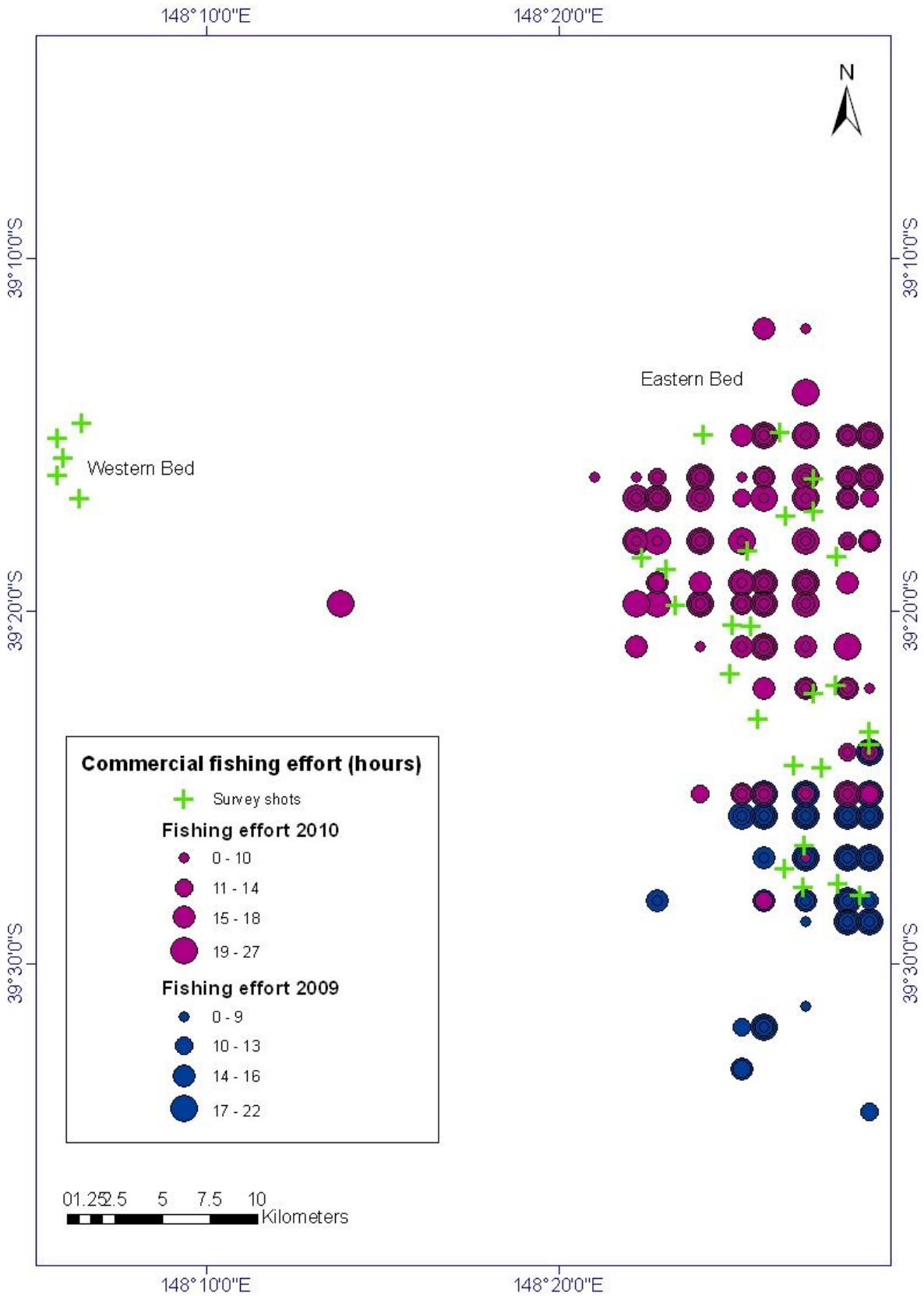


Figure 6.5. Survey dredge shots (crosses) superimposed on areas of commercial fishing effort for 2009 and 2010.

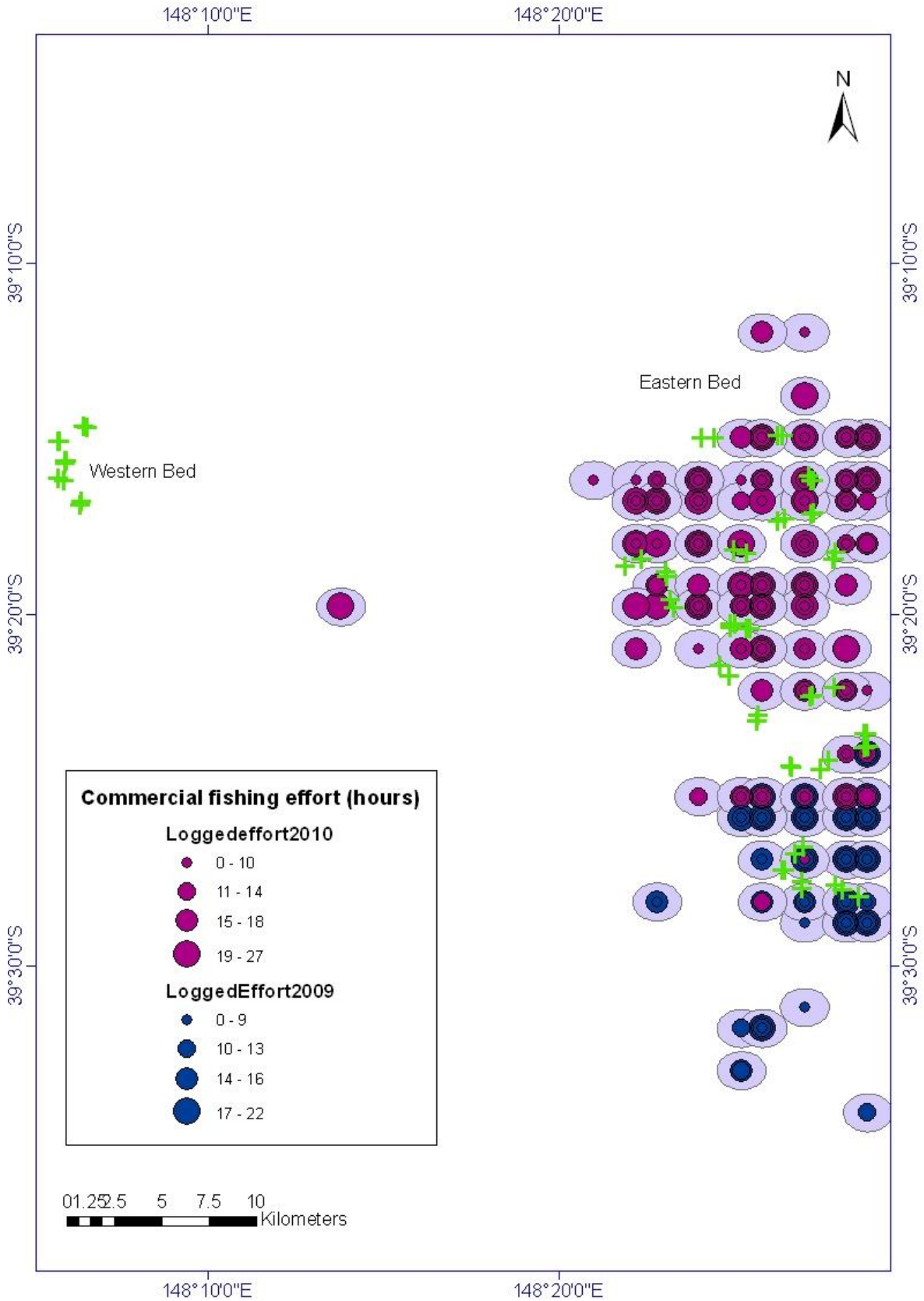


Figure 6.6. Survey dredge shots (crosses) that fell within areas of specific fishing effort in 2009 (blue) and 2010 (purple), according to average length of a standard trawl ~500m. Fishing effort, in hours fished, was overlaid on the map as an area of 1 km in diameter around logged dredge start locations.

Data Analysis

A sub-sample of the scallops caught in each tow was retained and their shell length (widest distance across the scale parallel to the hinge) measured (mm) and length frequency distributions calculated. The species richness and total abundance (total individuals caught) was calculated for all species and graphed to see if there were any visual differences between these measures before and after the fishing season, which would suggest impacts from dredge fishing. Differences between the fished and unfished areas before and after fishing were determined using analysis of multidimensional scaling (MDS) performed with PRIMER software (Plymouth Marine Laboratory, U.K.). The data were root transformed and clustered using the Bray-Curtis measure of sample similarity, then plotted using non-metric multi-dimensional scaling (MDS), following similar methods described by Clarke (1993).

Ranking each survey site using the Bray-Curtis resemblance model, which compares sample sites according to species richness and abundance, gives a representation of the compositional variation of the survey sites. ANOSIM (analysis of similarities) was used to test the significance of differences between composition of communities (species richness, numbers of species, and evenness, a measure of the proportional abundance of individuals from each species) from fished (dredged) and control (not dredged) sites. R values of 0.25 and less were taken to indicate similarity between tested groups as per Clarke and Warwick (2001). SIMPER (similarity percentages) was used to determine which species contributed most to the dissimilarities where differences occurred.

Fishing effort for each discrete GPS logged point within the study region was calculated as the number of fishing hours spent at that position during the open fishing season. The fishing effort was then divided into three levels low, medium and high. This fishing effort calculated for each tow was used to form an area around the research sample tow midline (with a 500 m diameter) to take into account the average trawl lengths (Fig.7.12).

The Bray-Curtis resemblance models were re-run using different levels of fishing effort, and on specific subsets of the data to ensure that the low catch levels of some of the species were not masking the effect of fishing and or region on the community structure estimates. Eleven key indicator species, or groups of related species were selected on the condition that they were all found in all fished areas and are all considered to have consistent catchability in dredges appearing in ≥20% or more of the tows.

Animals were grouped into categories based on taxonomic order (Table 7.16) and the more abundant species were analysed as a separate entity. The eleven groups selected in this way were:

1. Commercial scallops (*Pectin fumatus*)
2. Doughboy scallops (*Chlamys asperrimus*)
3. Oyster (*Ostrea angasi*)
4. Cockles (*Glycymeris* spp.)
5. Red rock whelks (*Charonia lampas*)
6. Wavy volute (*Amoria undulatae*)
7. Australian Tulip shell (*Pleuroploca australasia*)
8. Hermit crabs (*Strigopagurus* spp.)
9. Spider crab (*Leptomithrax gaimardii*)
10. 11-arm seastar (*Coscinasterias muricata*)
11. Astropectinid seastar (*Bollonaster pectinatus*)

6.3 EXAMINE THE IMPORTANCE OF SCALLOP DENSITY (SPAWNER BIOMASS) ON SYNCHRONISATION OF SPAWNING AND RECRUITMENT SUCCESS

6.3.1 Methods

Relationship between adult scallop abundances and recruitment intensity

Study Site
Surveys of adult scallops and collection of scallop spat (newly settled larvae) were conducted several times during 2009, 2010, and 2011 in each of a total of 40 sites within, or adjacent to Great Bay in the DEC Tasmania (Fig.7.4). Thirty-two of these sites were located within Great Bay itself, at different distances from a known and dense aggregation of adult commercial scallops. A further four sites were chosen from each of two locations (8 sites in total) adjacent to Great Bay. These two additional locations were spatially separated from the Great Bay population, and known to contain suitable scallop habitat that historically held dense scallop populations.

Spat collection
Numbers of collected spat were used as a proxy for larvae availability and abundance at each site. Mesh bag spat collectors were used to trap scallop spat during two seasons. The spat collectors were fabricated by enclosing a piece of plastic mesh (10 mm mesh size) inside a 1 mm mesh 'onion bag' that was anchored to the bottom by a rope attached to a cement block and held in a vertical position by a sub-surface buoy. Initially collectors were deployed in each of the 40 sites on the 24th and 25th November 2008 and retrieved from the 3rd to the 5th February 2009. A further array of 20 spat collectors were deployed within Great Bay on the 23rd December 2010, and these spat collectors were retrieved between the 3rd to the 5th April 2011. The contents of each collector was counted and measured.

Adult and recruit densities
Dive transects were conducted in May and September 2009, March, June, August 2010 and April 2011 at each of the 40 sites. For each site, a 100m transect was deployed in a random direction. Two scuba divers would then swim along the transect, counting and collecting all scallops found within one meter either side. Shell length was measured to the nearest mm for all scallops collected from all sites during the study period. The number of recruits per site (scallops with a shell length of between 2 and 40 mm, as per Fraschetti *et al.*, 2002) was obtained from the size frequency distributions in each sampling period. Size frequency also provided relative densities of adult scallops and an indication of successful recruitment and retention within each site (see above).

Statistical analysis
The relationship between the number of adults and recruits and adults and spat the subsequent year was examined for 2010 and 2011 using a Generalized Linear Model with a Poisson distribution, corrected for over-dispersion when necessary. This distribution is appropriate for count data, when there are no negative values and a high number of zeroes is expected. The model was calculated using the statistical package "R" (R Development Core Team 2006). Generalized lineal models were fitted using the glm (family=binomial, link=logit) function.

Effect of density on synchronisation of spawning

Study site
To investigate levels of gonad synchronization between individuals, samples of *P. fumatus* specimens were collected from within (high density) and outside (low density) of a scallop bed located in Great Bay, in the DEC over two spawning periods (2009 and 2010). The high density site was located at 147.33590° W and 43.22028° S and the low density site at 147.33590° W and 43.20227° S. The two sites were about 2km from each other, had similar depths, which ranged from 10 – 12 m, and sandy substrates. The density of adults at the beginning of the study (September 2009) was 1.88 ± 0.07 scallops.m^{-2} at the high density (HD) site and 0.05 ± 0.005 scallops.m^{-2} at the low density (LD) site. The density in August 2010 was estimated as 1.455 ± 0.035 scallops.m^{-2} at the HD site and 0.255 ± 0.005 scallops.m^{-2} at the LD site.

Monthly satellite sea-surface temperature (SST) data was sourced from the NASA Moderate Resolution Imaging Spectroradiometer (MODIS) website (modis.gsfc.nasa.gov/) and used as a proxy for temperature at the study area, from August 2009 to April 2011. Sampling occurred in two separate seasons, between June 2009 to February 2010 and August 2010 to March 2011. During each sampling season 20-30 adult scallops (measuring from 95 to 127 mm shell length) were collected by SCUBA divers from both sites either fortnightly or monthly.

Scallop Sampling
To estimate density at each site, a weighted 100 metre strip transect was laid from the boat in a random direction. Two divers would then swim along each side of the transect collecting all scallops within a metre of the line. This represented a total searched area of 200 m^2. The scallops were then processed in the laboratory where morphological measurements were taken from each scallop. Measurements included shell length, width, total weight, roe weight, wet meat weight, shell weight and digestive gland weight.

Gonadal mass index
To estimate spawning time and reproductive effort, the gonadal mass index was estimated for each specimen after Bonardelli and Himmelman (1995). This method scales gonadal mass to shell length, and has been proven to remove the effect of size (Bonardelli and Himmelman, 1995). First, we calculated the slope of the linear regression between the $\log_{(10)}$ length (mm) and $\log_{(10)}$ mass of gonad (g) for each collection date. The slope obtained for each date was used to calculate gonadal mass index for each scallop using the following formula as per Bonardelli and Himmelman (1995):

Gonadal mass index = (gonadal mass/shell length^b).k

Where:
b is the slope obtained in the regression of gonadal mass to shell length for fully mature animals;
k is a constant determined by the units adopted for gonadal mass and shell length, to obtain a value greater than zero.

This index was then used to calculate the mass for a standard scallop measuring 105 mm (the average length during the sample period). Standard gonad mass for each site was then compared over time.

Coefficient of variation
The coefficient of variation was used to determine the degree of inter-individual synchrony of gonad mass at the two study sites following Paulet (1997):

$$\text{Coefficient of variation} = \frac{\text{standard deviation of mass for standard scallop}}{\text{mean mass for standard scallop}}. 100$$

Gonad histology
Histological analyses of gonad samples were carried out between August 2010 and March 2011. A reduction in gonad mass index can occur as a result of spawning or resorption of gametes (atresia), and this can only be distinguished histologically (Barber and Blake, 2006). Each month, 20 to25 gonads were fixed in FAACC (formalin, acetic acid, calcium chloride) for later analysis. Samples were then transferred to 70% ethanol and stored for at least 48 hours prior to use. A piece of fixed tissue was embedded in paraffin and sectioned to 6µm with a microtome. Sections were stained with Haemotoxylin and Eosin and mounted with DPX for microscopic analysis.

Stages were identified for both female gonads following (Cantillanez *et al*., 2005; and Sause *et al*., 1987). The following stages were used: developing 1, developing 2 developing 3, mature, atresic, early spawning, spawning and fully spawned.

Statistical analysis
Synchronization of spawning was compared among dates and among low and high density sites using a logistic regression model, where the response variable was binary (spawned or not spawned).The model was calculated using the statistical package "R" (R Development Core Team 2006). Generalized lineal models were fitted using the glm (family=binomial, link=logit) function. The R-routine step AIC (stepwise technique) was applied. This routine considers all main effects and interactions. The significance of each variable to the model was tested using the null hypothesis that there was no significant difference from 0 using partial Z-tests (Wald statistics). Variables that were non-significant were removed and a reduced model refitted. Pearson's X^2 was used to evaluate the goodness of fit of the model. Significant levels of statistical procedures were set at p=0.05.

7. RESULTS AND DISCUSSION

7.1 GENETIC POPULATION STRUCTURE OF SCALLOPS (*P. FUMATUS*) IN SOUTHERN AUSTRALIA

7.1.1 Results and discussion

Microsatellite dataset statistics
The population genetic structure of 1124 scallops was examined using 15 microsatellite loci from 18 locations and three management jurisdictions; 218 scallops were analysed from four locations in Victoria, 142 from three locations in the Commonwealth, and 764 from 11 locations in Tasmania (Table 6.2, Fig. 6.1).
All 15 microsatellite loci were highly polymorphic, based on data pooled across all locations, with high numbers of alleles (13 - 70) and heterozygosities (0.38 - 0.93) per locus (Table 7.1). A detailed breakdown of genetic variation per microsatellite locus within each sampling location is provided in Appendix 3B.

Four of the microsatellite loci had null alleles whose predicted frequency was in excess of 7% (Loci A09, PeFu_P1_H11, PeFu_P2_D07, PeFu_P2_C07, Table 7.1) shown to deviate from Hardy Weinberg equilibrium (HWE). Two of these loci had high genotype failure rates across the 1124 scallops, which would be consistent with the presence of null allele homozygotes that would manifest as failed genotypes. The failure rates were 101/1124 when the null allele frequency was 0.17 (locus PeFu_P2_C07) and 72/1124 when null allele frequency was 0.23 (locus PeFu_P2_D07). The average percentage of missing genotypes per locus across the eleven loci was 4.49% (Table 7.1)[2].

Three of the remaining eleven microsatellite loci were out of HWE, but were retained in subsequent analysis as the proportion of observed to expected heterozygosities for these loci were similar (e.g. 0.82/0.85, 0.73/0.76 and 0.71/0.79, Table 7.1) and null allele frequencies were 0.05 or less.

Overall, deviation from linkage disequilibrium was slight; only one pair of loci (P1_E12 & A06) was significantly linked in three populations. There was no consistent pattern between pairs of loci judged to be linked when all data was combined, or when tests were performed on the three collections where more than 100 samples were taken (Great Bay, Banks Straits and Victoria_3). Significant linkages (i.e. $p < 0.05$) were detected between three locus pairs (P1_E12 and P1_C01, P1_E12 and P1_E04a, P1_E04a and P1_A11) on the pooled data, but none of these were repeated at specific collections locations.

[2] The fifteen-locus genotype data set for the eighteen locations is available at www. http://era.deedi.qld.gov.au/ A copy can be requested from the website, and the request will be sent to Jenny Ovenden for approval.

Table 7.1. Sampling locations by region and jurisdiction and scallop shell size for the 1124 scallops genotyped in this study.

Jurisdiction	Region	Location	Latitude	Longitude	n	Size class					
						< 40 mm	40-60 mm	60-90 mm	90-110 mm	>110 mm	Unsized
Tasmania	D'Entrecasteaux Channel (DEC)	Satellite Island	-43.3177	147.2373	32				32		
		Gordon Channel	-43.2655	147.2580	59				59		
		Great Bay 10	-43.2204	147.3113	42	42					
		Great Bay 25	-43.2112	147.3357	61	19			42		
		Great Bay	-43.2063	147.3348	120		89		20	11	
	White Rock	White Rock	-42.4478	148.0732	88	8		42	38		
	Eddystone	Eddystone Dp	-40.9974	148.4815	30						30
		Eddystone	-40.9569	148.4291	39						39
	Banks Strait	Banks Strait	-40.5095	148.4376	110		16	47	47		
	Babel Island	Babel Island	-39.9996	148.4197	93		50	43			
	West Flinders Island	W Flinders 2	-39.9437	147.6982	90	23	48	19			
				Total	**764**	**92**	**203**	**151**	**238**	**11**	**69**
Commonwealth	Commonwealth	Commonwealth SE	-39.4608	148.4506	47		25		22		
		Commonwealth W	-39.2584	148.0644	49				49		
		Commonwealth NE	-39.2482	148.4443	46				46		
				Total	**142**		**25**		**117**		
Victoria	Lakes Entrance	Victoria 1	-38.2682	147.6889	27				27		
		Victoria 2	-38.1290	147.7755	36			36			
		Victoria 3	-38.0352	147.7426	121		121				
	Port Phillip Bay	Port Phillip Bay	-38.0479	144.7542	34			34			
				Total	**218**		**121**	**70**	**27**		
				Overall	**1124**						

Table 7.2. Summary statistics across 15 microsatellite loci for all *P. fumatus*.

Locus	Locus Name	N	% missing genotypes	Na	Ho	He	p(HWE)	Null
Locus 01	A09	1065	5.25	38	0.38	0.48	0.0000	0.09
Locus 02	PeFu_P1_B05	1068	4.98	17	0.74	0.75	0.6303	0.00
Locus 03	PeFu_P1_E12	1055	6.14	72	0.93	0.95	0.3314	0.01
Locus 04	PeFu_P2_C12	1041	7.38	31	0.82	0.85	0.1725	0.02
Locus 05	A06	1096	2.49	33	0.86	0.88	0.6889	0.01
Locus 06	PeFu_P1_C01	1081	3.83	21	0.60	0.61	0.1986	0.02
Locus 07	PeFu_P1_E04a	1085	3.47	70	0.82	0.85	0.0000*	0.02
Locus 08	PeFu_P1_H11	1081	3.83	13	0.52	0.62	0.0000	0.07
Locus 09	PeFu_P2_D07	1052	6.41	27	0.44	0.89	0.0000	0.23
Locus 10	PeFu_P2_E11	1096	2.49	18	0.73	0.76	0.0126*	0.02
Locus 11	PeFu_P1_A11	1068	4.98	17	0.49	0.51	0.0745	0.02
Locus 12	PeFu_P1_F02	1092	2.85	47	0.74	0.76	0.3706	0.00
Locus 13	PeFu_P2_C07	1023	8.99	14	0.43	0.72	0.0000	0.17
Locus 14	PeFu_P2_C09	1094	2.67	21	0.80	0.83	0.3904	0.01
Locus 15	PeFu_P2_F01	1033	8.10	16	0.71	0.79	0.0000*	0.05

Samples analysed here, including sample size (N), number of alleles (Na), observed (Ho) and expected (He) heterozygosity, probability of HWE departure [p(HWE)] and frequency of null alleles (Null). Four loci (shaded) were excluded from further analyses due to presence of null alleles in high frequency. Three loci (*) were retained despite likely departure from Hardy-Weinberg equilibrium. Locus details (including formal locus names) are listed in Appendix 3A.

Genetic population structuring

Fine-scale

Using conventional F_{ST} measures, we tested whether scallops from various shell size classes were genetically homogeneous within beds. Scallops of more than one size class were collected from seven locations; Great Bay 10, Great Bay 25, Great Bay, White Rock, Banks Strait, West Flinders Island and Commonwealth SE (Table 7.1). We were unable to reject the null hypothesis of genetic structuring among size classes within collection locations, suggesting that scallops were genetically homogeneous across shell sizes. For these tests and other tests below, the statistical power of the microsatellites to reject the null hypothesis if F_{ST} was greater than zero was assumed to be sufficiently high to draw this conclusion, although power was not formally evaluated here. We concluded that the scallops of different size classes within beds were unlikely to be derived from genetically distinct spawning cohorts.

Likewise, we tested whether scallop samples from adjacent collection locations (i.e. separated by less than 45 km) were genetically homogeneous. In the case of Eddystone, the two collection locations represented samples taken from shallow and deep water. Closely spaced collections had been made from four regions. Five collections were made within the DEC region (Satellite Island, Gordon Channel, Great Bay 10, Great Bay 25 and Great Bay), two collections were made at Eddystone region (Eddystone Deep and Eddystone), three collections were made at Commonwealth (Commonwealth SE, Commonwealth W and Commonwealth NE) and three collections were made at Lakes Entrance (Victoria1, Victoria 2 and Victoria 3). The null hypothesis of genetic homogeneity within each of the four regions was unable to be rejected, which suggested that scallops were genetically homogeneous at this fine spatial scale (Table 7.3). For subsequent analyses, scallop samples were

pooled into nine regions. The regions were DEC, White Rock, Eddystone, Banks Strait, Babel Island, West Flinders Island, Commonwealth, Lakes Entrance and Port Phillip Bay.

Broad-scale

In contrast to a lack of genetic differentiation at a fine spatial scale, scallops from collection locations at the extremes of our sampling distribution were genetically differentiated. The pairwise F_{ST} between DEC in south eastern Tasmania and Port Phillip Bay in southern Victoria was 0.018 (Table 7.4). These scallop populations are not only isolated by distance, but they also occur in large coastal embayments that would restrict the exchange of recruits with inshore, open ocean locations.

Table 7.3. Pairwise F_{ST} (above the diagonal) and *p*-values (below diagonal) for adjacent locations within regions for *P. fumatus.*

Locations	(1 - 18)	n	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18
Channel, Tas																				
Satellite Is	1	32		-0.002	-0.004	-0.002	-0.002	0.000	0.000	-0.001	-0.001	0.001	0.002	-0.001	0.007	0.003	0.008	0.005	0.008	0.012
Gordon Channel	2	59	0.738		0.001	-0.001	0.002	0.002	0.002	0.004	0.005	0.003	0.006	0.009	0.007	0.005	0.011	0.008	0.011	0.019
Great Bay 10	3	42	0.385	0.292		0.001	0.000	0.000	0.003	0.001	0.003	0.001	0.006	0.002	0.009	0.007	0.013	0.008	0.010	0.015
Great Bay 25	4	61	0.861	0.890	0.278		0.003	0.001	0.004	0.006	0.004	0.004	0.004	0.006	0.007	0.002	0.008	0.007	0.010	0.022
Great Bay	5	120	0.754	0.969	0.517	0.277		0.002	0.002	0.002	0.004	0.003	0.005	0.003	0.010	0.008	0.011	0.009	0.012	0.017
White Rock, Tas																				
White Rock	6	88	0.504	0.025	0.664	0.730	0.033		0.001	0.000	0.001	-0.001	0.000	0.002	0.003	0.002	0.005	0.001	0.004	0.012
Eddystone, Tas																				
Eddystone Dp	7	30	0.110	0.272	0.212	0.302	0.199	0.086		-0.003	0.000	-0.001	0.000	-0.001	0.001	0.001	0.000	0.000	0.001	0.004
Eddystone	8	39	0.325	0.052	0.047	0.118	0.211	0.264	0.533		0.002	0.000	0.002	0.000	0.002	0.004	0.002	0.004	0.004	0.008
Banks Strait, Tas	9	110	0.409	0.049	0.271	0.036	0.001	0.503	0.375	0.106		0.001	0.000	0.001	0.000	0.000	0.002	-0.002	0.002	0.007
Babel Island, Tas																				
Babel Island	10	93	0.164	0.009	0.123	0.034	0.011	0.094	0.245	0.454	0.218		0.001	0.001	0.002	0.002	0.008	0.001	0.005	0.009
West Flinders, Tas	11	90	0.529	0.001	0.011	0.107	0.003	0.479	0.412	0.161	0.959	0.338		0.004	0.001	-0.001	0.003	-0.001	0.002	0.011
Commonwealth																				
Comm. SE	12	47	0.759	0.006	0.223	0.232	0.125	0.858	0.447	0.306	0.915	0.506	0.862		0.004	0.004	0.006	0.003	0.005	0.008
Comm. W	13	49	0.006	0.032	0.001	0.082	0.000	0.253	0.273	0.152	0.178	0.072	0.268	0.226		0.001	0.001	0.001	-0.001	0.008
Comm. NE	14	46	0.325	0.022	0.023	0.811	0.000	0.424	0.346	0.099	0.760	0.302	0.829	0.864	0.625		0.001	-0.002	0.003	0.011
Lakes Entrance, Vic																				
Victoria 1	15	28	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA		0.002	-0.002	0.008
Victoria 2	16	35	0.197	0.039	0.144	0.156	0.028	0.215	0.441	0.423	0.857	0.229	0.834	0.875	0.067	0.972	NA		-0.002	0.004
Victoria 3	17	121	0.053	0.000	0.002	0.004	0.000	0.021	0.242	0.012	0.200	0.001	0.738	0.410	0.444	0.739	NA	0.715		0.005
Port Phillip Bay, Vic	18	34	0.006	0.000	0.001	0.007	0.000	0.001	0.023	0.002	0.025	0.005	0.002	0.032	0.044	0.098	NA	0.357	0.057	

Regions are named in bold and sample sizes per collection location (n) are presented. Boxes indicate comparison among collections locations separated by less than 45 km. Some comparisons were significant after B–Y FDR correction ($\alpha = 0.05$, critical *p*-value = 0.00891, in bold). *P*-values for some comparisons could not be estimated by Fstat software because all genotypes had some missing data (NA).

Table 7.4. Pairwise F_{ST} (above the diagonal), *p*-values (below diagonal) and whether those comparisons are significant after B–Y FDR correction ($\alpha = 0.05$, critical p-value = 0.01198) among nine pooled locations of *P. fumatus*.

Location (1 to 9)		n	1	2	3	4	5	6	7	8	9
D'Entrecasteaux Channel	1	314		0.001	**0.003**	**0.004**	**0.003**	**0.005**	**0.005**	**0.011**	**0.018**
White Rock	2	88	0.013		0.001	0.001	-0.001	0.000	0.001	0.004	**0.012**
Eddystone	3	69	**0.003**	0.054		0.002	0.001	0.002	0.001	**0.003**	**0.007**
Banks Strait	4	110	**0.000**	0.499	0.042		0.001	0.000	0.000	0.001	0.007
Babel Island	5	93	**0.000**	0.094	0.272	0.218		0.001	0.001	**0.005**	**0.009**
West Flinders Island	6	90	**0.000**	0.476	0.048	0.957	0.336		0.001	0.002	**0.011**
Commonwealth	7	142	**0.000**	0.743	0.018	0.680	0.195	0.427		0.001	0.008
Lakes Entrance	8	184	**0.000**	0.028	**0.002**	0.324	**0.002**	0.770	0.248		0.005
Port Phillip Bay	9	34	**0.000**	**0.001**	**0.001**	0.025	**0.005**	**0.002**	0.040	0.069	

As well as being genetically distinct from each other, scallop samples taken from the DEC (south-eastern Tasmania) and Port Phillip Bay (southern Victoria) were significantly genetically differentiated from most other locations. Pairwise F_{ST} between Port Phillip Bay and the other eight locations ranged from 0.005 (Lakes Entrance) to 0.012 (White Rock); four of the seven comparisons were significantly different based on the corrected *p*-value (0.01198). *P*-values for the remaining three comparisons were small (0.025, 0.040 and 0.069). Pairwise F_{ST} between the DEC ranged from 0.001 (White Rock) to 0.011 (Lakes Entrance) and these were significant at the corrected *p*-value (Table 7.4).

Scallops from the Lakes Entrance location on the south eastern Victorian coastline were genetically differentiated from other regional collections. Pairwise F_{ST} was significant for three out of eight comparisons of Lakes Entrance to other regions (DEC, pairwise F_{ST} 0.011; Eddystone, pairwise F_{ST} 0.003 and Babel Island, pairwise F_{ST} 0.005). Two other comparisons to Lakes Entrance had small *p*-values; Lakes Entrance compared to White Rock (*p*-value 0.028) and Lakes Entrance compared to Port Phillip Bay (*p*-value 0.069). There was one other comparison with a low, but insignificant *p*-value (0.018) associated with the pairwise F_{ST} of 0.001 between Commonwealth and Eddystone locations (Table 7.4).

Based on these results, we explored the possibility that geographic and genetic distance between collections locations may be proportional by testing for the presence of isolation-by-distance (IBD). Formal tests for IBD indicated that 47% of the genetic variation among the nine regional collection locations was explained by geographic distance (Fig. 7.1). However, this pattern seemed to be predominantly driven by the genetic distinctiveness of collections from the embayment locations of DEC (south-eastern Tasmania) and Port Phillip Bay (southern Victoria), which were also at the extremities of the study area. When these two locations are removed tests for IBD among the remaining locations were not significant (Fig. 7.2).

Discriminant analysis of principal components (DAPC) - (Fifteen-locus dataset D1.dat)
As an alternative to F-statistics to detect population structure, a relatively new approach (DAPC) was trialled. One hundred principal components were retained in the DAPC analysis, which explained approximately 90% of the variance (Fig. 7.3a). Figure 7.3b suggested that there were approximately four clusters. When four clusters are modelled, one distinctive cluster stands out as being predominant (Fig. 7.4). However, there was no clear

association pattern between the discriminant analysis clusters and the sample locations (Table 7.4).

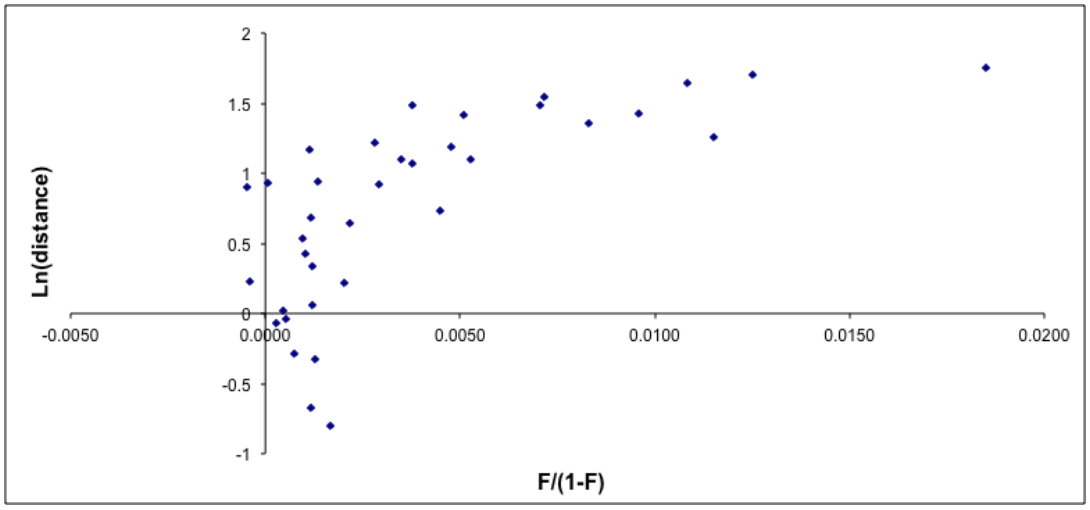


Figure 7.1. A plot of genetic distance (F_{ST} / (1- F_{ST})) and geographic distance (ln km) for nine regional sampling locations of *P. fumatus* at 11 microsatellite loci. Mantel test for isolation by distance was significant ($p < 0.00087$).

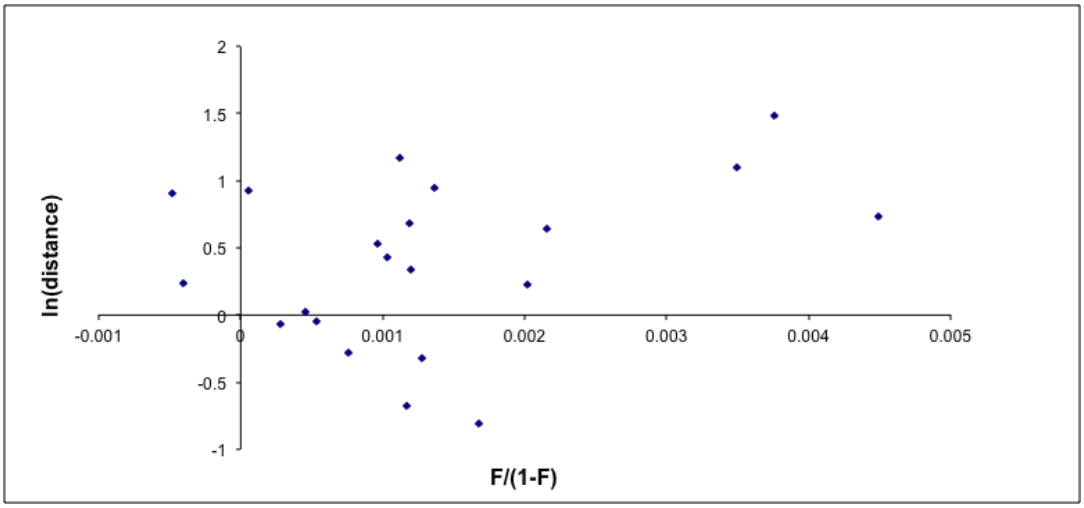


Figure 7.2. A plot of genetic distance (F_{ST} / (1- F_{ST}) compared to geographic distance (ln km) for seven regional sampling locations in open waters (i.e. without embayment locations of Port Phillip Bay and D'Entrecasteaux Channel, DEC) of *P. fumatus* at 11 microsatellite loci. Mantel test for isolation by distance was insignificant ($p < 0.256$).

(a) (b)

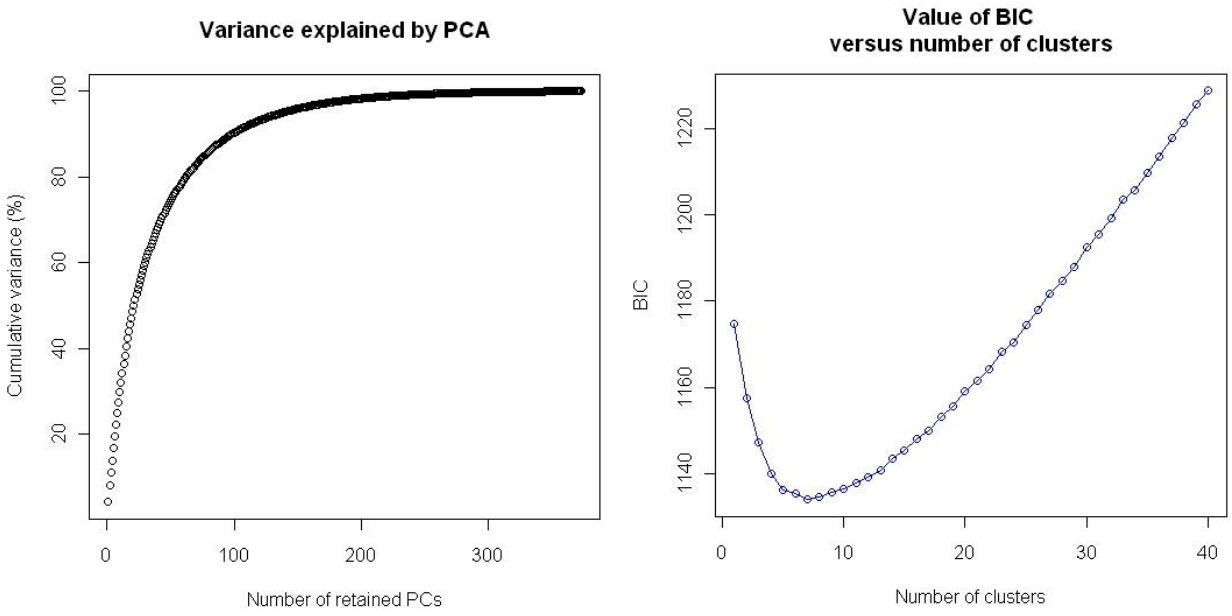


Figure 7.3. Analysis of 15 locus scallop (*P. fumatus*) genotypes (D1.dat, see table 6.1): (a) variance explained by number of retained principal components (PSs) and (b) Bayesian Information Criterion (BIC) to assess the best supported model i.e. the number of clusters in the fifteen locus dataset.

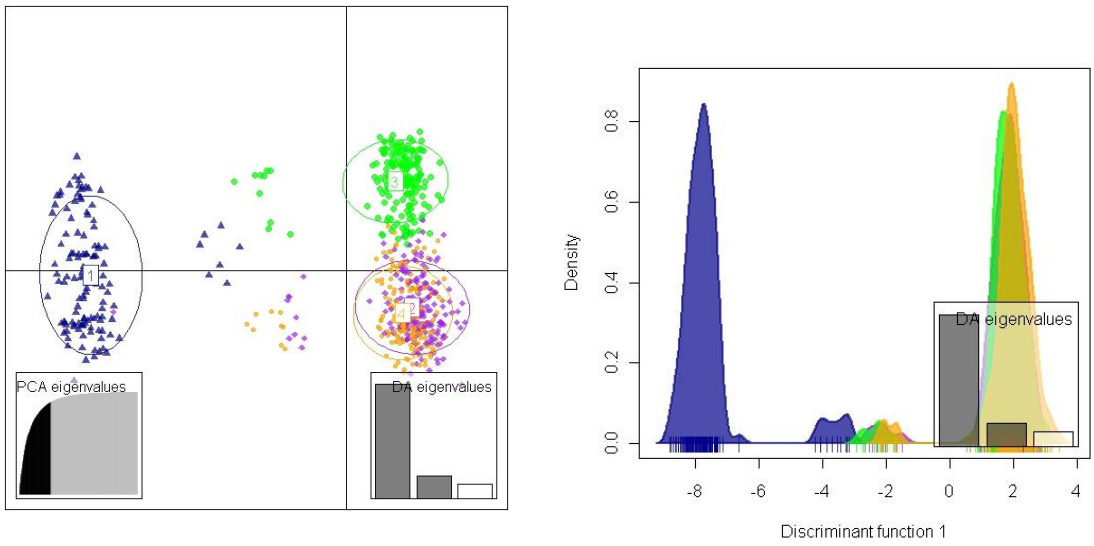


Figure 7.4. Analysis of 15 locus scallop (*P. fumatus*) genotypes (D1.dat, see table 6.1): discriminant analysis with four clusters (a) plot of first by second principal component (b) first principal component plotted against density in the fifteen locus dataset.

Table 7.5. Number and percentage of samples from each sample location grouped within each cluster.

Location	Number in cluster				Cluster percentage			
Cluster	1	2	3	4	1	2	3	4
Satellite Island	6	6	8	1	0.29	0.29	0.38	0.05
Gordon Channel	12	14	15	3	0.27	0.32	0.34	0.07
Great Bay 10	8	15	9	4	0.22	0.42	0.25	0.11
Great Bay25	6	14	13	7	0.15	0.35	0.33	0.18
Great Bay	23	21	23	6	0.32	0.29	0.32	0.08
White Rock	16	24	17	11	0.24	0.35	0.25	0.16
Eddystone Deep	6	3	4	4	0.35	0.18	0.24	0.24
Eddystone	8	7	6	6	0.30	0.26	0.22	0.22
Banks Strait	18	22	22	16	0.23	0.28	0.28	0.21
Babel Island	13	17	20	15	0.20	0.26	0.31	0.23
West Flinders 2	18	13	13	15	0.31	0.22	0.22	0.25
Commonwealth S^{th} eastern	9	8	9	8	0.26	0.24	0.26	0.24
Commonwealth western	14	8	7	7	0.39	0.22	0.19	0.19
Commonwealth N^{th} eastern	5	7	8	16	0.14	0.19	0.22	0.44
Victoria 2	3	2	1	0	0.50	0.33	0.17	0.00
Victoria 3	12	9	7	7	0.34	0.26	0.20	0.20
Port Phillip Bay	1	3	1	0	0.20	0.60	0.20	0.00

The results in Table 7.5 would be consistent with the cryptic presence of more than one species of scallop amongst the samples, as the clusters were distributed over the different locations. If this was so, and because random mating should occur within but not between putative species, we hypothesized that there would be a reduction (if not an elimination) in the number of loci that deviated from HWE within each cluster. This hypothesis was tested by measuring HWE in cluster 1 which was the largest outlier compared to the other clusters (Fig. 7.4). Genotypes in cluster 1 had three loci that deviated from HWE ($P<0.01$) and we therefore concluded that the cluster pattern was due to null alleles causing deviations from HWE and not due to the presence of cryptic species.

Discriminant analysis of principal components (DAPC) - (Eleven-locus dataset D2.dat)
Four loci that deviated from HWE were removed from the data, leaving 11 loci (D2.dat, table 6.1). One hundred principal components were retained in the analysis that explained approximately 90% of the variance (Fig. 7.5a). Figure 7.5b suggests that approximately five to seven clusters were supported by the data. When five or seven clusters were modelled no distinctive cluster stands out as being predominant (Fig. 7.4). Tables 7.6 and 7.7 show no clear association pattern between the discriminant analysis clusters and the sample locations, that is all sample locations had genotypes in at least three clusters.

A control discriminant analysis of principal components using genotypes randomly generated from empirical allele frequencies gave a similar pattern to the empirical data analysis indicating that the best supported model using Bayesian Information Criteria does lead to a false positive cluster pattern (Fig. 7.7). This supports the hypothesis that scallop genotype samples are largely from an admixed population.

(a) (b)

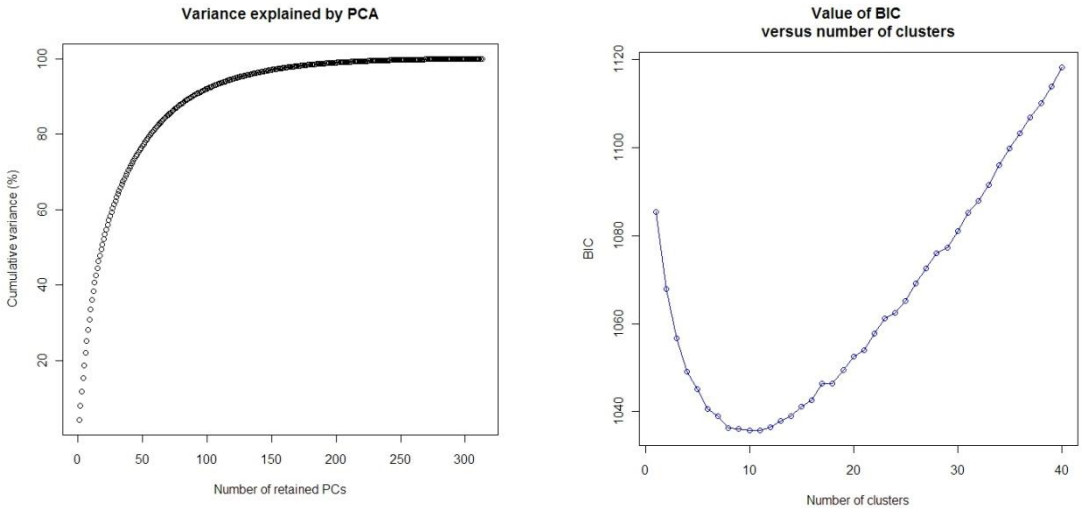


Figure 7.5. Analysis of *P. fumatus* genotypes with 11 loci (D2.dat, table 6.1): (a) variance explained by number of retained principal components (PSs) and (b) Bayesian Information Criterion (BIC) to assess the best supported model i.e. the number of clusters in the eleven locus dataset.

(a) (b)

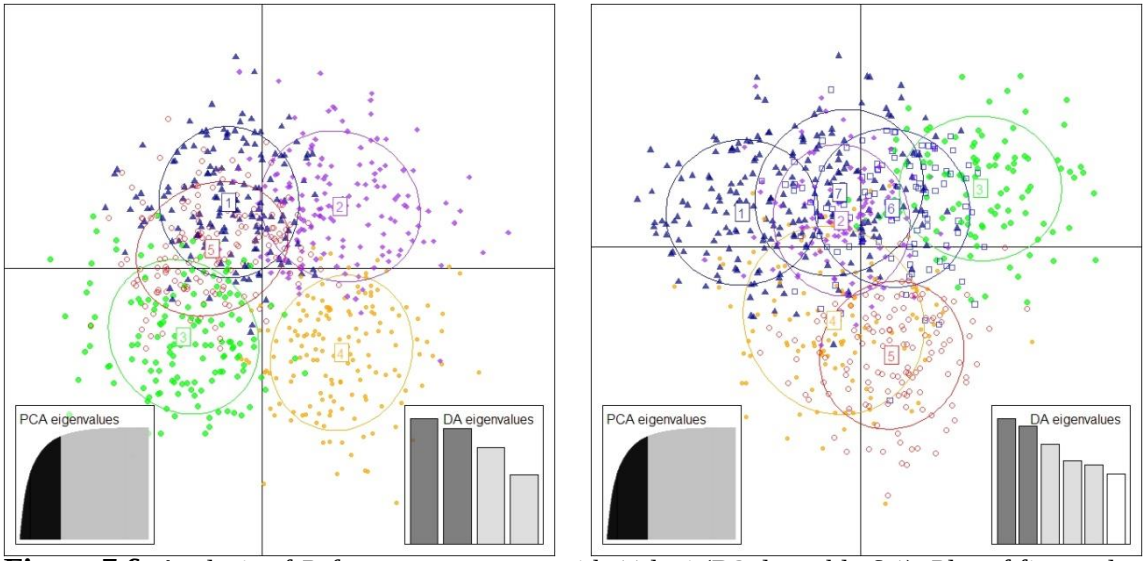


Figure 7.6. Analysis of *P. fumatus* genotypes with 11 loci (D2.dat, table 6.1): Plot of first and second principal components with (a) five clusters and (b) seven clusters.

Table 7.6. Number and percentage of *P. fumatus* from each collection location grouped within each cluster of fine clusters using the 11 loci dataset (D2.dat, table 6.1).

Location	Number of genotypes	Percentage of genotypes in each cluster (1 to 5) within location				
		1	2	3	4	5
Satellite Island	25	0.20	0.16	0.24	0.12	0.28
Gordon – Channel	52	0.19	0.15	0.10	0.40	0.15
Great Bay 10	40	0.13	0.23	0.25	0.18	0.23
Great Bay 25	47	0.21	0.19	0.17	0.19	0.23
Great Bay	84	0.21	0.14	0.15	0.15	0.33
White Rock	75	0.19	0.24	0.19	0.16	0.23
Eddystone Deep	21	0.33	0.14	0.10	0.33	0.10
Eddystone	28	0.18	0.18	0.21	0.29	0.14
Banks Straight	86	0.23	0.19	0.22	0.15	0.21
Babel Island	72	0.14	0.21	0.21	0.18	0.26
West Flinders 2	62	0.23	0.29	0.19	0.19	0.10
Commonwealth S^{th} eastern	38	0.13	0.18	0.34	0.11	0.24
Commonwealth western	44	0.18	0.25	0.18	0.23	0.16
Commonwealth N^{th} eastern	40	0.30	0.25	0.10	0.15	0.20
Victoria 2	10	0.20	0.30	0.10	0.20	0.20
Victoria 3	41	0.22	0.22	0.15	0.27	0.15
Port Phillip Bay	9	0.22	0.00	0.33	0.44	0.00

Table 7.7. Number and percentage of samples from each sample location grouped within each cluster of 7 clusters using 11 loci: (D2.dat, table 6.1).

Location	Number of genotypes	Percentage of genotypes in each cluster (cluster 1 to 7) within location						
		1	2	3	4	5	6	7
Satellite Island	25	0.16	0.00	0.28	0.08	0.12	0.20	0.16
Gordon – Channel	52	0.19	0.12	0.23	0.12	0.13	0.08	0.13
Great Bay 10	40	0.13	0.15	0.13	0.10	0.18	0.10	0.23
Great Bay 25	47	0.26	0.06	0.11	0.13	0.15	0.17	0.13
Great Bay	84	0.20	0.07	0.10	0.07	0.19	0.11	0.26
White Rock	75	0.12	0.11	0.20	0.17	0.19	0.05	0.16
Eddystone Deep	21	0.24	0.19	0.00	0.05	0.14	0.24	0.14
Eddystone	28	0.11	0.07	0.18	0.18	0.21	0.00	0.25
Banks Straight	86	0.08	0.15	0.12	0.15	0.20	0.17	0.13
Babel Island	72	0.08	0.13	0.17	0.14	0.19	0.14	0.15
West Flinders 2	62	0.15	0.11	0.13	0.26	0.21	0.08	0.06
Commonwealth S^{th} eastern	38	0.05	0.16	0.16	0.08	0.24	0.13	0.18
Commonwealth western	44	0.02	0.09	0.11	0.23	0.16	0.27	0.11
Commonwealth N^{th} eastern	40	0.20	0.25	0.08	0.08	0.15	0.13	0.13
Victoria 2	10	0.20	0.50	0.00	0.10	0.00	0.10	0.10
Victoria 3	41	0.15	0.17	0.12	0.24	0.12	0.15	0.05
Port Phillip Bay	9	0.11	0.44	0.00	0.00	0.22	0.22	0.00

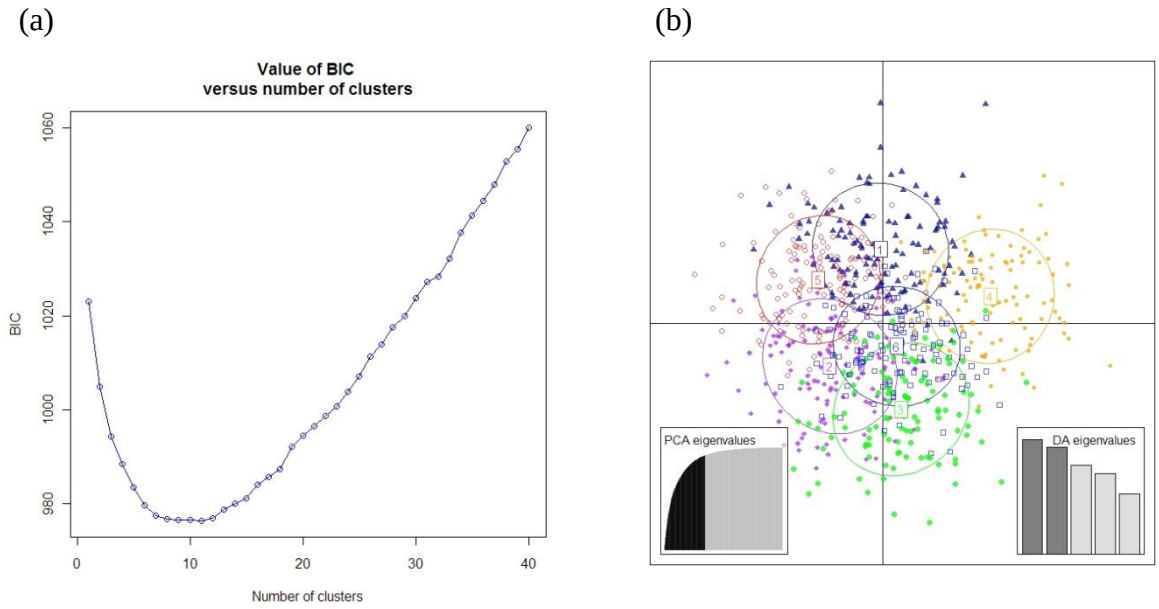


Figure 7.7. Discriminant analysis of principal components from a random genotype dataset generated from empirical allele frequencies (a) Bayesian Information Criterion (BIC) to assess the best supported model and (b) scatter plot of the first two principal components in a model with six clusters selected.

Recruitment analysis

Two approaches were taken to detect self-recruitment; firstly, by searching for related pairs of individuals in the entire dataset and secondly, by searching for related pairs of individuals in a series of closely-spaced beds in an enclosed embayment of the DEC. Self-recruitment would be more likely to occur within the enclosed embayment.

The fifteen-locus scallop genotype dataset consisting of 1124 individuals was subsampled to create two separate data files. The first consisted of data from all locations with data trimmed by removing four loci that deviated from HWE (Table 6.1) and by removing any genotypes with missing loci; leaving 774 genotypes (D1.dat). The second dataset consisted of individuals from the DEC region only with data trimmed by removing any genotypes with missing loci leaving 214 genotypes amongst the five locations within the channel (D3.dat). Samples with missing (i.e. incomplete) genotypes were removed to reduce the number of false positive relationships per pairwise comparison. The software (MLRELATE) is unable to accept missing genotypes with missing allelic determinations.

Pooled scallop populations (774 genotypes with 11 loci: D1.dat)

Relationships (i.e. parent-offspring, PO; full-sibling, FS; half-sibling, HS and unrelated, U) between pairs of individuals were determined from a lower diagonal matrix of 774x(774-1)/2= 299,151 pairwise comparisons. In order to evaluate the relationships found in the empirical data, we searched for relationships in random, simulated data, where no relationships should exist. The average number of relationships identified from 50 simulated data sets from randomly generated genotypes each with 774 samples is shown in Table 7.8. By chance, there were 173 false positive PO relationships (on average) identified among 774 unrelated genotypes.

Table 7.8. Number of MLRELATE Parent Offspring (PO), Full Sib (FS) and Half Sib (HS) relationships identified in unrelated simulated data containing 774 genotypes.

	PO	FS	HS
Mean	173	714	32007
Minimum	128	623	31510
Maximum	229	778	32689
Standard deviation	24	29	242

About the same number of relationships were found in the empirical data. The number of relationships identified from the analysis of empirical data (Table 7.9) was not significantly different from the results of simulated random genotypes in Table 8. If there were many true relationships, we would have expected significantly more PO, FS and HS matches in Table 7.9 compared to those found in Table 7.8. Thus, the parent-offspring, full-sibling and half-sibling matches in the empirical data (Table 7.9) were probably false positive matches.

Table 7.9. Number of MLRELATE Parent Offspring (PO), Full Sib (FS) and Half Sib (HS) relationships found in empirical data with 11 loci containing 774 genotypes.

	PO	FS	HS
Empirical data	133	621	28541

Another way to determine the rate at which false positive matches occur is by looking at the distribution and magnitude of the likelihood of each pairwise comparison. Assuming genotypes were sampled from a single population, the 50th highest likelihood from the 50 pooled MLRELATE analyses should yield about one false positive for each of the relationship classes. For example, the 50th highest likelihood from the 50 pooled simulated files represents the average likelihood at which one false positive should occur. Similarly the 100th and 200th highest ranked likelihood should yield about two and four false positives as they represent the average likelihood at which two and four false positives occur respectively. Table 7.10 lists the log likelihoods for each of the relationship classes from simulated data that could be used as thresholds to infer putative relationships.

Table 7.10. Log likelihood thresholds on the highest ranked value from 50 pooled simulation runs.

Rank Relationship	50th	100th	200th
PO	-51.02	-52.27	-53.50
FS	-51.38	-52.26	-53.64
HS	-52.33	-52.88	-53.54

Assuming the thresholds were unbiased, if there were many pairwise likelihoods from the empirical data that were greater than the 50th ranked likelihood (threshold), we would expect that one of these would occur by chance and that one less than the number of pairs above this threshold would be the approximate number of true relationship assignments.

For each of the three relationship classes (PO, FS and HS), by chance there was not one pairwise match for empirical data that was above the 50th ranked log likelihood threshold (Table 7.11). Compared to the likelihood thresholds of Table 7.10, we would expect on average four false positives for each of the relationship classes above the 200th ranked

likelihood of the 50 simulated data sets. Here, we had 1, 2 and 0 pairwise matches that were above the 200th ranked threshold for PO, FS and HS relationships, respectively, indicating once again that there were no significant numbers of that type of relationship within the empirical genotypes.

Table 7.11. Pairwise likelihoods form empirical data for highest three likelihoods within each relationship class: Parent Offspring (PO), Full sib (FS), Half Sib (HS).

Relationship	Log likelihood	Rank	Pair	
PO	-52.50	1	Pefu0470	Pefu0915
PO	-54.39	2	Pefu0899	Pefu1007
PO	-55.13	3	Pefu1962	Pefu0905
FS	-52.79	1	Pefu1576	Pefu0915
FS	-53.07	2	Pefu0470	Pefu1394
FS	-54.90	3	Pefu0470	Pefu0058
HS	-53.88	1	Pefu0380	Pefu0076
HS	-54.55	2	Pefu0380	Pefu0470
HS	-54.63	3	Pefu0380	Pefu0915

As described in the methods, we added six genotypes comprising two groups of three full-sibs to the empirical data prior to estimating relationships as a test to see if we could find true relationships. Twelve true PO relationships and six true FS relationships (Fig. 6.1) were added. MLRELATE found eleven correct PO relationships, but they had relatively low likelihoods (i.e. pairwise likelihoods of -61.25, -64.92, -68.22, -68.68, -69.98, -72.47, -73.75, -76.16, -76.38, -79.17 and -79.49 amongst 146 putative PO matches). The likelihoods of the simulated relationships were less than the thresholds in Table 7.10, which demonstrated that there was insufficient statistical power to delineate true relationship pairs when genotypes were pooled across all locations.

The same result applied to the identification of full sibling pairs. Of the six true FS pairs, five were correctly identified with pairwise likelihoods of -70.70, -71.26, -72.32, -74.14 and 77.60 amongst 623 putative FS matches. One true FS pair was falsely identified as a PO pair. Of the 28543 false positive HS pairs detected in this analysis 401 were between the 6 additional genotypes added.

D'Entrecasteaux Channel (DEC) populations (214 genotypes with 15 loci: D3.dat)
In order to test for the presence of pedigree relationships in this population in an enclosed embayment, we increased the detection power by utilising all 15 microsatellite loci. This meant that we included some loci that deviated from Hardy-Weinberg equilibrium. There were 214 fifteen-locus genotypes with no missing alleles, which resulted in 22,791 pairwise comparisons.

Once again, we first determined the average number of relationships identified from 50 simulated data sets from randomly generated data each with 214 samples (Table 7.12).

Table 7.12. Number of MLRELATE Parent Offspring (PO), Full Sib (FS) and Half Sib (HS) relationships identified in unrelated simulated data containing 214 genotypes.

	PO	FS	HS
Mean	4.1	25.7	2045
Minimum	0	13	1960
Maximum	11	37	2140
Standard deviation	2.2	5.4	48.5

The number of relationships identified from the analysis of empirical data is provided in Table 7.13, with and without correcting for deviations in Hardy-Weinberg equilibrium (HWE) in the implementation of MLRELATE. The numbers of related pairs of scallops in the empirical data was similar to the number in the simulated, random data (Tables 7.12 and 7.13). The correction for HWE did not make a large difference in the number of putative relationships found (Table 7.13). Across the range of all likelihoods there was a high correlation (r=0.99) between relationships with and without correction for null alleles using MLRELATE. This indicated that the correction made little difference to our not finding significant numbers of PO, FS and HS relationships within the DEC.

Table 7.13. Number of MLRELATE Parent Offspring (PO), Full Sib (FS) and Half Sib (HS) relationships found in empirical data containing 214 genotypes with and without correcting for null alleles.

Null allele correction	PO	FS	HS
No	0	17	1781
Yes	4	19	1958

Table 7.14 lists the sample pairs for FS and HS relationships that had the highest log likelihoods (no null allele correction). Both the log likelihoods in Table 7.14 were smaller than the 200th highest log likelihood from random genotypes (Table 7.15), so we can conclude that the highest ranked likelihoods presented in Table 7.14 are not significantly greater than that observed by chance.

Table 7.14. Pairwise likelihoods form empirical data (first ranked match) with likelihood showing rank within relationship class: Full sib (FS), Half Sib (HS).

Relationship	Log likelihood	Rank	Pair	
FS	-74.48	1	Pefu1808	Pefu1033
HS	-73.12	1	Pefu1857	Pefu1036

Table 7.15. Log likelihood thresholds on the highest ranked value from 50 pooled simulation runs using D'Entrecasteaux Channel (DEC) allele frequencies.

Rank Relationship	50th	100th	200th
PO	-73.48	-76.91	-80.23
FS	-70.88	-72.58	-74.30
HS	-68.65	-69.71	-70.21

As a control, two groups of three full-siblings were simulated by randomly choosing parental genotypes from the DEC samples. As before, this created 12 true PO relationships and 6 true FS relationships. The six genotypes were added to the empirical data with pairwise

relationship likelihoods determined. MLRELATE found ten correct PO relationships with seven of these having log likelihoods above the threshold of -80.23 (Table 15). There was one false positive PO with a likelihood of -81.27, which was a true FS pair. Of the six true FS pairs, four were correctly identified. Two of these pairwise matches had log likelihoods greater than -74.30 (Table 15). There were 91 false positive HS relationships from the six simulated genotypes with all pairwise log likelihoods being less than -83.33 a value much smaller than the -70.21 threshold shown in Table 15. Overall, these results indicate that a major proportion of PO and FS pairwise relationships could have been identified if they had existed in the DEC genotypes. The simulation also shows that not all true pedigree relationships could be identified with fifteen loci and that more statistical power, with more loci and alleles, is required to reduce false positive relationships.

Bio-physical modelling

Figures 7.8, 7.10, 7.12 and 7.14 show examples of dispersal trajectories and end points following runs of the bio-physical model of larval connectivity. Notably, Fig. 7.8 demonstrates an eddy facilitating a high degree of self-recruitment around the east Flinders Island region (Fig. 7.12 and Fig.7.14 also show eddy features) and Fig. 7.10 demonstrates propagules ‘running ashore’ prior to reaching a competent settlement age and not being recruited to the population.

Figures 7.9, 7.11, 7.13 and 7.15 show aggregate compilations of the dispersal end points from all release days by year for each of the four spawning boxes. For the east Flinders Island spawning box (Fig. 7.9), 2004 shows a high degree of self-recruitment to the spawning box and broader dispersal to other areas from where scallops are fished. 2005 shows a degree of self-recruitment and also a disproportionate number of larvae being dispersed in the vicinity of the mid-east Tasmanian coast (White Rock region). 2006 shows a degree of self-recruitment but also very good recruitment to the Commonwealth BSCZ scallop beds and particularly into the Victorian (Lakes Entrance region) beds. 2007 shows the highest and most intense degree of self-recruitment for all years tested.

For the Lakes Entrance spawning box (Fig. 7.11) in general there was limited recruitment. This result appears to corroborate the results of scallop surveys run in Victorian waters in 2009 and 2012 (see Appendix 4), which showed poor recruitment, although recruits to Lakes Entrance do originate from other spawning boxes run in the model e.g. east Flinders and Commonwealth BSCZ (see above and below). There was some self-recruitment in 2005-2007, particularly 2006. 2005 shows some dispersal of larvae to the Commonwealth BSCZ, the east Flinders Island region and the Eddystone region. 2007 shows some dispersal of larvae to near the west Flinders Island region.

For the Commonwealth BSCZ spawning box (Fig. 7.13), there was self-recruitment in all years, but particularly 2006 and 2007. There was also some dispersal of larvae to all other regions, but more strongly into the Victorian (Lakes Entrance region) beds (2004 - 2006) and to a lesser extent east Flinders Island (2004-2007).
For the Eddystone spawning box (Fig. 7.15), there was significant self-recruitment and recruitment around east Flinders Island in 2004, 2006 and 2007 and significant recruitment around the mid-east coast (White Rock region) in 2004 and 2005.

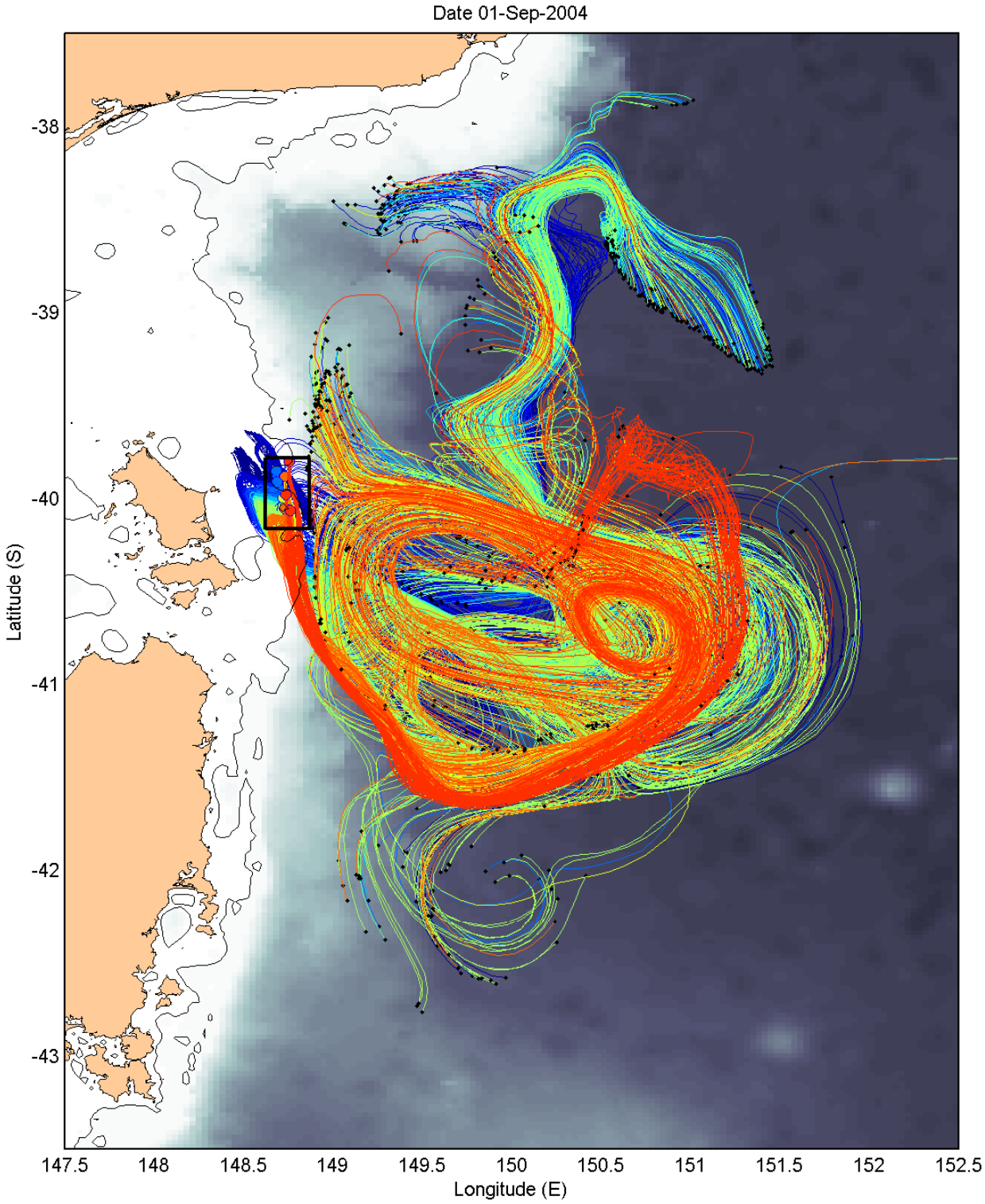


Figure 7.8. An example showing the spawning nodes (coloured circles within black box), dispersal trajectories (coloured lines corresponding to spawning node colours) and end points (black points) from 10 of the 30 spawning nodes off East Flinders Island.

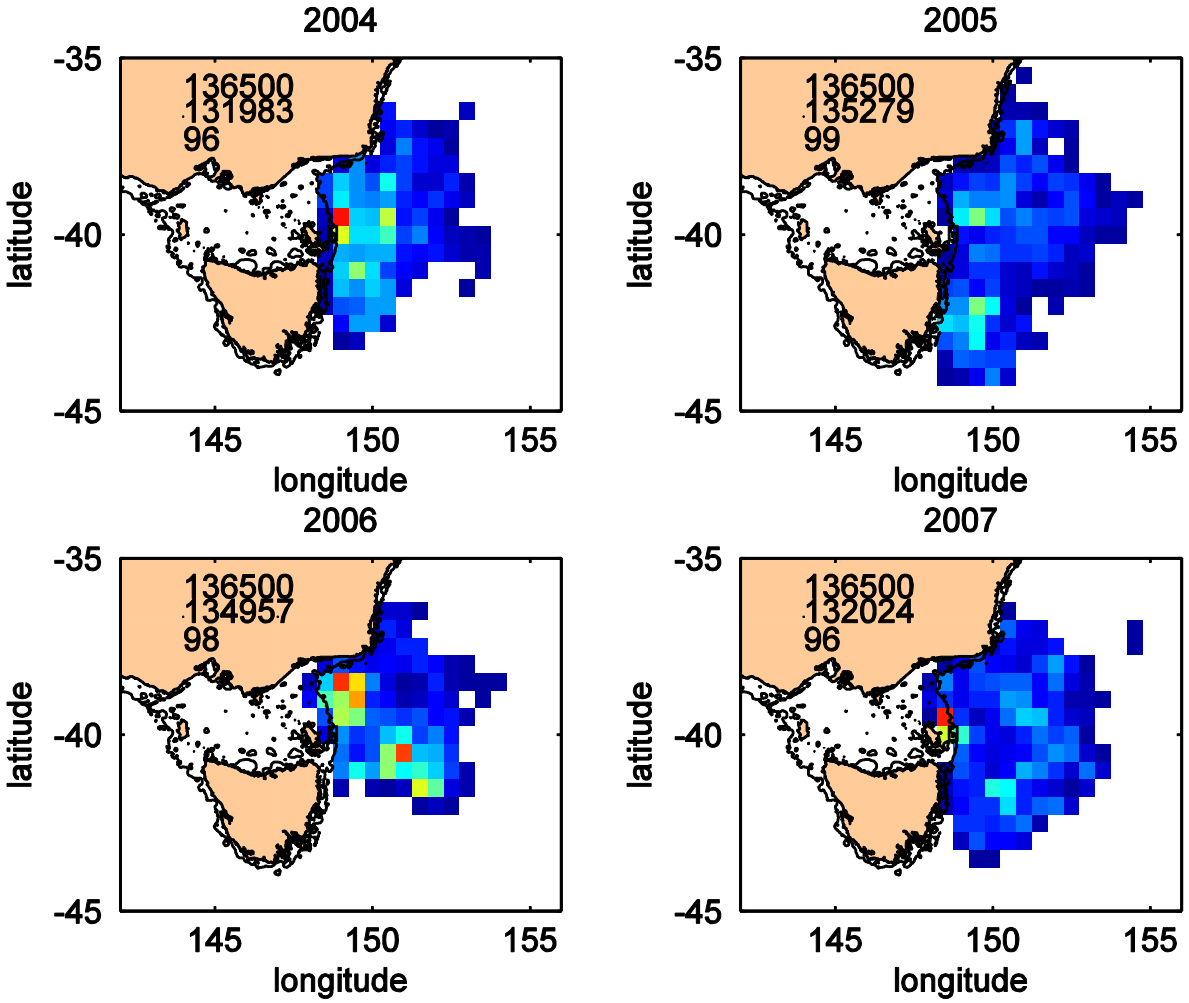


Figure 7.9. Aggregate compilation of the dispersal end point from all release days by year, from blue to red indicates a higher number of scallops in the ½ degree block.

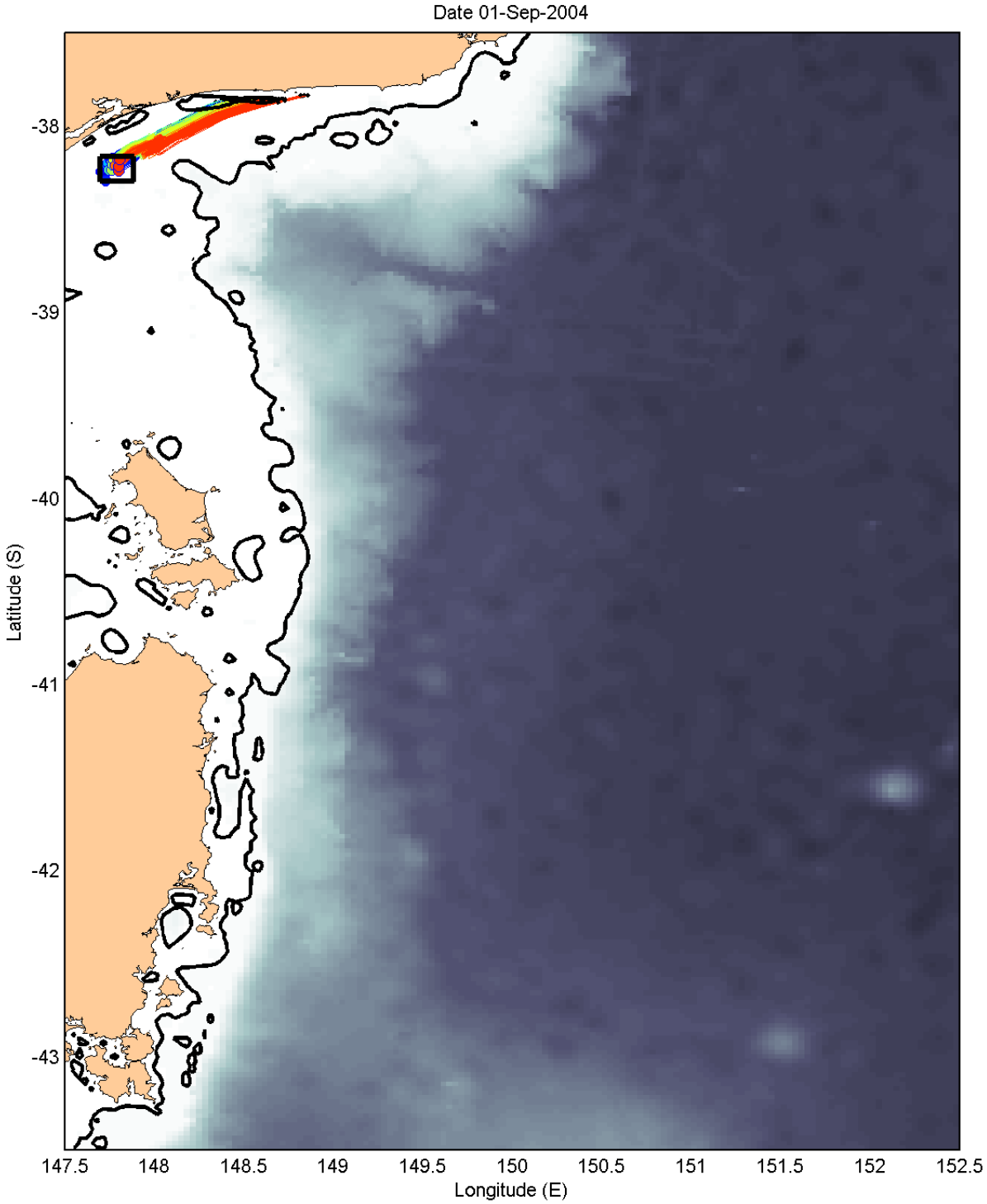


Figure 7.10. An example showing the spawning nodes (coloured circles within black box), dispersal trajectories (coloured lines corresponding to spawning node colours) and end points (black points) from 10 of the 30 spawning nodes off Lakes Entrance.

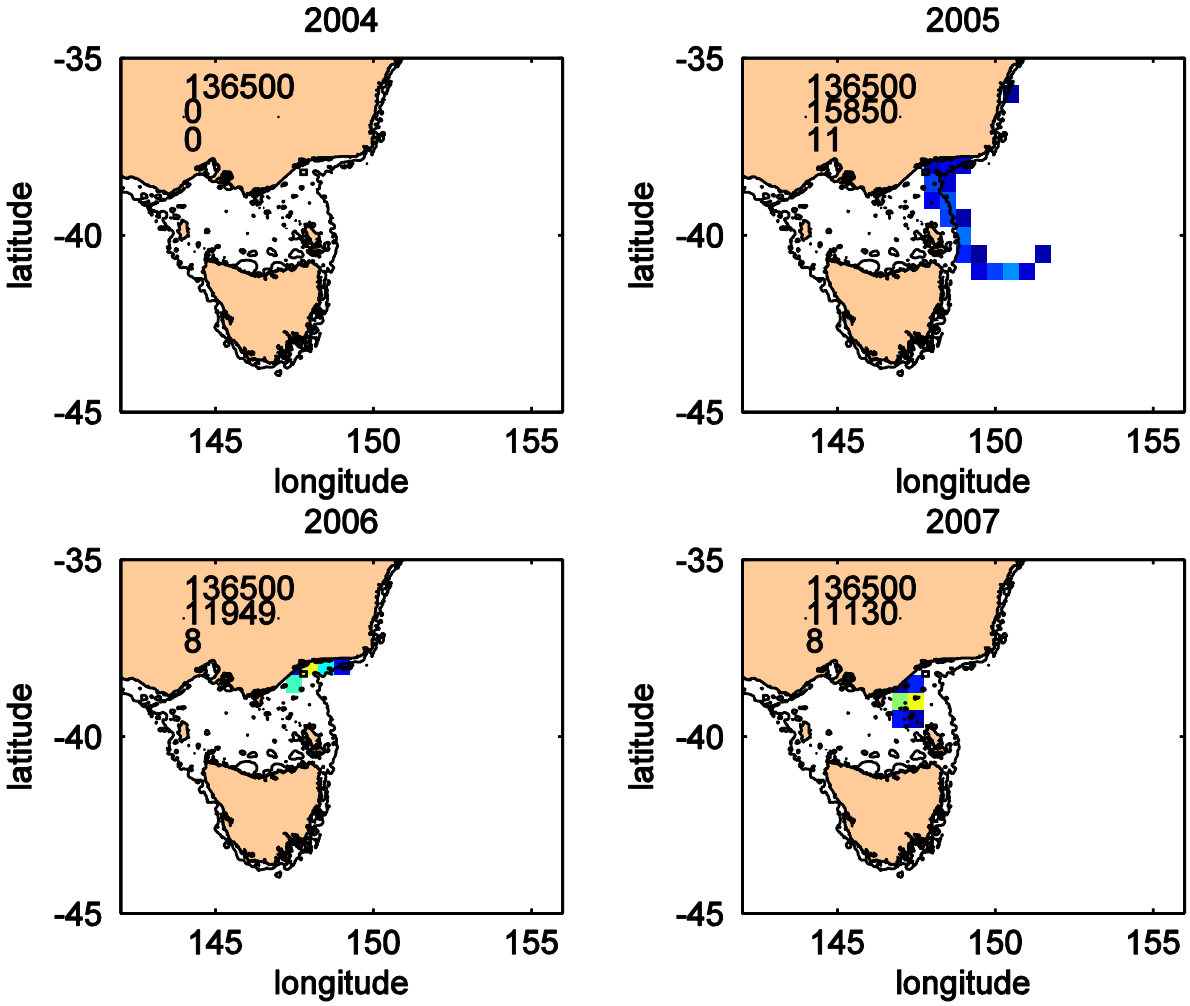


Figure 7.11. Aggregate compilation of the dispersal end point from all release days by year, from blue to red indicates a higher number of scallops in the ½ degree block.

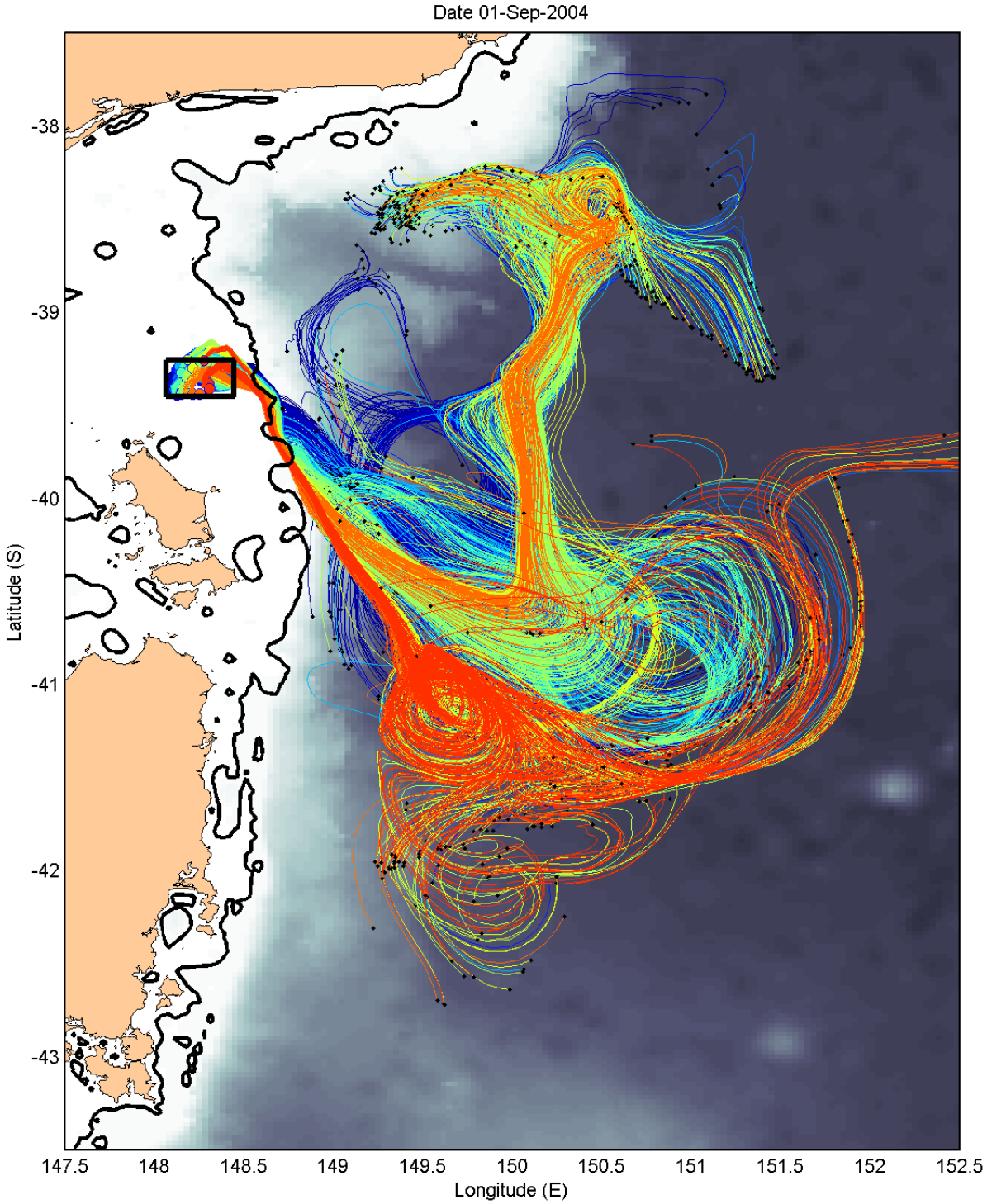


Figure 7.12. An example showing the spawning nodes (coloured circles within black box), dispersal trajectories (coloured lines corresponding to spawning node colours) and end points (black points) from 10 of the 30 spawning nodes in the Commonwealth BSCZ.

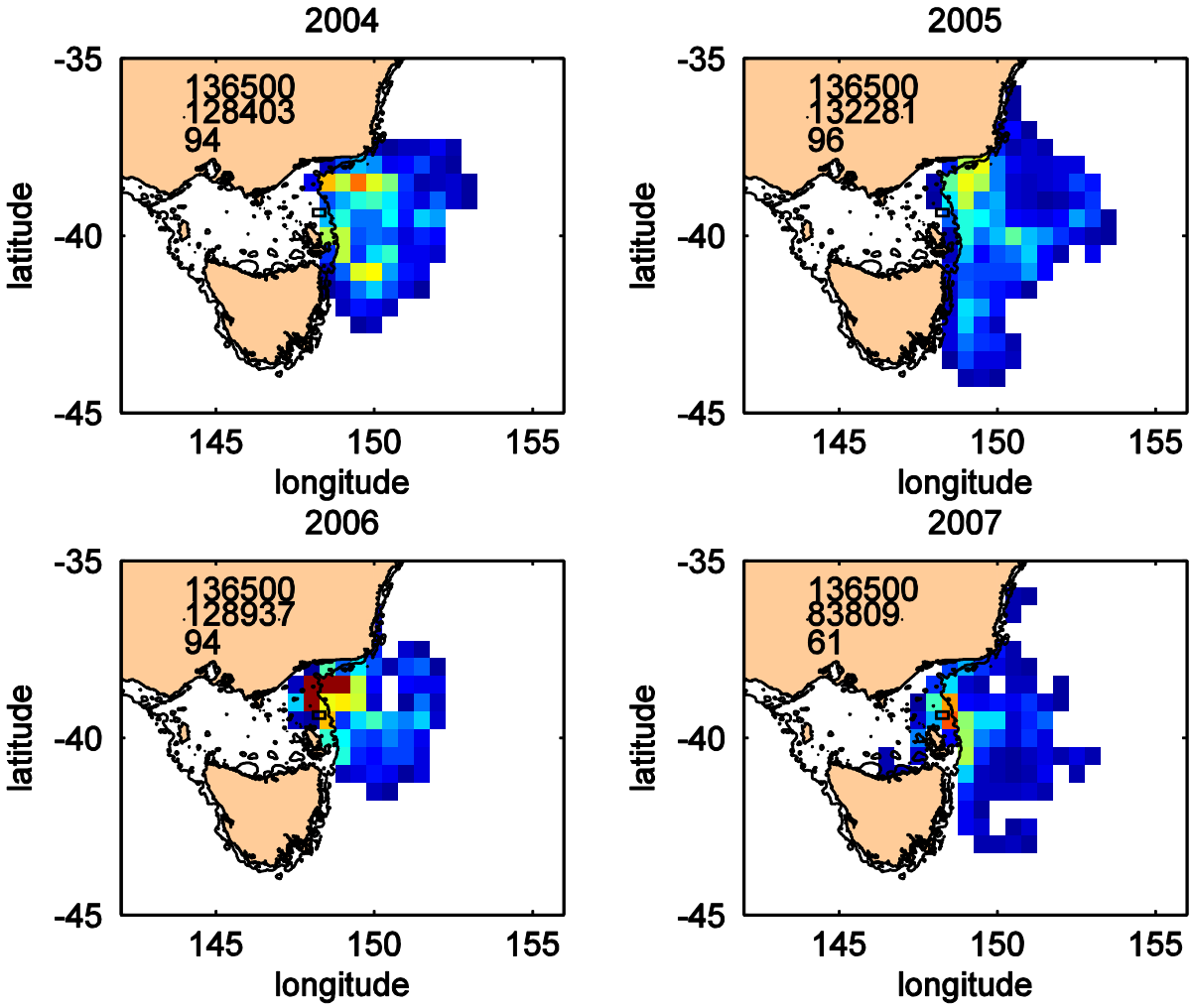


Figure 7.13. Aggregate compilation of the dispersal end point from all release days by year, from blue to red indicates a higher number of scallops in the ½ degree block.

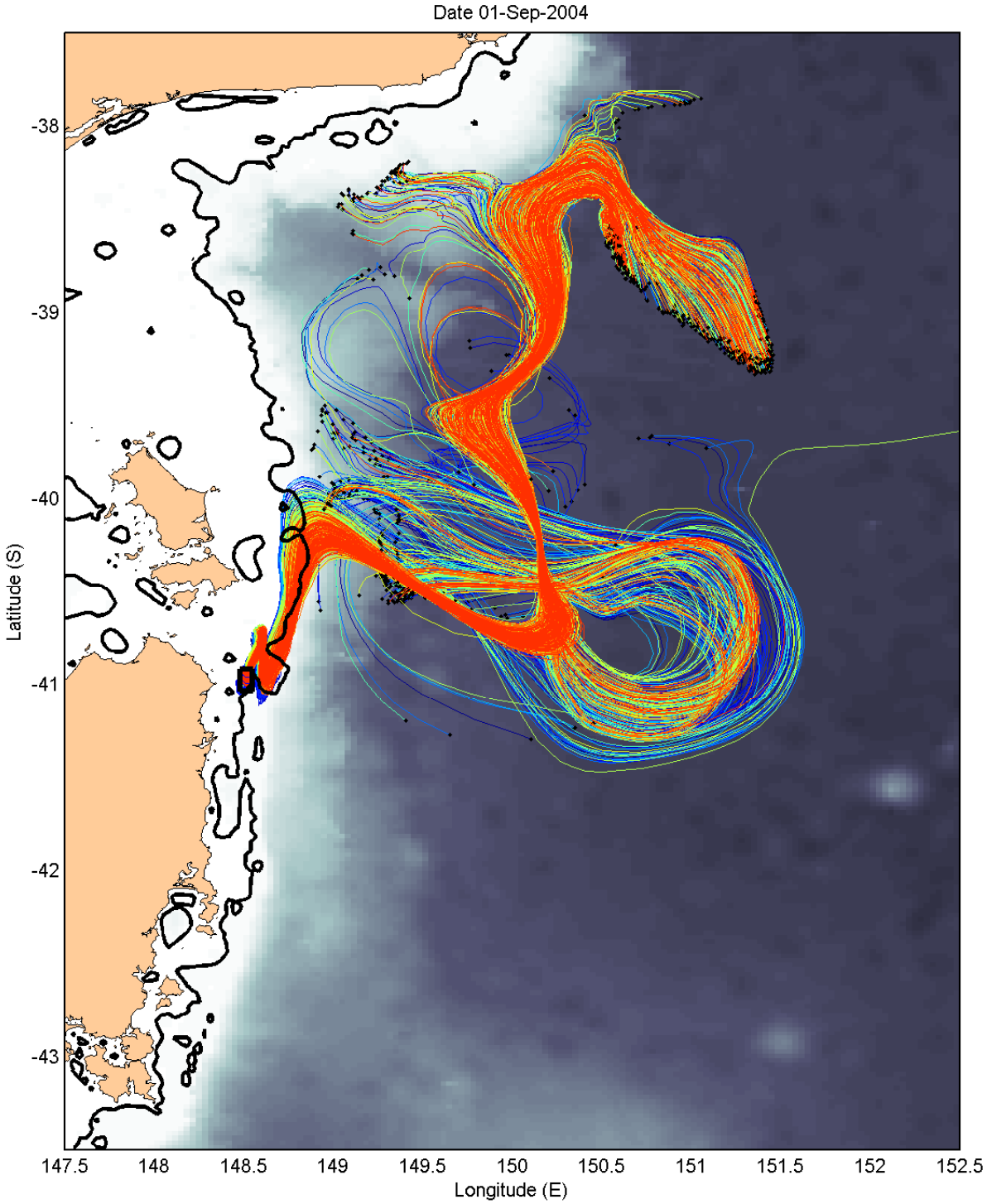


Figure 7.14. An example showing the spawning nodes (coloured circles within black box), dispersal trajectories (coloured lines corresponding to spawning node colours) and end points (black points) from 10 of the 30 spawning nodes off Eddystone Point Tasmania.

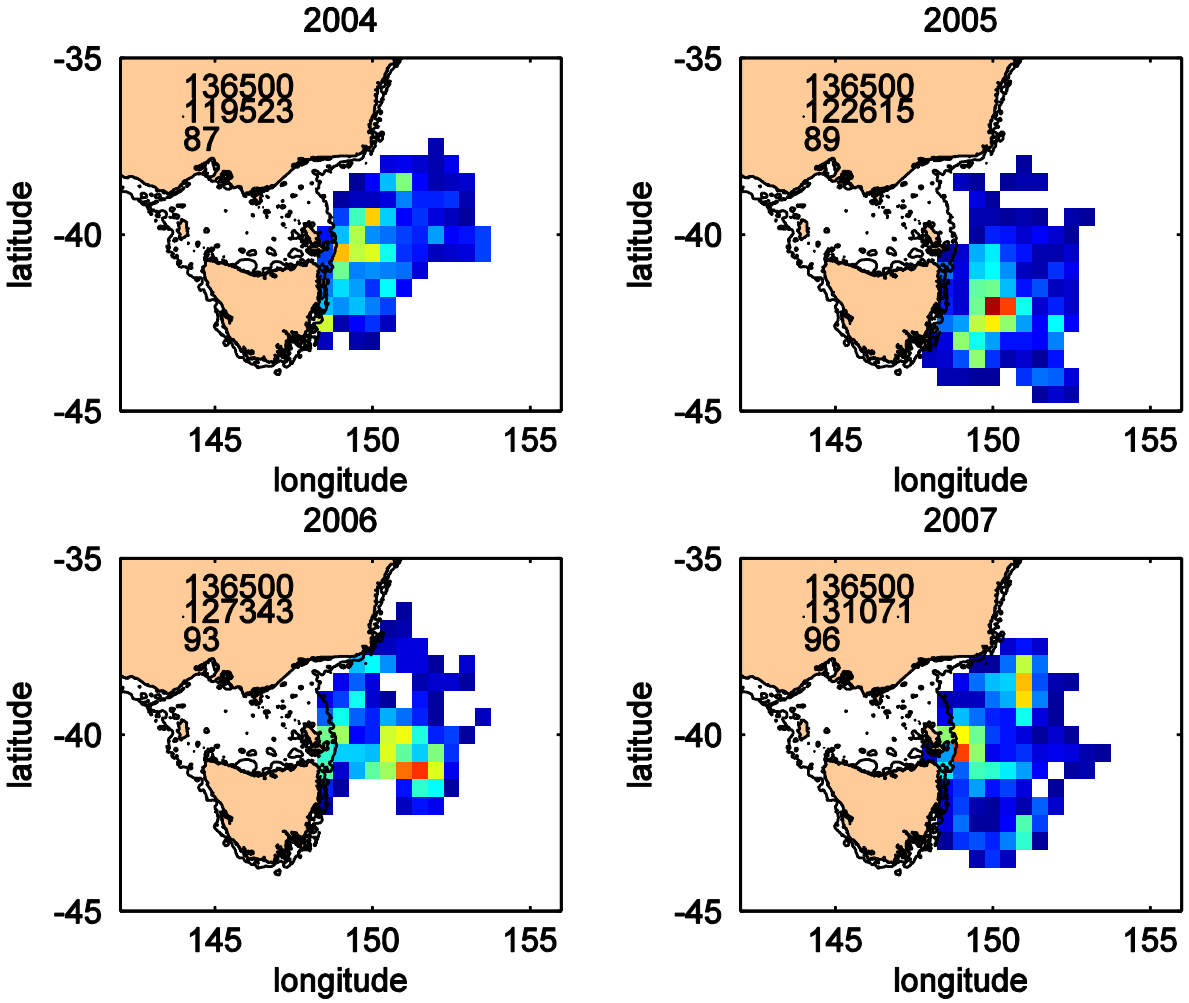


Figure 7.15. Aggregate compilation of the dispersal end point from all release days by year, from blue to red indicates a higher number of scallops in the ½ degree block.

Discussion

Microsatellite loci in Pecten fumatus

The genetic results presented here are derived from a set of eleven, reliable microsatellite loci. But, like others working with microsatellite loci in molluscs, we experienced problems in arriving at this set of loci. Over one thousand individuals were genotyped with 15 loci, but a significant amount of this data could not be used in the majority of analyses. Despite our best efforts, four of the 15 loci had possible null alleles (frequencies of 7, 9, 17 and 23%) and consequently these loci were not included in downstream analyses. Another three loci showed evidence of departure from Hardy-Weinberg equilibrium (HWE) and all of the loci showed positive values for F_{IS}, indicating an overall deficit of heterozygotes.

McInerney *et al.* (2011) suggested two features of molluscan genomes that could be responsible for problems associated with the development of microsatellite loci. Microsatellite flanking regions across loci can either be too similar or too variable in this group. Similarity can be due to the occurrence of cryptic repetitive sequence, or they can be too variable due to the insertion-deletion of consecutive sequence (indels) or other mutations. Cryptic repetitive sequence leads to the amplification of products of unexpected sizes or difficulty in the amplification of products representing alleles of a single locus. Primer-pairs that amplified products like this in our study were discarded, and we have no information about whether this could have been due to cryptic repetitive sequence. However, our study did appear to suffer from flanking region sequence that was too variable. Again, if this had led to complete failure of PCR, then the primer-pair would have been discarded. But, some features of our data could indicate partial primer binding and subsequent poor amplification consistent with highly variable flanking regions. There were null alleles in high frequencies at four loci, a further three failed the HWE test and all loci showed heterozygote deficit (i.e. inbreeding coefficient F_{IS} greater than zero) that is known to occur in the presence of null alleles.

We were potentially interested in using the inbreeding coefficient (Appendix B, F_{IS}) to flag the possible occurrence of inbreeding, selfing or Wahlund effects (e.g. Duran *et al.*, 2004), but in our mollusc study bias in F_{IS} would have been more likely to be associated with variable flanking sequence, so this was not pursued.

Broad-scale stock identification

Extent of stock structure and correspondence between analysis methods

The objective of the genetic part of this project was two-fold; to detect and define stock structure using samples collected throughout the fishery from Port Phillip Bay (Victoria) to DEC (south eastern Tasmania) including locations in between, and to test for a signal of self-recruitment using microsatellite genotypes. Stock structure is a standard application of genetics to wild fisheries populations, while testing for self-recruitment is more speculative, although being widely trialled worldwide (e.g. Planes and Lenfant, 2002; Saenz-Agudelo *et al.*, 2009; Saenz-Agudelo *et al.*, 2011).

Scallops have pelagic larvae of approximately 30-day duration and spawn in the waters of Bass Strait and eastern and southern Tasmania that experience strong and variable current

flow. Under these conditions, larval advection would be expected to lead to genetic homogeneity among adult populations (beds). Jungle perch (*Kuhlia rupestris*) have a similar larval duration (45 days) and adults of this species cannot disperse because they are restricted to freshwater. Larval advection alone was shown to be responsible for the genetic similarity of adult populations on either side of the Coral Sea (eastern Queensland compared to Noumea and Vanuatu). (Feutry *et al.*, Submitted). The scale of the Coral Sea is larger than the scallop fishery, so genetic homogeneity between beds of adult scallops would be the expectation. This was the conclusion of Woodburn (page 235, 1988) who concluded from scallop allozyme data that "the gene pool in Bass Strait appears especially cohesive, with the population in Port Phillip Bay, New South Wales and South Australia relatively isolated from it".

Fifteen years later, results from our microsatellite study almost exactly matches the allozyme results of Woodburn (1988). Like Woodburn (1988), we found that scallops in Port Phillip Bay and the DEC were genetically distinct from each other (population pairwise F_{ST} 0.018). These two sampling locations were also largely distinct from scallops in Bass Strait and eastern Tasmania (Table 7.3). There are two ways in which scallops in Port Phillip Bay and the DEC could maintain their genetic distinctiveness. Firstly, the scallops occur in isolated embayments and may rarely exchange larvae with adjacent populations. Secondly, larval exchange over large distances (i.e. several hundred kilometres) is presumably less likely than over shorter distances. In this case, the most likely explanation is that both processes are occurring. A strong isolation-by-distance signal was detected (Fig. 7.1).

Populations outside embayments occur in open water, and were sampled here in eastern Bass Strait (from Lakes Entrance on the southern Victorian coast to Eddystone Point on the north-eastern tip of Tasmania) and from the eastern coast of Tasmania (White Rock). The geographic distance between them is 500 km or less and most of them lie well within the expected dispersal distance of pelagic larvae with a 30 day duration based on expected current patterns. This should lead to genetic homogeneity within the region encompassing eastern Bass Strait and eastern Tasmania.

However, the samples from Lakes Entrance, in the northern part of eastern Bass Strait, were significantly different to two Bass Strait beds (Eddystone, F_{ST} 0.003; Babel Island, F_{ST} 0.005) and possibly to the bed at White Rock on the eastern Tasmanian coast (F_{ST} 0.004, *p*-value 0.028). The Eddystone Point bed was geographically more distant from Lakes Entrance beds compared to Babel Island beds. The Eddystone location was in the south eastern part of Bass Strait on the northeaster tip of Tasmania, whereas the Babel Island bed was on the northeaster tip of Flinders Island. There were three beds in Bass Strait that were not genetically differentiated from Lakes Entrance, and these were Banks Strait (*p*-value, 0.324), West Flinders Island (*p*-value, 0.770) and Commonwealth (*p*-value, 0.248). Of these three, the Commonwealth beds were closest to Lakes Entrance, so the genetic similarity between them is not surprising.

The F_{ST} values involved in these comparisons are small, indicating genetic differences are low. F_{ST} ranges from 1.0 when the populations are completely different (such as closely related but separate species) to zero when the populations are genetically identical. The *p*-values used to test the statistical significance of the F_{ST} values are derived by bootstrapping, where individuals are randomly allocated to groups of the same size as in the original dataset.

The *p*-value is a measure of the number of times the true F_{ST} value exceeds the F_{ST} value produced from bootstrap replicates. It is a best-practice method of assessing whether the true F_{ST} value is significantly larger than zero.

It is difficult to understand biological mechanisms that could give rise to this genetic pattern. Given the scale of larval dispersal, genetic distinction between beds within Bass Strait should not occur. However, it appears that the pattern of larval interchange between beds is not completely random. The processes involved are completely unknown, and there are many possible explanations. For example, some beds could be more permanent and act as larval 'sources', while other beds could be larval 'sinks'. There could also be hidden, physical barriers to larval interchange, possibly associated with bathymetric features.

Several other lines of evidence support the hypothesis of non-random larval interchange in Bass Strait. Two other scallop beds within eastern Bass Strait (Commonwealth and Eddystone) may be genetically different from our microsatellite dataset (F_{ST} 0.001), as the *p*-value (0.018) for the F_{ST} was similar to the false discovery rate *p*-value of 0.012. Secondly, the multidimensional scaling of Roger's modified genetic distance performed by Woodburn (page 233, Woodburn, 1988) on allozyme results found that Babel Island was the most divergent population in the Bass Strait group. We found this with microsatellites; Babel Island was identified as different from Lakes Entrance. Persistent ocean gyres have been identified in eastern Bass Strait that could regularly bring larvae produced from a particular bed back to that general area (see Bio-physical modelling section and Figures 7.8, 7.9, 7.12-7.15). Although preliminary and with limitations of where data is available around the coast which effects the model, all four regions which had a spawning box for the bio-physical model showed some degree of self-recruitment due to ocean gyres. This was particularly the case for the regions east of Flinders Island (Figs. 7.8 and 7.9), where Babel Island sits, and around Eddystone Point (Figs. 7.14 and 7.15), both of which were genetically differentiated from Lakes Entrance. Repeatable current features that could facilitate self-recruitment within Bass Strait would be consistent with the genetic results, because genetic characteristics are long-standing (i.e. multi-generational), repeatable features of population structure. However, it should be noted that this genetic structuring relates to current oceanographic patterns, which may change as a result of the East Australian Current (EAC) extending over the past 60 years approximately 350 km further south from southern New South Wales into the east coast of Tasmania (Ridgway, 2007).

The 'new' method to test for the presence of genetically structured populations (DAPC, Jombart *et al.*, 2010) did not provide resolution that matched the conventional *F*-statistics approach. This method makes fewer assumptions about population structure (e.g. stepping stone, island model) and Hardy-Weinberg equilibrium (HWE). However, when loci were included that were out of HWE (i.e. D1.dat, Table 6.1), the method gave a false positive result. Jombart *et al* (2010) claim that it is more sensitive than STRUCTURE (Pritchard *et al.*, 2000; Falush *et al.*, 2003) in detecting population groupings, but the F_{ST} values between collections locations (Table 7.5) were small. For the scallop dataset, we assume that the genetic signal showing differences among locations may have been below the level that can be reliably detected with DAPC. While DAPC is rapid (particularly for large datasets), we need a clearer understanding of its strengths. More trials are needed where DAPC analyses are compared to other methods when the levels of spatial genetic differentiation are low.

Comparison with previous genetic studies on scallops

Three recent genetic studies of scallops in the northern hemisphere match the geographic range of this analysis in south eastern Australia. Hemond and Wilbur (2011) studied the population structure of the bay scallop *Argopecten irradians* in the Gulf of Mexico and adjacent Atlantic locations. On the northeaster Pacific coast of North America, Gaffney *et al* (2010) studied another scallop species (weathervane scallops, *Patinopecten caurinus*) from locations in the Gulf of Alaska and the adjacent Bering Sea. The Pacific lion-paw scallop (*Nodipecton subnodosus*) was studied on the western coast of the US in and around the Gulf of California (Petersen *et al.*, 2010). The three studies used microsatellites alone or in combination with other genetic markers.

Two of the three studies found genetic differentiation among populations of scallops. Hemond *et al* (2011) reported that F_{ST} between two geographically distant populations (Gulf of Mexico compared to western North Atlantic) exceeded 0.120, which was larger than we found here between Port Phillip Bay and DEC (F_{ST} 0.018). The magnitude of the microsatellite F_{ST} from six populations inside the Gulf of Mexico was similar to what we found among the populations in Bass Strait. Hemond *et al* (2011) believe that their large F_{ST} (that was an order of magnitude above our largest values) was due to possible selection on adaptive genes linked to microsatellite alleles, and they argue that this is important baseline data for resource management and conservation. The microsatellite F_{ST} between populations of lion-paw scallops inside and outside the Gulf of California were genetically distinct (F_{ST} 0.032 to 0.045) (Petersen *et al.*, 2010). These F_{ST} values were more similar to the upper range of the values reported here for *P. fumatus*.

The null hypothesis of genetic homogeneity could not be rejected for weathervane scallops, however. The overall F_{ST} was 0.0004 for populations extending 2500km in the Gulf of Alaska and the Bering Sea (Gaffney *et al.*, 2010) based on microsatellite loci. Similarly low F_{ST} 's were obtained from the same samples using other genetic marker systems (allozymes and mitochondrial DNA). Gaffney *et al* (2010) conclude that the apparent lack of population structure does not rule out the presence of locally adapted populations, although their study found no evidence of genes under selection.

Overall, these studies show that populations of scallops with disjunct distributions are likely to be genetically differentiated. Just like *P. fumatus* populations that were genetically distinct between embayments in south eastern Australia (i.e. Port Phillip Bay and DEC), populations of scallops inside and outside both the Gulf of Mexico (Hemond and Wilbur, 2011) and the Gulf of California (Petersen *et al.*, 2010) were genetically distinct. This would be consistent with attenuation of larval interchange between beds of adults, presumably due to lack of water current exchange between embayments and adjacent open water. Unlike this study, these studies did not report genetic differentiation among beds in open water. Adjacent beds on coastlines (Petersen *et al.*, 2010; Hemond and Wilbur, 2011) or in the Gulf of Alaska (Gaffney *et al.*, 2010) were not genetically differentiated.

Recruitment patterns

Lack of knowledge of recruitment patterns is considered a major bottleneck to the management of the scallop resource for sustainability and profitability. In this project, a large

amount of effort was expended towards testing for the presence of self-recruitment. We developed 15 new, highly variable (i.e. powerful) microsatellite markers and assayed over 1000 individuals representing beds from enclosed and open waters. We used the latest analysis methods and developed unique simulation approaches to detect and evaluate genetically related pairs of scallops (i.e. parent-offspring pairs, full and half-sibling pairs) whose presence would have indicated self-recruitment. However, all the pairs of related scallops that were found were false-positive matches, and none were true relatives.

Insufficient sampling intensity was the most likely reason for not detecting true relatives among the samples from the enclosed embayment (i.e. DEC). Here, the lack of water exchange with open inshore waters in south eastern Tasmania almost guarantees some degree of self-recruitment. Failure to detect pairs of relatives in the Channel could be because a) there were no related pairs to detect, b) there was insufficient genetic power to identify relatives, or c) there were too few true relatives in the data from which to draw any inferences. The ability to detect true relationships by adding a small number of control relationships rules out scenario (b), and we believe related pairs of individuals would have been present among the Channel beds due to self-recruitment. In other words, our sample size was just too small compared to the size of the scallop breeding population to genetically detect self-recruitment.

The genetic effective population size (*Ne*, a surrogate for the number of breeding individuals under certain conditions, Ovenden *et al.*, 2007; Hare *et al.*, 2011) of scallops in the Channel is likely to be high. Using the eleven-locus dataset, the lower 95% confidence interval for *Ne* was estimated to be 5,000 in the DEC. These calculations were performed using the LDNE software (Waples and Do, 2008). The actual estimate of *Ne*, and upper 95% limits of *Ne* were much greater. In a full factorial mating of 3,000 males and 3,000 females, where all parents contribute the same number of offspring, the chance of picking up two samples that have a full sib relationship equals $1/(3000)^2$. There were 744 genotypes in the eleven-locus data set, so there were 299,151 pairwise comparisons. The chance of finding a pair of full siblings is that multiplied by $1/(3000)^2$. This equals 0.03, which is a small chance of finding the full sib pair. It is however unlikely that a full factorial mating of this size would occur, and it is also likely that the breeding population size would be much greater than 3,000. Thus, there was little chance of finding pedigree relationships within the scallop population in the Channel population given the numbers sampled.

Perhaps greater precision in pedigree assignment could have been achieved using a joint likelihood approach such as implemented in the software COLONY (Wang, 2004). This analysis method is potentially more accurate as it builds up information from putative parental genotypes, which are built into the likelihood equations. The major difficulty with this approach is that a single likelihood is obtained for the entire group of genotypes in the dataset making it difficult to address false positives. In data sets with few relationships, such as the scallop data, the joint likelihood approach may not be much better than pairwise likelihood methods such as MLRELATE as the likelihoods calculated by COLONY can only be improved with the existence and identification of true groups of full and half-siblings.

MLRELATE can account for Hardy-Weinberg disequilibrium per locus, but does not account for missing data. Thus, a subset of the data with no missing alleles was necessary for this analysis. But unfortunately, this also reduced the sample size, which reduced the chance of

finding relatives. Another limitation of MLRELATE is that the likelihoods are determined assuming there are no mistakes in identifying one allele from another (genotyping errors). Two related samples would have a lower likelihood of being relatives if there was a genotyping error in one of the genotypes but not as low had an error model been implemented.

There are three major take home messages from the genetic self-recruitment analysis; (1) there was a lack of related pairs of individuals within the data and the implication is that a significant increase in sample size would be required to detect recruitment patterns between populations, however (2) increasing sample size would exponentially increase the number of pairwise comparisons (Macbeth *et al.*, 2011) and thus would require more microsatellite loci to address an increased level of false positives at a given likelihood value, and (3) even without a larger sample size, more microsatellite loci would assist the partitioning of log likelihood distributions for each of the relationship classes (PO, HS and FS) with current sample sizes.

Future research in this area would benefit from more genetic markers and more intensive sampling of a few spatially close scallop beds and their spat from an enclosed embayment (e.g. DEC, Port Phillip Bay). This approach should increase the chance of finding relatives from which to draw inferences about recruitment dynamics. In practice, the likely large effective population sizes of scallops, even within the DEC, will make the detection of relationship inferences challenging.

Appropriate scales of management

The objective of this study was to resolve the pattern of recruitment among scallop beds in Bass Strait. Beds outside Bass Strait within the embayments of Port Phillip Bay and DEC were included to provide contrast in the data, and to test methodology for detecting self-recruitment. Results from embayment beds conformed to expectations: they were shown to be genetically distinct from the remainder. As such, they should be treated as separate stocks and be managed with spatially appropriate restrictions on harvesting.

In the open water of Bass Strait, the expectation of genetic homogeneity appears to be subtly disrupted. In eastern Bass Strait, this seems to be occurring within a radius of 200 – 400 km. Several lines of evidence, from previous genetic studies to observations by fishers, appear to support the hypothesis of non-random dispersal and subsequent settlement of larvae. Circulating currents (see Bio-physical modelling section and Figures 7.8, 7.9, 7.12-7.15) could entrain pelagic larvae and return them as recruits on a regular basis into natal beds. The genetic analyses were unable to directly test this hypothesis by providing evidence of close relatives (e.g. parent – offspring pairs) within beds. Embayment studies showed that the microsatellite loci were powerful enough to detect relatives if they were there, but the ratio between the numbers of animals genotyped and the population size of a scallop bed was not high enough to include related animals in the sample.

This outcome departs from the widely accepted model of population genetic stock structure in fisheries. Generally, genetic data is used to make inferences about restrictions to gene flow, which is used to divide the range of a continuously distributed species into spatially discrete stocks. Within Bass Strait, and despite preliminary evidence from the bio-physical modelling that ocean gyres may be causing self- recruitment, it was not possible to explain the genetic

pattern as spatially discrete stocks. Future analyses of larger samples of individuals or genes may resolve this situation. Even though the general model does not seem appropriate, there is value in these microsatellite results for the management of scallops in Bass Strait.

At a population level, genetic markers provide information about micro-evolutionary processes such as genetic drift, natural selection, mutation and gene flow. Three of these forces may be operating at low levels in the Bass Strait scallop population. The genetic results appear to be inconsistent with spatial barriers to gene flow. The microsatellite loci used here are neutral with respect to natural selection, and the rate of appearance of mutations is inversely related to effective population size. If these three forces can be ruled out, then the genetic signal in Bass Strait may be originating from genetic drift. Genetic drift describes the change in gene frequencies across generations due to random sampling, and is most pronounced when the numbers of individuals that successfully reproduce each year is small (Ovenden *et al.*, 2007). In other words, scallops in Bass Strait may not be as reproductively successful as their biology would lead us to believe (this may be due to insufficient adult densities – see section 7.3). This suggests that a 'fine-scale rotational harvest strategy' may be the most appropriate management model for Bass Strait, particularly if the genetic effect is occurring within a finite radius (i.e. 200 – 400km).

7.2 EVALUATE THE EFFECTS OF INTENSIVE ROTATIONAL DREDGE FISHING ON SCALLOP BEDS AND SCALLOP RECRUITMENT EVENTS.

7.2.1 Results and discussion

A total of 96,567 individual organisms from 60 species, or groups of related species where identification to individual species was not possible, were collected during the two before and two after BACI surveys. The target species of the fishery the commercial scallop, *P. fumatus*, was the most abundant species and the only species caught in each of the 118 tows, with an average abundance of 0.2 scallops per m^2 (± 0.28) (Table 7.16).

Species and relative abundance

Commercial scallops accounted for 88% of the total individuals caught during the four surveys, however, the vast majority of species occurred in very low abundances and accounted for less than 1% of the total individuals caught during the surveys (Fig. 7.16). Molluscs were by far the most dominant group found within the surveyed regions, accounting for 96.5% of the total individuals caught during the four surveys (Fig. 7.16b). Each of the remaining animal categories accounted for less than 2% of the total individuals caught (Fig. 7.16 b).

Other than scallops, only hermit crabs (*Strigopagurus strigimanus*, and other unidentified species), Australian tulip shells (*Pleuroploca australasia*), and cockles (*Glycymeris* spp.*)* were found in greater than 50% of the sample tows conducted (Fig. 7.16). Approximately half the species identified were observed in less than 5% of the sample tows conducted (Table 7.16). When considering the animal categories identified in Table 7.16, hermit crabs, bivalves, other molluscs, seastars and other crustaceans categories were observed in 94%, 82%, 80%, 59% and 52% of the tows conducted respectively.

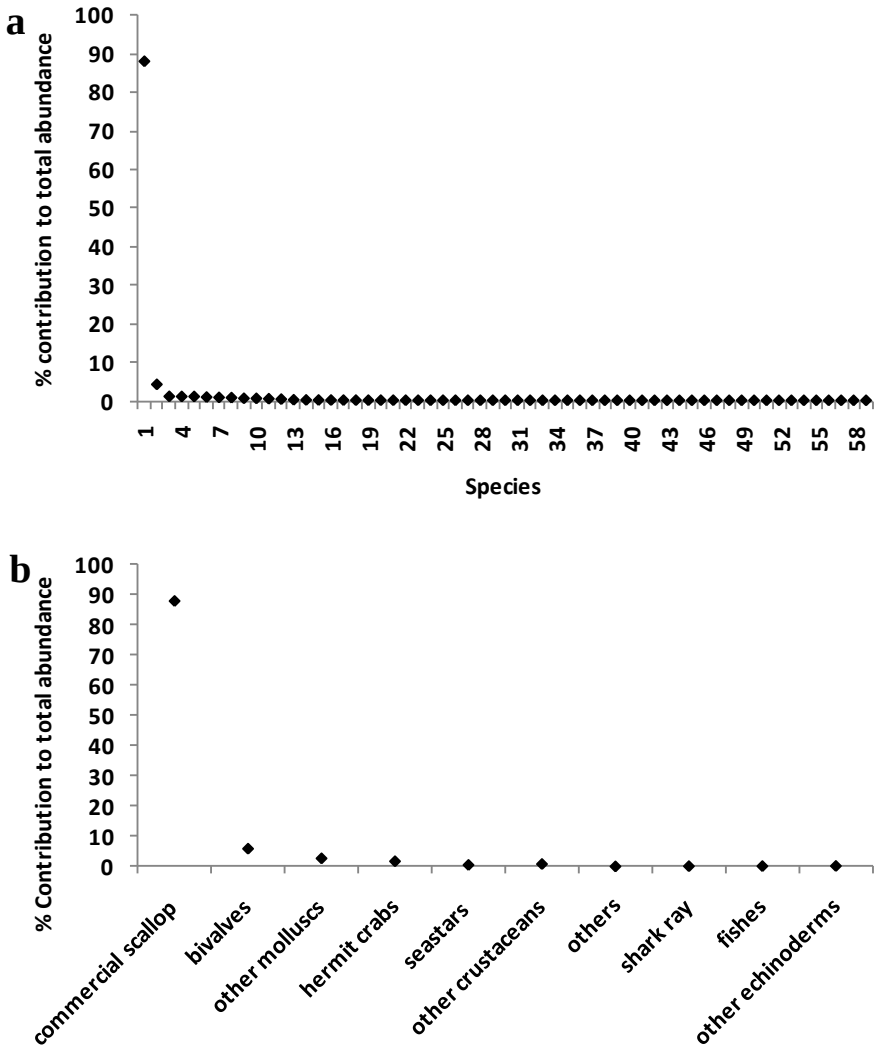


Figure 7.16. The percentage contribution (a) each species and (b) animal category (as per Table 7.16) made to the total number of individuals caught during the four surveys.

Table 7.16. Species list showing animal categories, scientific names, common names, average abundance caught per 1m^2 sampled area (± SE) and the number of tows this species occurred in. Note the total number of tows conducted during the four surveys was 118.

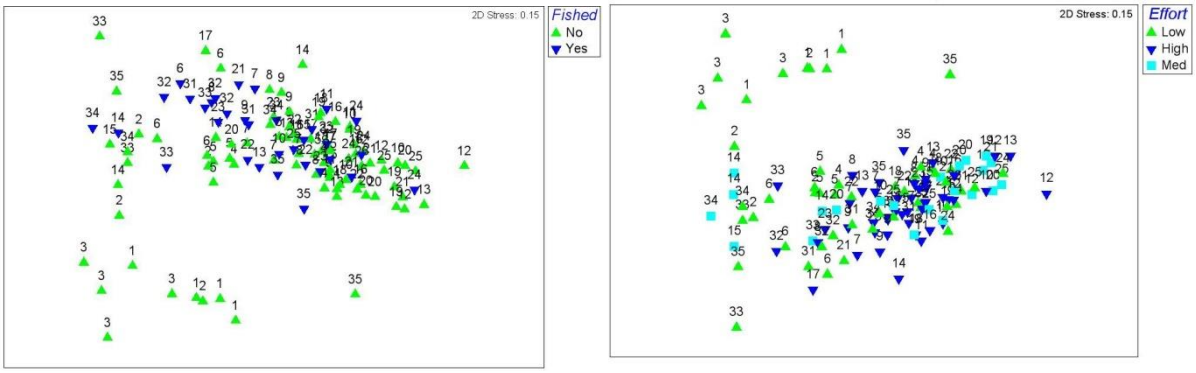
Category	Scientific name	Common name	av. Abund /m^2 (± SE)	Tows
1.Scallop				
	Pecten fumatus **	Commercial Scallop	0.21261 ± 0.28	118
2.Bivalves				
	Chlamys asperrimus **	Doughboy Scallop	0.01001 ± 0.00478	47
	Mytilus edulis	Mussel	<0.00001	2
	Ostrea angasi **	Mud / Flat Oyster	0.00203 ± 0.00161	22
	Neotrigonia margaritacea	Brooch Shell	<0.00001	1
	Bassina pachyphylla	Faintly-Frilled Venus Clam	<0.00001	1
	Bassina disjecta	Frilled Venus Shell	<0.00001	1
	Solen vaginoides	Southern Razor Shell	0.00003 ± 0.00002	6
	Glycymeris striatularis **	Striated Dog Cockle		
	Glycymeris radians **	Radiant Dog Cockle	0.00182 ± 0.00038	67
	Glycymeris grayana **	Grays Dog Cockle		
	Fulvia tenuicostata	Thin-Ribbed Cockle	<0.00001	1
	Eucrassatella kingicolca	King Island Whelk	0.00034 ± 0.00021	22
3.Other Molluscs				
	Maoricolpus roseus	New Zealand Screwshell	0.00242 ± 0.00136	8
	Philine angasi	Angas Bubble Shell	<0.00001	1
	Semicassis pyrum	Pear Helmut Shell	<0.00001	1
	Charonia lampas **	Red Rock Whelk	0.00127 ± 0.00123	11
	Fusinus novaehollandiae	New Holland Spindle Shell	0.00005 ± 0.00002	7
	Amoria undulata **	Wavy Volute	0.00016 ± 0.00005	30
	Cypraea hesitate	Umbilicated Cowrie	0.00004 ± 0.00004	2
	Pleuroploca australasia **	Australian Tulip Shell	0.00241 ± 0.0004	85
	Calliostoma armillata	Top Shell	0.00007 ± 0.00004	4
	Sepioteuthis australis	Southern Calamary	<0.00001	1
	Octopus pallidus	Pale Octopus	0.00008 ± 0.00003	12
	Octopus berrima	Southern Keeled Octopus		
4.Hermit Crabs				
	Strigopagurus strigimanus **	Hairy Hermit Crab	0.00249 ± 0.00041	103
	Unidentified Sp. **	Wavy Hermit Crab	0.00168 ± 0.00025	81
5.Other Crustaceans				
	Pilumnus tomentosus	Hairy Shore Crab	0.00018 ± 0.00005	19
	Leptomithrax gaimardii **	Spider Crab	0.00099 ± 0.00035	44
	Ibacus alticrenatus	Wollongong Bug	0.00003 ± 0.00002	5
	Ovalipes australiensis	Surf Crab	0.00002 ± 0.00001	3
6.Seastar				
	Coscinasterias muricata **	11-Arm Seastar	0.00073 ± 0.0003	22
	Bollonaster pectinatus **	Astropectinid Seastar	0.00123 ± 0.00022	59
7.Other Echinoderms				
	Amblypneustes ovum	Urchin	<0.00001	1
	Heliocidaris erythrogramma	Common Urchin	0.00004 ± 0.00002	6
	Unidentified Sp.	Heart Urchin	<0.00001	1

Table 7.16. Continued

Category	Scientific name	Common name	av. Abund /m^2 (± SE)	Tows
8.Fishes				
	Lophonectes gallus	Crested Flounder	0.00002 ± 0.00001	6
	Rhombosolea tapirina	Greenback Flounder	0.00001 ± <0.00001	2
	Aracana aurita	Shaws Cowfish	<0.00001	1
	Diodon nicthemerus	Porcupine Fish	<0.00001	1
	Platycephalus bassensis	Sand Flathead	0.00001 ± <0.00001	3
	Neoplatycephalus richardsoni	Tiger Flathead	0.00007 ± 0.00002	15
	Muraenichthys breviceps	Southern Worm Eel	<0.00001	1
	Foetorepus calauropomus	Common Stinkfish	0.00002 ± 0.00001	4
	Lepidotrigla papilio	Spiny Gurnard	0.00002 ± 0.00002	3
	Lepidotrigla Vanessa	Butterfly Gurnard	0.00004 ± 0.00001	10
	Kathetostoma leave	Common Stargazer	0.00004 ± 0.00001	11
	Paristiopterus labiosus	Giant Boarfish	<0.00001	1
9.Sharks and Rays				
	Narcine tasmaniensis	Tasmanian Numbfish	0.00003 ± 0.00001	8
	Trygonorhina guanerius	Southern Fiddler Ray	<0.00001	1
	Raja whitleyi	Whitley's Skate	<0.00001	1
	Urolophus paucimaculatus	Sparsely Spotted Stingaree	0.00023 ± 0.00004	36
	Urolophus cruciatus	Banded Stingaree	0.00001 ± 0.00001	3
	Heterodontus portusjacksoni	Port Jackson Shark	<0.00001	1
	Cephaloscyllium laticeps	Draughtboard Shark	<0.00001	2
10.Other Species				
	Unknown spp.	Sponge Large	0.00005 ± 0.00002	11
	Unknown spp.	Sponge Small	0.00011 ± 0.00004	13
	Sarcoptilus grandis	Sea Pens	0.00003 ± 0.00001	9
	Pyura stolonifera	cunjevoi	0.00011 ± 0.00007	4
	Unknown spp.	Polychaete worm	0.00007 ± 0.00005	5
	Unknown spp.	Polychaete worm sea mouse	<0.00001	1
	Unknown spp.	corals and bryazoans	0.00003 ± 0.00002	6

Community comparison

Looking at the entire survey region over both years, there appears to be little impact on community structure due to fishing pressure. MDS ordinations show no difference in community structure between fished and control (not fished) sites. Species abundance rankings between fished and non-fished regions overlapped considerably, with no indication of separation within the MDS model (and thus no evidence for differences between them) (Fig.7.17a). Allocation of the three levels of fishing effort to each site did not reveal any segregation between the sites either (Fig.7.17b), which is consistent with the anosim results (R = 0.001 p = 4.74).



a b

Figure 7.17. a): Multi-dimensional scaling (MDS) using the Bray Curtis resemblance to compare species abundance rankings between a) survey sites that were fished (blue inverted triangles) and control (green triangles) sites and b) survey sites located in areas of different levels of fishing pressure. Survey sites are numbered, with 1- 6 belonging to the western bed and the rest to the Eastern region (multiple numbers are due to multiple surveys).

Despite this, there is some distinct grouping in Fig. 7.17, with sites labelled 1 to 6 tending to be more distinct from the rest of the sites according to community structure. These sites were all located in the western area, which was not fished. The two survey regions, western and eastern, were 30 km from each other, and samples from these two regions showed indications of a difference in community structure. MDS ordinations of the sites according to regions also revealed some difference in community structure between the two regions (Fig. 7.19) consistent with Anosim results. An Anosim R value of 0.39 was weakly significant at 0.001 indicating that the similarities between samples within the different beds are greater than the similarities in samples between the different beds.

A SIMPER test allowed dominant species to be identified for each region and indicated the species responsible for the largest differences in the community comparisons; commercial scallops contributed the most to differences (42 %) as would be expected, with cockles and hermits contributing the next most significant levels (Table 7.17). The two sites had a dissimilarity of 63 %, with the Eastern bed having 50% fewer species with significant catch rates, and a 30% higher contribution of scallops to the total catch. There was a much reduced presence of cockles, doughboys and screw shells from the eastern region (Table 7.17).

Table 7.17. Proportion of main species in the total catch by region. The Eastern bed and Western Bed had an average dissimilarity of 62.85.

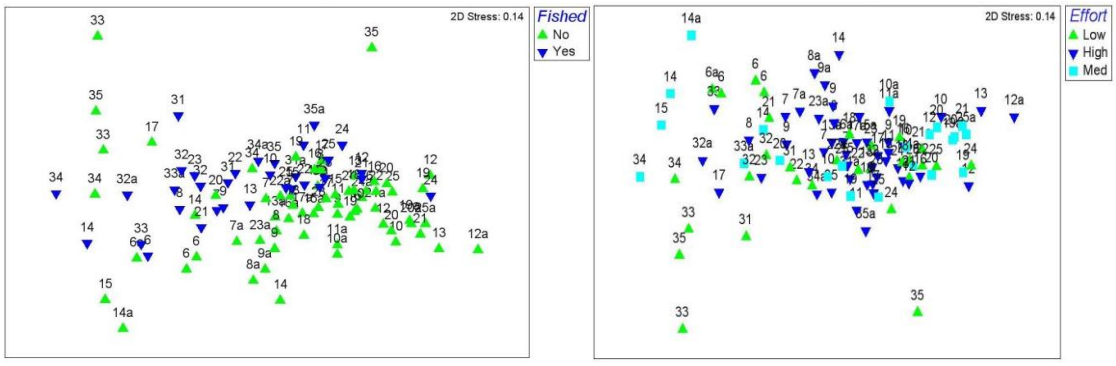
Western Bed

Species	*Av.Abund*	*Av.Sim*	*Sim/SD*	*Contrib%*	*Cum.%*
P. fumatus	0.16	17.60	1.57	42.65	42.65
Glycymeris spp	0.05	7.16	1.23	17.35	60.00
S. strigimanus	0.04	5.63	1.31	13.64	73.63
P. australasia	0.03	3.42	1.13	8.29	81.92
M. roseus	0.05	1.17	0.24	2.84	84.76
B. pectinatus	0.01	0.84	0.50	2.04	86.79
C. asperrimus	0.02	0.76	0.42	1.85	88.64

Eastern Bed

Species	*Av.Abund*	*Av.Sim*	*Sim/SD*	*Contrib%*	*Cum.%*
P. fumatus	0.42	36.23	2.26	73.22	73.22
S. strigimanus	0.04	3.79	1.27	7.65	80.87
P. australasia	0.04	2.02	0.84	4.07	90.48

Given the differences in community structure between the two beds, data from the eastern region was separated from the western region, however running the MDS on sites from the eastern region only did not change the level of differences seen. Comparing fished to non – fished sites within the eastern bed showed no significant difference between community structure (R 0.15, p = 0.02), nor was there any difference between sites with different levels of fishing effort (R 0.13, p = 0.02) (Fig. 7.18).

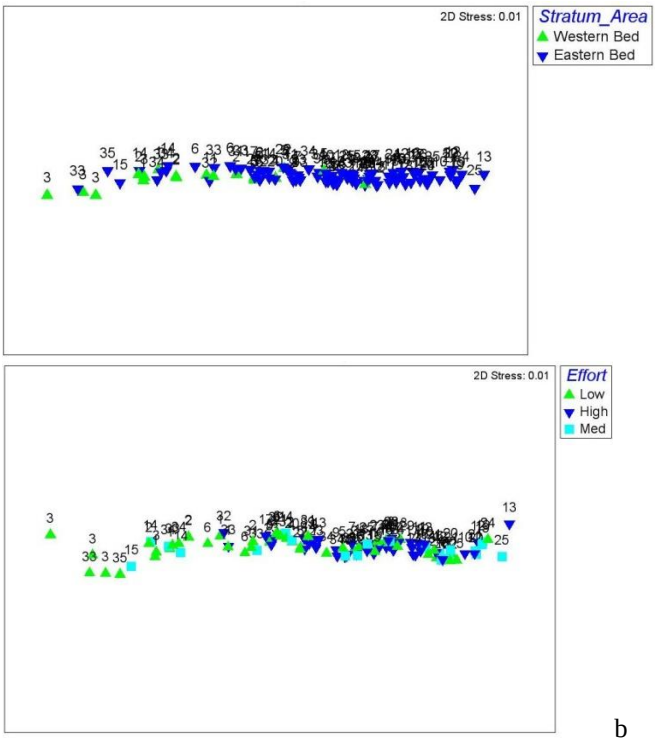


a b

Figure 7.18. MDS ranking of sites within the eastern region only at levels of a) fished or control, and b) three levels of fishing effort.

To account for the low catch abundances of the different species the model was run again with the commercial scallop abundance data only (Fig 7.19), as it was the dominant species and contributed 40.44% to total abundance across the surveyed sites. The survey region(either western or eastern) did not have a distinct impact on scallop abundance (Fig.

7.19) nor did the level of fishing effort (Fig. 7.19b) (R = 0.002, p=4.2%).



b

Figure 7.19. Multi-dimensional scaling (MDS) using the Bray Curtis resemblance to compare scallop abundance rankings a) across the two regions and b) between fished and non-fished sites at three levels of fishing effort.

Size distribution of commercial scallops

On comparing the size frequency distributions for scallops caught in the 2010 post fishing survey, there were relatively similar size distributions, allowing for growth over time and the removal of fished individuals, in all areas regardless of whether they were not fished, fished for a single year (2010) or fished twice in consecutive years (2009 and 2010) (Fig. 7.20). In terms of recruitment, there were no signs of new recruits regardless of fishing history.

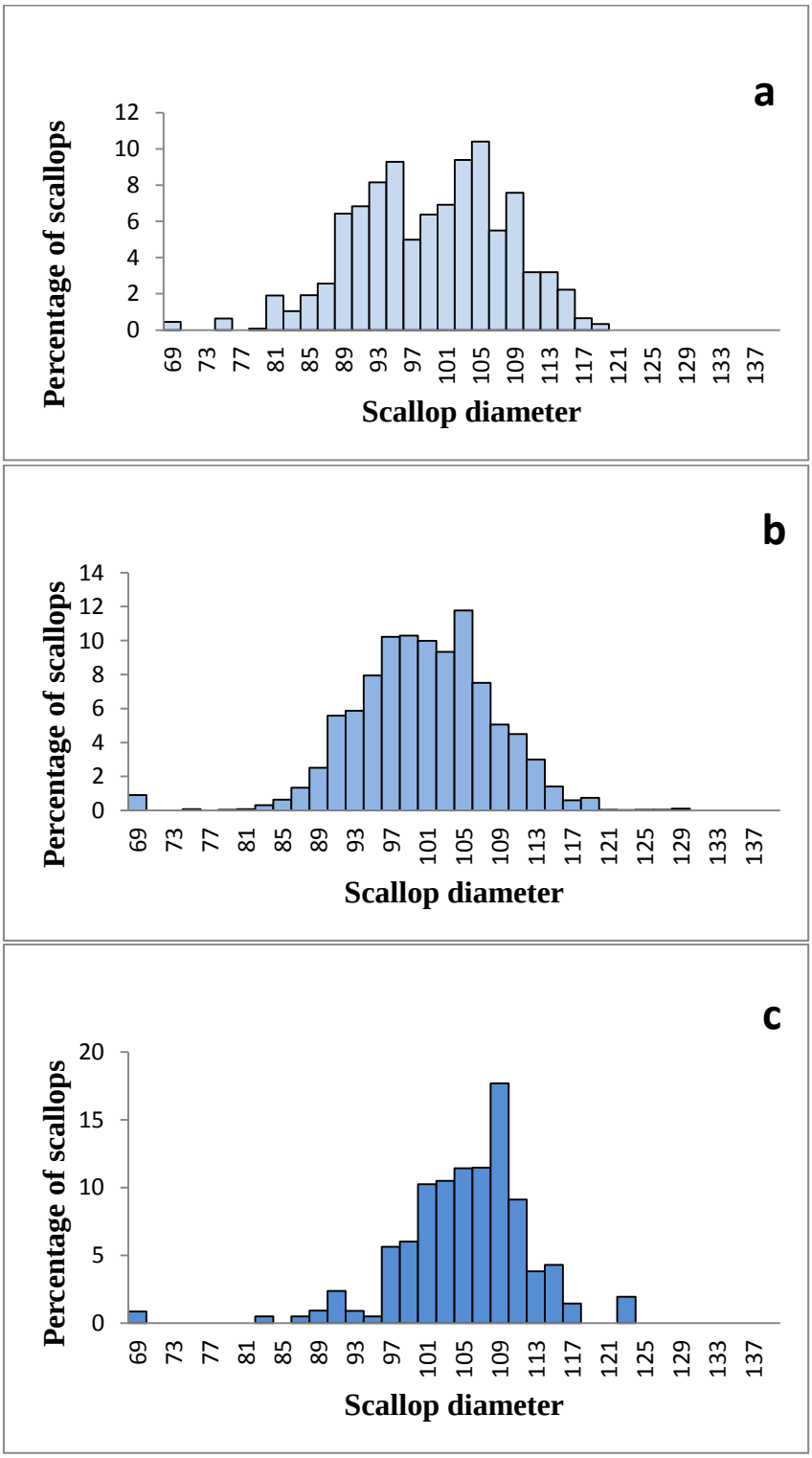


Figure 7.20. Comparison of size frequencies for scallops caught during the 2010 post fishing season survey from sites that were: (a) never fished n = 233; (b) fished for a single year, during the 2010 season (note that all sites that were fished in 2009 were also fished in 2010) n = 1767; and (c), fished in both 2009 and 2010 n = 211.

Discussion

With a view to ensuring the ecological sustainability of the scallop fishery, particularly under a spatially managed harvest strategy, this study explored the effect of dredging activities within the BSCZSF on the composition and abundance of the species assemblage selective to dredge fishing. Abundance of all species (commercial scallop and all by catch) comprising the assemblages did not differ significantly between fished and non-fished areas. Community structure did not differ significantly either, with the species assemblages heavily dominated by commercial scallop both before and after fishing. This suggests that scallop dredging appears to have a relatively low short- to medium-term impact on the species assemblage selective to dredge fishing within the BSCZSF, allowing for beds to potentially be rotationally fished after relatively short temporal closures if they meet the harvest strategy decision rules.

This similarity between fished and unfished scallop beds may in part be explained by the history of fishing in the area. Knowing the history of fishing grounds is important, as long term effects of fishing can change the habitat by reducing the abundance of structural components. As an example, areas dominated by seagrass exposed to dredge fishing can be reduced to habitats where the sea grass is replaced by unvegetated sand flats (Peterson *et al*. 1987). These changes in habitat and species dominance can be long-lasting, and it is expected that some functional groups are more vulnerable to fishing disturbance than others (Malaquias *et al*, 2006; Kaiser *et al*., 2002; Jennings *et al*., 2001) and may exist only at very low levels in areas where fishing pressure has historically been continuous.

The BSCZSF has been fished since the 1970s, and the small differences in species assemblages selective to dredge fishing between fished and non-fished sites found in this study may be due to ‘historical impacts’ the dredge fishery may have had on the benthic community. Repeated dredging over many years may have shifted the entire community to one which is more resilient and which can withstand dredge fishing pressure as has been found in other studies (Bradshaw, 2001). Those species that are most effected by dredging may now be too rare to be effectively sampled using dredge surveys.

Previous studies have also shown that changes in community structure following seasonal weather events can be more significant than those changes associated with fishing (Currie, and Parry 1996). Communities within the BSCZSF are more exposed to environmental variability than other regions where commercial scallops are or have been fished, perhaps further explaining why changes in species abundance were not observed in this study, but were observed for commercial scallops in inshore waters (see Currie and Parry, 1996; Harrington *et al*., 2008). Despite this, heavily fished inshore regions also show resilience to fishing, with species abundances similar to those prior to dredging within six to nine months after fishing in the Port Phillip Bay Scallop fishery (Currie and Parry, 1996), which was fished close to continually for around 30 years

It should be noted that the species collected in dredges has been shown to not be completely representative of the entire benthic community, indeed when nets are placed behind dredges a wide range of species are collected including many that are not brought up by the dredge itself (Roberts and Polunin, 1991). Much of the infauna is dislodged from the sediment and

passes through the dredge cage mesh, and more mobile species can evade the dredge completely (Currie and Parry, 1999). So the very low levels of species abundance may in some cases be merely due to the difficulty of catching them with a scallop dredge, and these species that aren't captured in dredges may be more vulnerable to disturbance through fishing. It is also important to note that during our study the target species of the fishery, the commercial scallop, had a higher variance than mean abundance, and that may indicate that the sampling was too patchy to allow valid assertions to be made about the impact of dredge fishing. This needs to be further examined.

There was no recruitment in either fished or unfished sites examined in this study, so it is not possible to determine if fishing had any influence on recruitment. However, in the White Rock region in Tasmania, which is in more sheltered coastal waters than the BSCZSF, scallops had recruited back into dredged areas within two months of the completion of a single fishing season (Harrington *et al*., 2008). Despite this, there is evidence that scallop dredging makes benthic communities more homogeneous, and this may have consequences on larval settlement. Bradshaw *et al*. (2001) measured community effects of dredging in the Irish Sea and found that the closure of areas to commercial dredging resulted in the development of more heterogeneous communities, with a tendency for a larger abundance of scallops (*Pecten maximus*) after just one year, and increased proportion of older scallops compared to neighbouring fished scallop beds after three years. Temporal closure of appropriate beds to fishing in the BSCZSF may be expected to have similar effects on the commercial scallop, and supports the current use of a spatial management system, where areas are rotated through periods of fishing and temporary closure. Given that there appeared to be little short- to medium-term impact of dredge fishing on abundance and species composition on the species assemblage selective to dredge fishing in the BSCZSF, the main consideration for choosing which beds to close under a rotational harvest strategy and the length of closure should be selecting those beds that are more likely to provide recruitment to the fishery (e.g. those with high adult density - see Chapter 7) and allowing them sufficient time to do so.

The down side of temporal closures is you can only work with those beds that are available and in certain years there may not be beds available that are likely to provide recruitment to the fishery (e.g. poor condition). The alternative is to have permanently closed areas that are known to have sites that scallops traditionally recruit to, as is the case in Tasmania, with dredge prohibited areas. The down side of this approach is that given you are closing an area not a scallop bed, in some years you may not be protecting any spawning stock. It is difficult to compare the merits of the two approaches, however, as the fisheries are quite different, with Tasmania predominantly an inshore fishery and the BSCZSF an offshore fishery.

7.3 EXAMINE THE IMPORTANCE OF SCALLOP DENSITY (SPAWNER BIOMASS) ON SYNCHRONISATION OF SPAWNING AND RECRUITMENT SUCCESS

7.3.1 Results and discussion

Relationship between adult scallop abundances and recruitment intensity

Most recruits (scallops measuring less than 40 mm in length) were found in sites in the DEC, Tasmania with large numbers of adult scallops (Fig. 7.21). From the summary of the generalised linear model we see that there is strong evidence (Table 7.18; $p < 0.002$) that the density of recruits in March 2010 is related to the density of adults in the previous year (September 2009, Fig. 7.22). Density of recruits increased by a factor of 2.15 for every unit increase in adult density ($ind.m^2$). For the recruitment pulse in 2011, there is also strong evidence (Table 7.18) that the number of recruits in April 2011 is related to the density of adults in the previous year (August 2011). For every unit increase in adult density, the expected density of recruits increased by a factor of 10.8. There was a strong decrease in the number of adults in 2011 (compare X-axis values between Fig.7.22a and b).

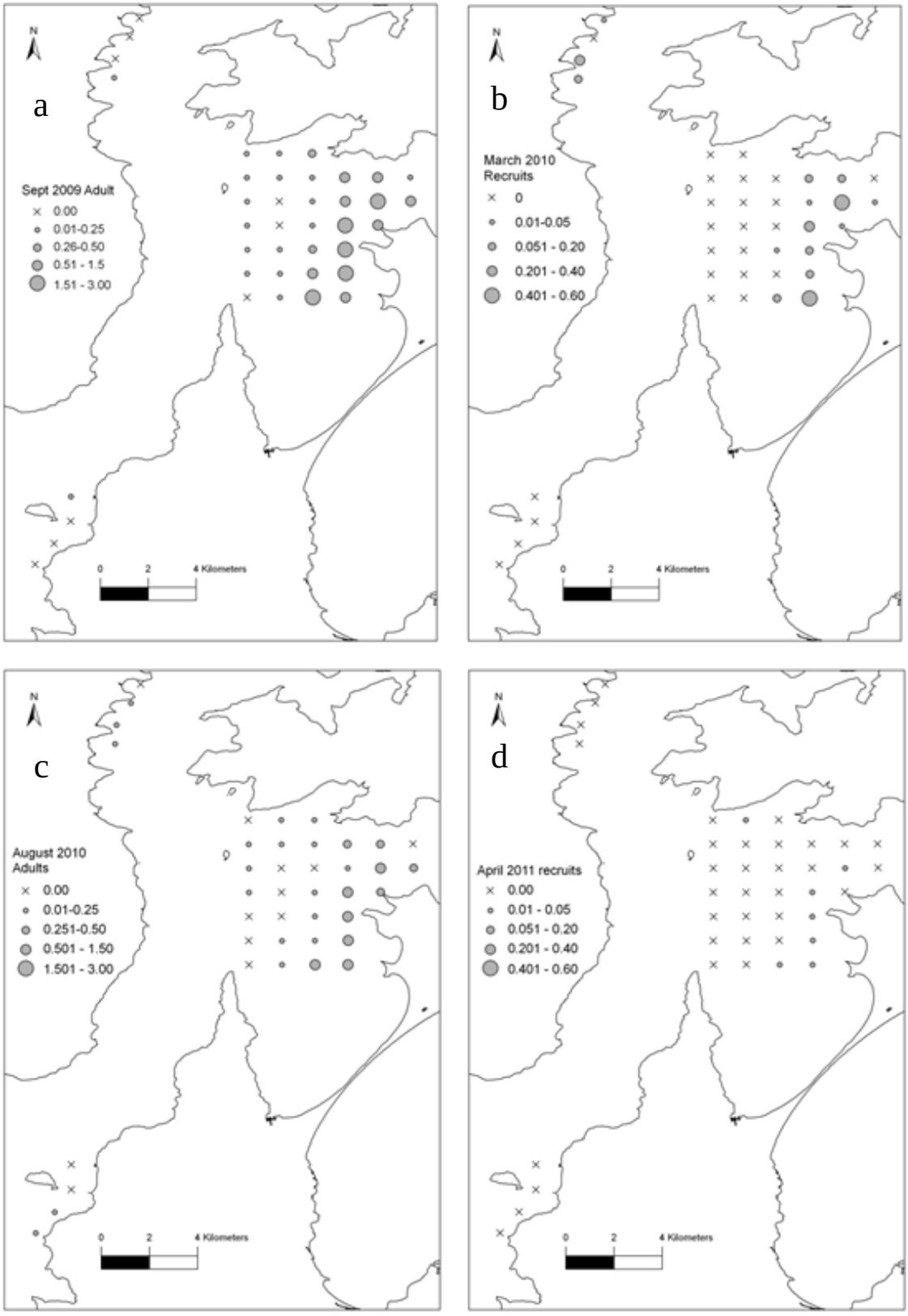


Figure 7.21. a) Number of adult scallops (>40mm in length) collected during the dive transect survey in May 2009; b) spat collected per spat collectors retrieved in February 2009 as a proxy for larvae abundance and c) Number of new recruits (<40mm) in May 2009. With 32 sites in Great Bay, and four each near Satellite Island in Alonnah bay in the south and Trial bay in the north.

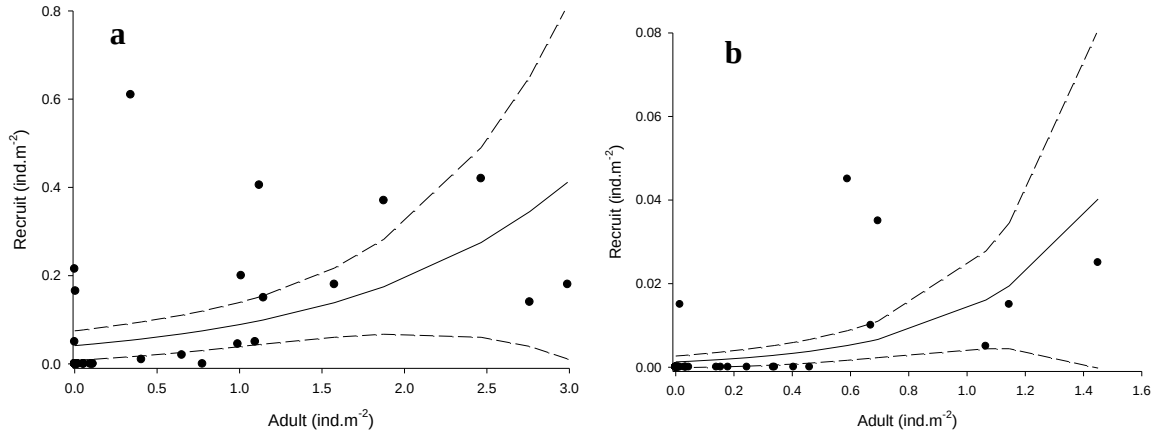


Figure 7.22. Relationship between adult and recruit density in a) 2010 and b) 2011. Black dots are the data points, continuous line indicates the model fit and dashed lines are the upper and lower 95% confidence intervals.

Table 7.18. Parameter estimates for the generalized linear model with Poisson distribution for adult-recruitment relationship in 2010 and 2011.

Recruitment 2010					Recruitment 2011				
	Estimate	St. Error	T value	Pr(>t)		Estimate	St. Error	T value	Pr(>t)
Intercept	-3.1856	0.4132	-7.710	$2.32e^{-9}$ ***	Intercept	-6.6637	0.5611	-11.877	$1.58e^{-14}$ ***
Adult	0.7687	0.2392	3.214	0.0263 **	Adult	2.3799	0.5838	4.077	0.000218***
Null deviance: 8.1736 on 40 degrees of freedom Residual deviance: 5.9850 on 39 degrees of freedom					Null deviance: 0.58793 on 40 degrees of freedom Residual deviance: 0.34908 on 39 degrees of freedom				

Despite collections of large numbers of spat using artificial collectors some distance from dense aggregations of scallop beds in February 2009 (Fig. 7.23 a and 7.23 b), these numbers did not necessarily translate into successful juvenile settlement to the benthos in May 2009 (Fig. 7.23 c). Recruits were mostly present in areas were adult scallops were found (see analysis above). However, the patterns of recruit abundances did not persist into adulthood. There was considerable reduction in abundance of recruits through time as can be observed from the length frequency distribution analysis in Fig. 7.24.

Figure 7.23. a) Number of adult scallops (>40mm in length) collected during the dive transect survey in May 2009; b) spat collected per spat collectors retrieved in February 2009 as a proxy for larvae abundance and c) Number of new recruits (<40mm) in May 2009. With 32 sites in Great Bay, and four each near Satellite Island in Alonnah bay in the south and Trial bay in the north.

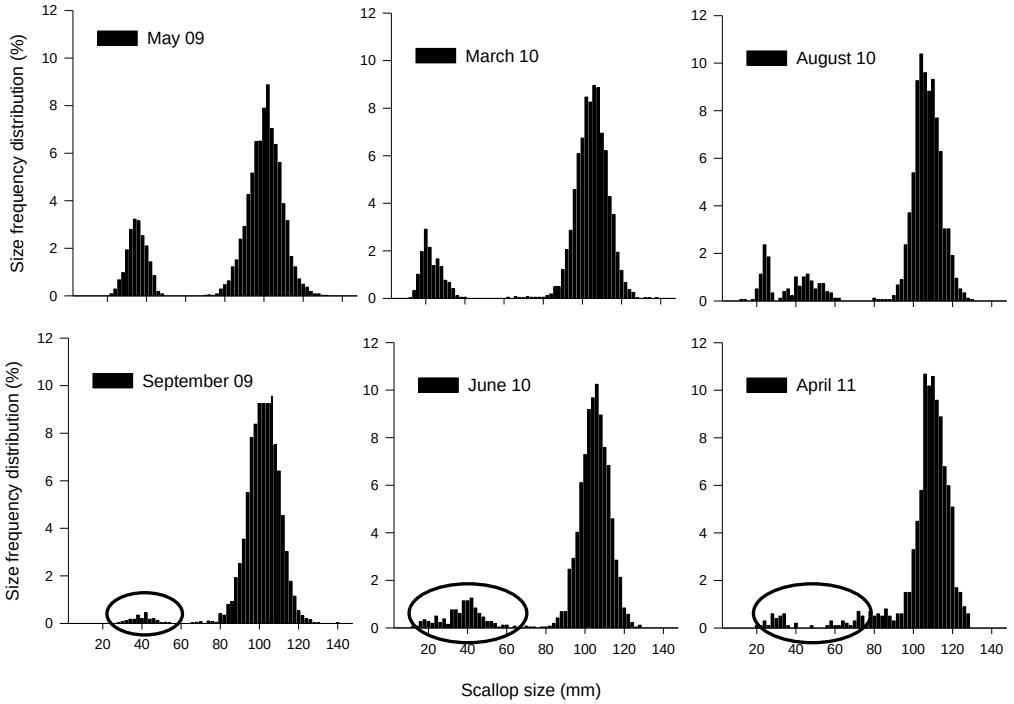


Figure 7.24. Length frequency distribution for scallops measured within the Great Bay sampling locations (32 sites) at each sampling period. Black circles show the reduced number of recruits that survived the post-settlement period.

Retention of recruits was analysed in more detail in the three sites showing the strongest recruitment pulse in 2009 and 2010. A strong recruitment pulse was detected in May 2009, however, four months later the length frequency distributions showed a significant reduction in number of recruits (Fig. 7.25). In 2010 the recruitment pulse was detected in March and five months later the number of recruits was very low (Fig. 7.25).

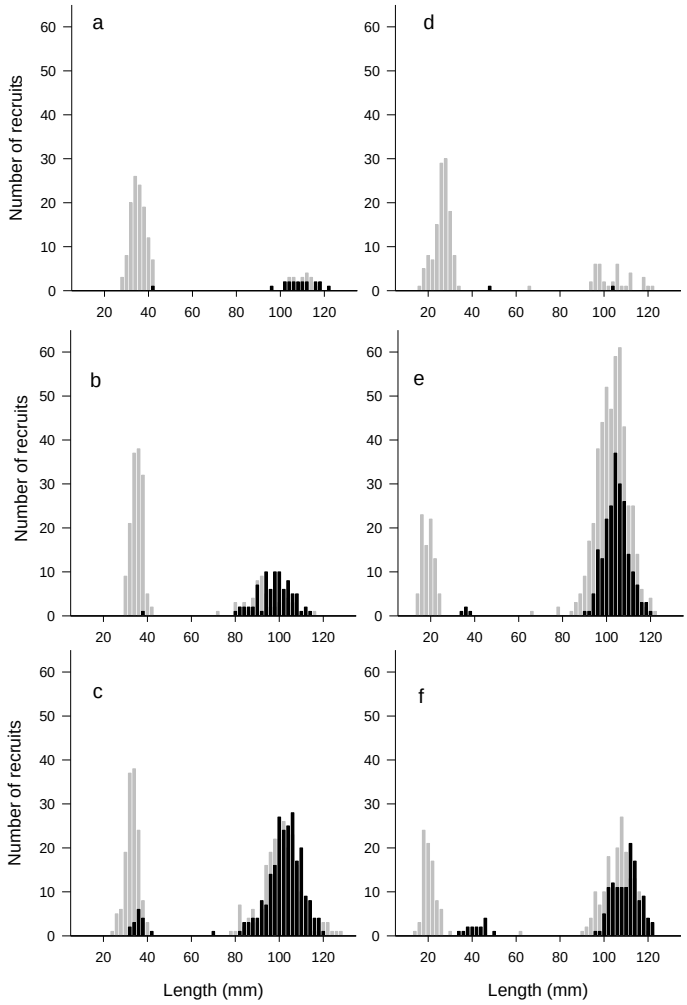


Figure 7.25. Length frequency distribution for scallops in three sites with strongest recruitment pulse in 2009 (a-c) in May (grey bars) and September (black bars) and in 2010 (d-f) in March (grey bars) and August 2010 (black bars).

Effect of density on synchronisation of spawning

The relationship between spawning stock and recruitment is very complex. A combination of different processes including larval production, transport, settlement and post-settlement all influence the actual number of recruits at a particular site (Pineda *et al*., 2009). This study showed that larval supply may not explain the abundance patterns of juvenile scallops in the DEC. The number of spat (measured as a proxy for larvae) retrieved from artificial collectors did not correlate with the number of adults at each site. Spat was collected far away from scallop beds; however, this did not translate into successful settlement to the benthos in these areas (Fig. 7.23).

Recruits were mostly present in areas were adults were found (Fig. 7.22), suggesting that successful recruitment is a function of site physical and biological characteristics and/or density of adult scallops. These results are supported by Young *et al* (1989) who postulated

that the number of organisms settling to the bottom is dependent upon some physical or biological factors at the settlement site. This relationship between adult and recruit densities is supported by data from the yearly recreational surveys throughout the DEC (Tracey and Lyle, 2011). Adult and recruit densities were highest in 2006, which coincided with the opening of the recreational fishery. Subsequently, since 2007, the recruitment levels have been very low (Fig. 7.26).

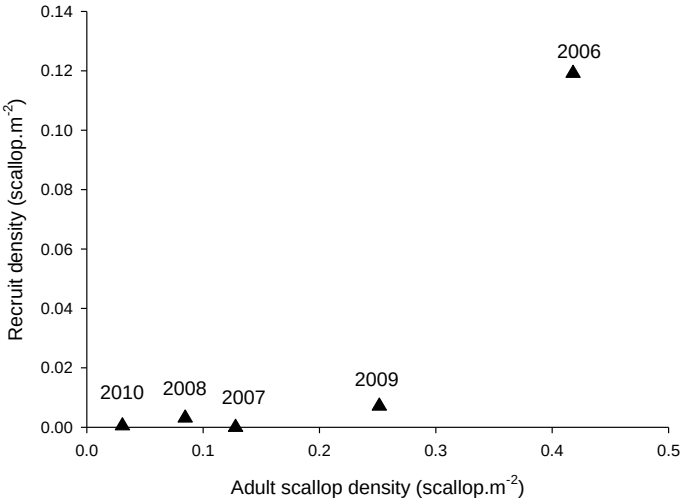


Figure 7.26. Relationship between density of adults and density of recruits in 24 sites throughout the DEC from 2006-2010.

Our observations are consistent with the "recruitment limitation" hypothesis (Peterson and Summerson, 1992) where patterns of population abundance vary as a function of larval abundance rather than being set by subsequent post-settlement processes. Indeed recruitment failure of most beds of *P. fumatus* occurred in southern Australia after a period of intense commercial fishing (Young and Martin, 1989). It would seem that for the commercial scallop, recruitment is positively correlated with stock size, hence, at low density levels of spawning stock, strong recruitment is a rather exceptional event (Orensanz *et al*., 2006). These findings would support the idea of some level of protection of scallops within areas of high density spawning stock to increase the probability of steady and/or significant recruitment pulses. Exactly how this protection of dense spawning stock is carried out operationally would depend on the number and location of beds in the fishery at any given time.

Even though the numbers of recruits are mainly affected by the number of spawning adults the previous year, this study demonstrated a significant reduction in the number of recruits after only a few months of detecting a recruitment pulse, suggesting a strong effect of post-settlement processes on the abundance pattern of scallops. Because dispersal of settled scallops is rather limited (Brand, 2006), it is most probable that this reduction in numbers is caused by predation on small-sized scallops. This suggests that large recruitment events are needed in order for a significant number of recruits to be retained through to adulthood.

Gonadal mass index

A gonad mass increase was observed from June to August 2009 (Fig. 7.27). After mid-August a strong decrease in gonad mass occurred, probably indicating the beginning of spawning. Gonad mass decreased until February 2010. For the spawning season 2010-11 (second data set), a gonad increase was noticed from August to beginning of September, followed by a decrease until the beginning of October suggesting a possible minor spawning. From then on there is an increase in gonad weight until mid-November and a sharp decrease at the end of November. From December onwards, there is not much change in the gonad mass index until the beginning of April. It seems that in spawning season 2010-11 less energy was used for reproductive effort. During the 2009-10 spawning season a standard scallop measuring 105 mm in length gonad mass would reach an average of 8 g, during the next years spawning season, gonad mass for a standard scallop measuring 105 mm was 4.5g

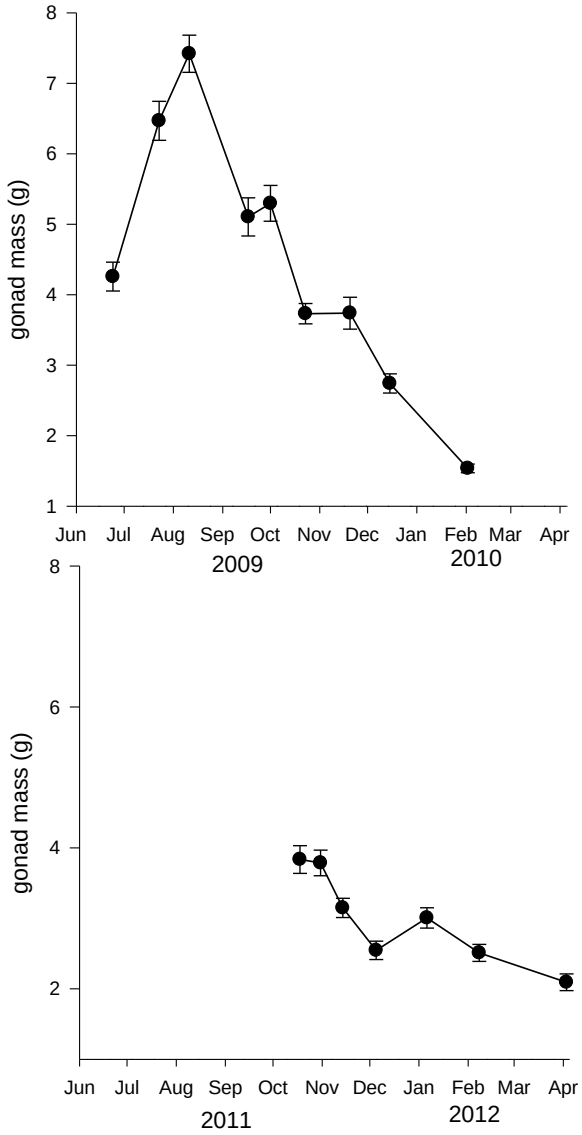


Figure 7.27. Gonadal mass for a standard scallop measuring 105 mm for a) spawning season 2009-10 and b) season 2012-11.

We used the coefficient of variation of the gonad mass index to assess synchrony of the reproductive process. The mean value in spawning season 2009-10 was 45% and in spawning season 2010-11, 40%. These high values would indicate a low level of synchrony of reproductive events within this population.

Comparing the gonad mass variation with the sea surface temperature, it is evident that the highest gonad mass occurred when temperature was the lowest (Fig. 7.28). Conversely, with higher temperatures the gonad mass was smaller. During the second spawning season (2010-2011), the highest and lowest temperatures recorded were not as extreme as during the first spawning season, and this coincided with lower gonad weights in the second season.

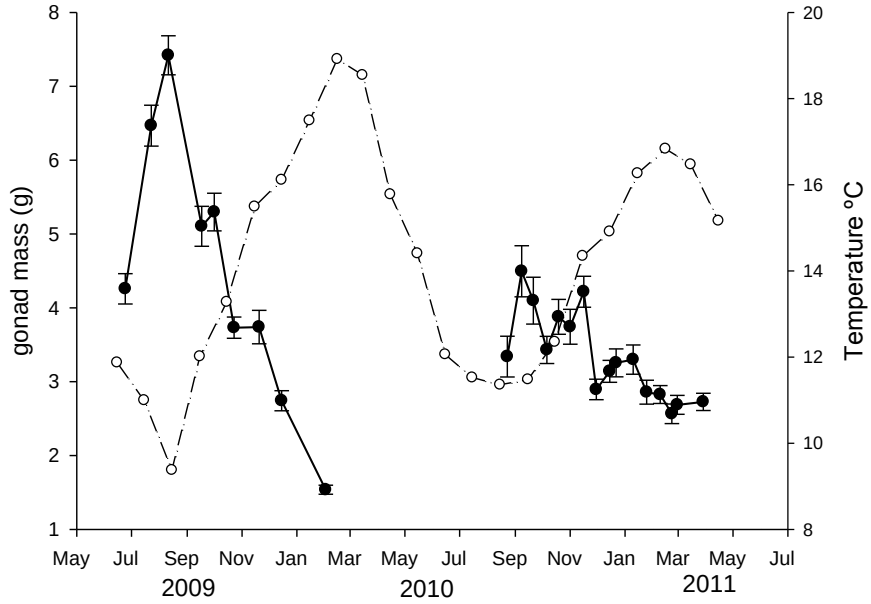


Figure 7.28. Gonad mass index (black dots) and average monthly sea surface temperature (white dots) estimated from MODISA satellite data.

Gonad mass index at low and high density sites

For spawning season 2009-10, mean gonad mass for a standard scallop measuring 105 mm was very similar between both sites from July to September (Fig. 7.29). From the beginning of October there was a slight increase in gonad mass for the HD area, which seems to continue until February, when both indices are very similar again. For spawning season 2010-11, there was no clear pattern of one area (HD or LD) having greater gonad mass than the other before November (Fig. 7.29), however, the HD area generally had a higher gonad mass than the LD area from November to February, which was similar to that for 2009-10. Mean values of coefficient of variation were higher in the LD area for both spawning seasons (46.4% compared to 42.5% in the HD area during spawning season 2009-10 and 42% compared to 37% during spawning season 2010-11), suggesting a lower level of synchrony of reproductive events within the LD area compared to the HD area.

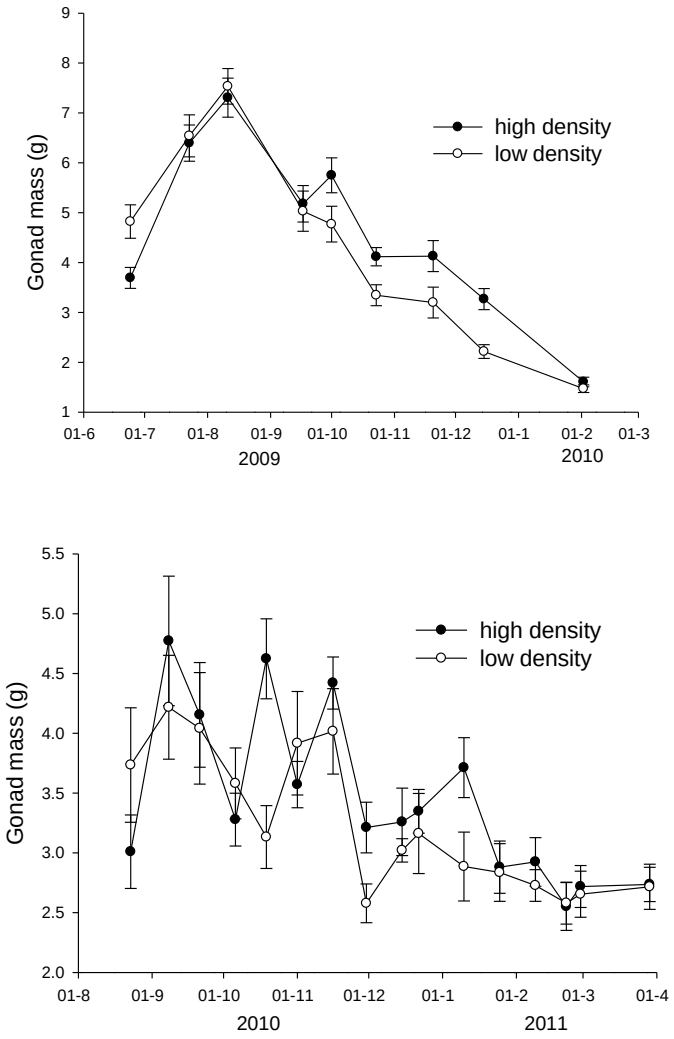
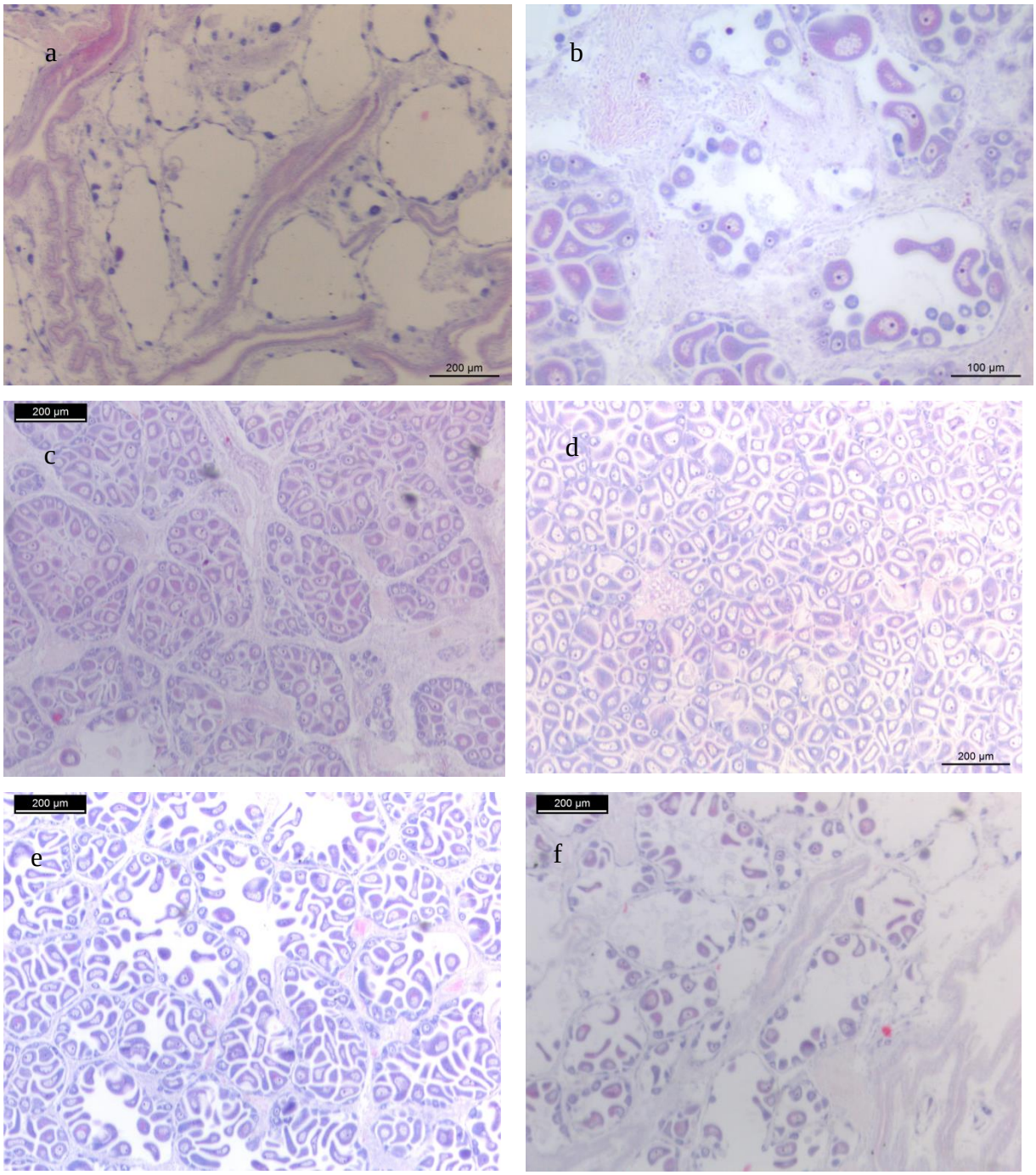


Figure 7.29. Gonad mass for high density and low density areas during spawning season 2009-10 a) and 2010-11b).

Gonad histology

Histological staging for the female component is shown in Fig. 7.30. In all stages the acini (bulb shaped structures composed of an outer layer of connective tissue) were clearly visible. The lumen of the acinus is more or less filled with oocytes in varying stages of gametogenesis, depending on the reproductive stage of the gonad. During the developing stages, the inter-acinal connective tissue occupies greater areas in the gonad (Fig. 7.30 a-c). The developing gametes gradually fill the lumina in the acini, and when the gonads are mature, the inter-acinal space is greatly reduced and the acini are full with oocytes (Fig. 7.30-d). During the spawning stages the oocytes are evacuated (Fig. 7.30-e-g). Atresia (or lysis), when the oocytes breakdown and are reabsorbed by the scallop, usually occurs in mature gonads (Fig. 7.30-h).


a
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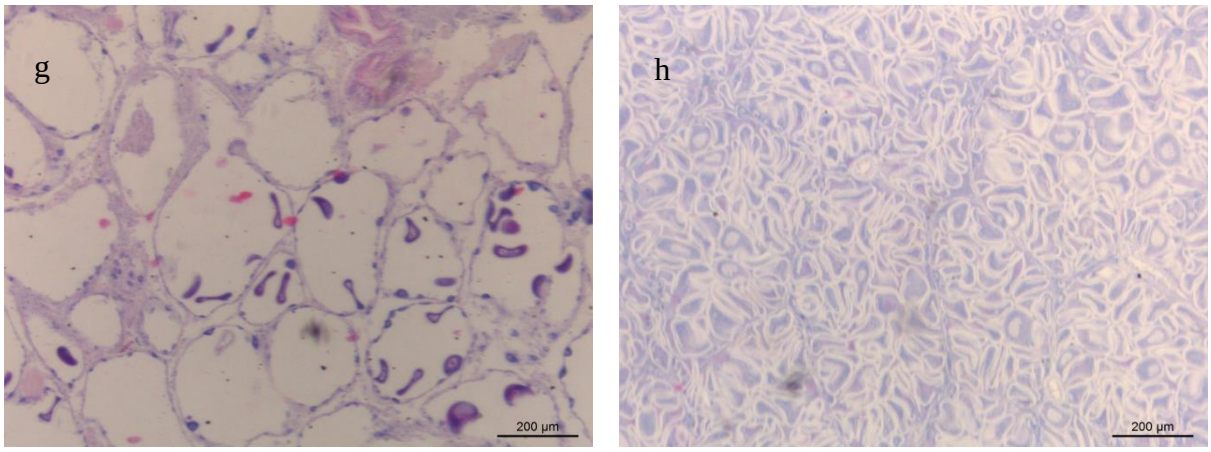

Figure 7.30. Histological sections of *P. fumatus* gonad showing different ovarian maturity stages (scale 200 microns). a)developing 1, b) developing 2, c) developing 3, d) mature, e) early spawning, f) spawning, g) fully spawned, h) atretic oocytes.

Gametogenic cycle

Results of the histological analysis showed strong inter-individual variations of gonad maturity stages over the same sampling dates (Fig. 7.31). The cycle was characterised by the continuous presence of mature gametes. Early spawned gametes were found in October and November while spawned and almost fully spawned (late spawning) gametes were found from December to March. *Pecten fumatus* showed a protracted spawning strategy (more than 150 days) with spawned gonads encountered from October 2010 until March 2011. Mature gametes coincided with a greater gonad mass than during later spawning stages. Lowest values of gonad mass coincided with a high percentage of partially or fully spawned individuals (Fig. 7.31).

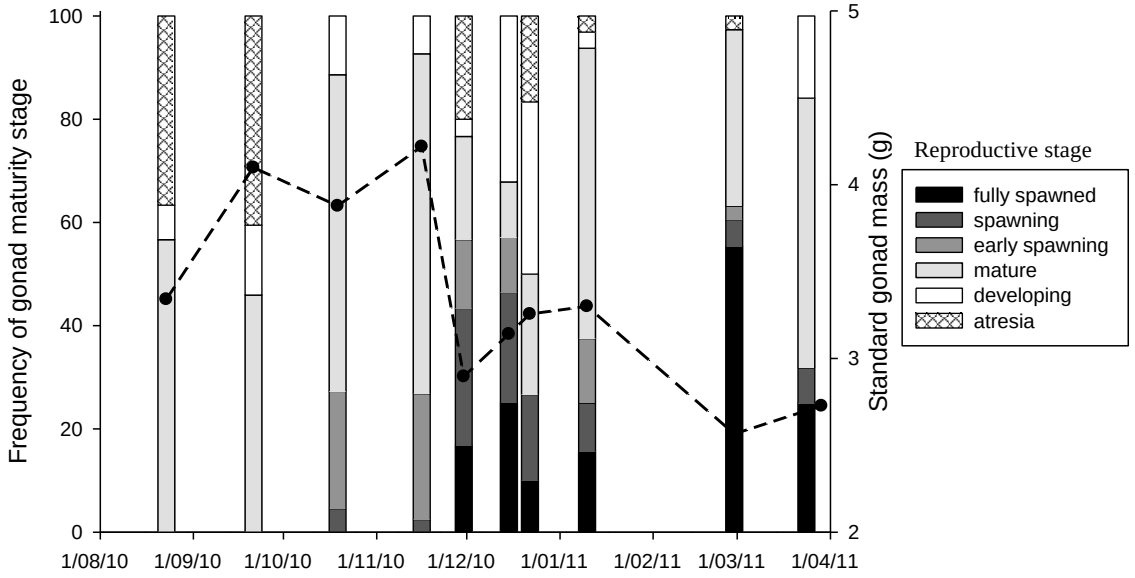

Figure 7.31. Relative frequency of gonad maturity stages in *P. fumatus* between August 2010 and March 2011 and average gonad mass (dashed line) for a standard scallop measuring 105 mm.

Lowest temperature values concurred with mature and atresic oocytes in August and September. When temperature began to rise, early spawning and spawning stages occurred. Highest temperatures were associated with higher frequencies of fully spawned gonads (Fig. 7.32).

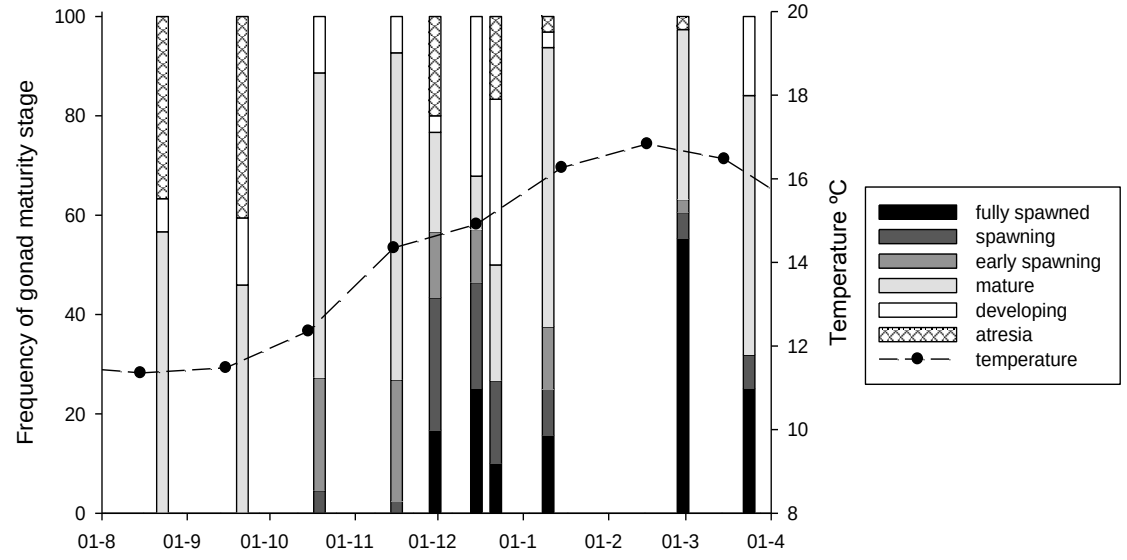

Figure 7.32. Relative frequency of gonad maturity stages in *P. fumatus* between August 2010 and March 2011 and monthly average temperature.

Synchronisation of spawning in high and low density sites

The HD area had an overall higher frequency of spawning stages (beginning to spawn, spawning and fully spawned) than the LD area (Fig. 7.33). There was an overall higher frequency of fully spawned individuals in the HD area. The spawning season also lasted longer in the HD area than in the LD area (Fig. 7.33)

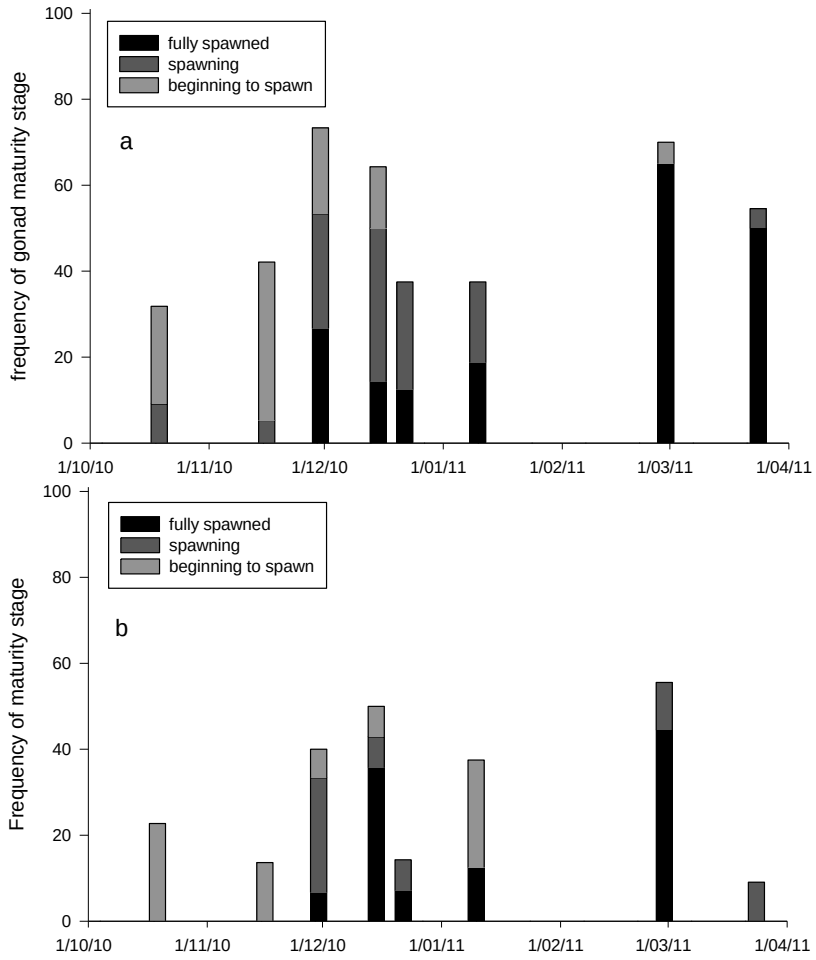

Figure 7.33. Relative frequencies of spawning stages (beginning to spawn, spawning and fully spawned) in a) high and b) low density areas from October 2010 to March 2011.

A logistic regression model was used to analyse the relationship between spawning (a binary response, either spawned or not spawned) and categorical (site density) and continuous (scallop size, temperature and roe weight) predictors. Only site density and temperature had a significant effect on synchronisation of spawning (Table 7.19). The model predicted that the odds of spawning increase 2.5 times in the HD area compared to the LD area and that for every unit (degree Celsius) increase in temperature, the odds of spawning increase 1.56 times (Fig. 7.34). Pearson's X^2 was used to evaluate the goodness of fit of the model. It was not significant (0.08) indicating no evidence for lack of fit of the model.

Table 7.19. Parameter estimates for the reduced logistic regression model.

Coefficient	Estimate	St. Error	Z value	Pr(>Z)
Intercept	-7.8178	1.14119	-6.851	< 0.000001
Density	0.9247	0.25104	3.638	0.00023
Temperature	0.4471	0.07398	6.044	< 0.000001
Null deviance: 445.68 on 354 degrees of freedom Residual deviance: 389.02 on 352 degrees of freedom Akaike Information Criterion: 395.02				

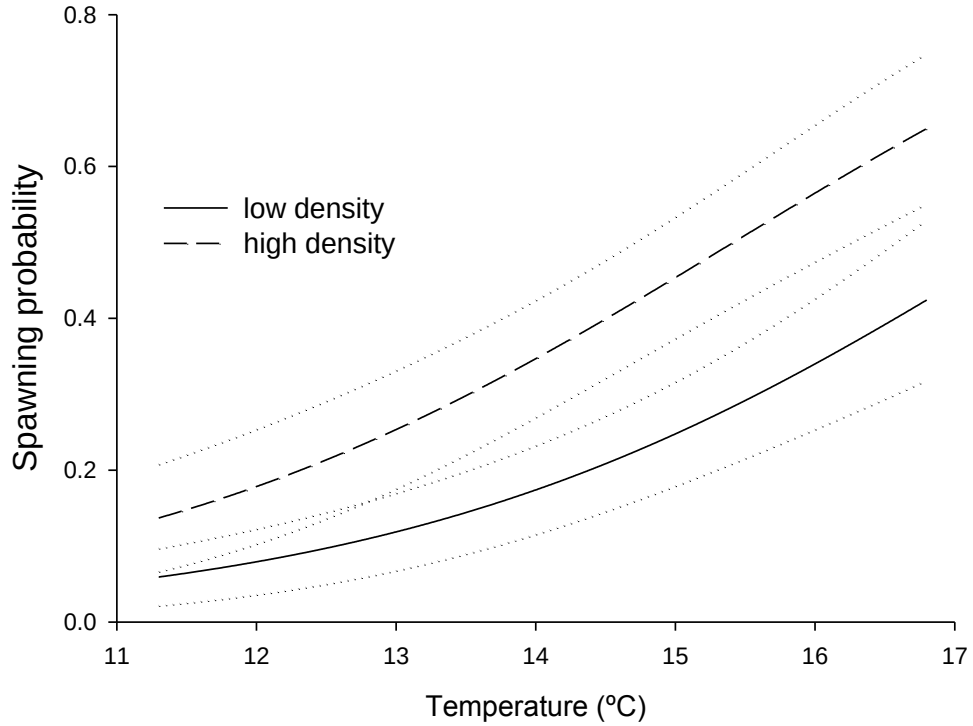

Figure 7.34. Spawning probabilities at different temperatures in a high density and low density site. Dash lines represent the model for high density and continuous line is the model for low density.

Reproductive cycle

The gonadal mass index and histological data collected for *P. fumatus* shows a protracted spawning process over at least four months starting in Spring. These results are supported by (Harrison, 1961) who studied the annual reproductive cycle of *P. fumatus* in the DEC about 50 years ago. Studies at both Banks Strait and King Island also showed that most spawning events for *P. fumatus* started in spring and lasted for at least a few months (Young *et al*., 1999). All these observations indicate that *P. fumatus* generally spawns in spring and that the spawning process lasts at least a few months, progressing into summer, in Southern Australia.

Gonad growth and gametogenic cycle have been correlated with temperature for several pectinid species (see review in Barber and Blake, 2006). Gonadal index mass and spawning stage were clearly influenced by temperature (Fig. 7.22 and 7.27), with an increase in temperature triggering the beginning of spawning during spring. *Pecten fumatus* in the DEC initiated spawning at temperatures between 10-12 ºC.

The coefficient of variation was used as a measure to assess synchrony of the reproductive process. Overall, the high values of this coefficient suggested that there was a low level of synchrony of reproductive events within the population of *P. fumatus*. This result was supported by histological techniques which showed strong inter-individual variations of gonad maturity stages over the same sampling dates and a low synchronisation of spawning events. It has been hypothesised that if conditions are not optimal, scallops may adopt a "dribble" spawning strategy to ensure that at least some gametes find suitable conditions for survival (Langton *et al*., 1987). A series of partial spawnings may be an adaptation of some scallop species when environmental conditions are not ideal for mass spawning.

Synchronisation of spawning: relationship with density
On average, inter-individual synchronisation was higher in the HD areas than in the LD areas during both spawning seasons. Our model showed that the odds of spawning increased 2.5 times in the HD area compared to the LD area. However, these results should be interpreted cautiously; given that only two sites were surveyed and other factors such as site-specific environmental conditions, or differences in arrival of spawning cues could be confounding the results. Nevertheless, the study shows a significant difference in spawning intensity and synchronisation between sites that were located only about 2 km away from each other. It has been suggested that the degree of synchronisation over the spawning period may be more important to recruitment than reproductive effort or reproductive production (Langton *et al*., 1987). The lack of understanding of reproductive spatial dynamics is an area of research that needs further development if we want to understand recruitment intensity changes and potentially increase fertilization success of scallops. However, our results do suggest that maintaining dense areas of adult scallops may increase the probability of recruitment, through increased spawning intensity and synchronisation.

8. BENEFITS AND ADOPTION

For the commercial scallop *Pecten fumatus* fisheries in the Commonwealth, Tasmanian and Victorian jurisdictions, this project has provided significant benefits though an improved understanding of the population linkages across jurisdictions, the role of scallop density in promoting spawning and recruitment and the impact of dredging in light of the current harvest strategies adopted across the fisheries. Given that all jurisdictions are currently looking at their harvest strategies and the recent review of options for improving management of the commercial scallop resource in south east Australia (Sen, 2011), there is great scope for adoption of the research and its integration into spatial management. Specific adoption measures that can be taken are (but not limited to):
Incorporation of population structure into commercial scallop harvest strategies across all jurisdictions; greater adoption of the rotational harvest strategy across the jurisdictions, given the limited effects of this strategy on community structure; the high importance of density for increasing synchronisation and intensity of spawning and promoting recruitment accounted for in harvest strategies across the jurisdictions.

9. FURTHER DEVELOPMENT

In the open water of Bass Strait, the expectation of genetic homogeneity, given the 30 day commercial scallop larval duration, appears to be subtly disrupted. In eastern Bass Strait, this seems to be occurring within a radius of 200 – 400 km. Several lines of evidence, from previous genetic studies to observations by fishers, appear to support the hypothesis of non-random dispersal and subsequent settlement of larvae. Circulating currents (see bio-physical modelling section) appear to entrain pelagic larvae and return them as recruits on a regular basis into natal beds. The genetic analyses were unable to directly test this hypothesis by providing evidence of close relatives (e.g. parent – offspring pairs) within beds. Embayment studies showed that the microsatellite loci were powerful enough to detect relatives if they were there, but the ratio between the numbers of animals genotyped and the population size of a scallop bed was not high enough to include related animals in the sample. This outcome departs from the widely accepted model of population genetic stock structure in fisheries. Generally, genetic data is used to make inferences about restrictions to gene flow, which is used to divide the range of a continuously distributed species into spatially discrete stocks. Within Bass Strait, and despite preliminary evidence from the bio-physical modelling that ocean gyres may be causing self-recruitment, it was not possible to explain the genetic pattern as spatially discrete stocks. Future analyses of larger samples of individuals or genes may resolve this situation. Further bio-physical modelling is also needed to better explain the role gyres may be having in scallop population connectivity, as the analyses provided here are preliminary and had some inherent limitations. This is important, as the strength and temporal patterns of these gyres are predicted to change in the future due to climate change.

Despite our results suggesting that maintaining dense areas of adult scallops may increase the chances of recruitment, through in part increased spawning intensity and synchronisation, there is still a general lack of understanding of scallop reproductive spatial dynamics. This is an area of research that needs further development if we want to better understand recruitment intensity changes and potentially increase fertilization success of scallops.

This study found little change in community structure due to the impact of scallop dredging. However, this only applies to those species captured by the dredge, with much of the infauna dislodged from the sediment and passing through the dredge cage mesh, and more mobile species evading the dredge completely. As such, there is scope for further research on the effect of dredging on those species that aren't captured by the scallop dredge.

10. PLANNED OUTCOMES

Objective 1:
Adoption of harvest strategies by all three jurisdictions of the commercial scallop fishery that sufficiently take in to account small- and large-scale population linkages and stock structure. If it is shown that there is only one stock in SE Australia, then a uniform harvest strategy across all three jurisdictions would be adopted.

Our findings demonstrated that the south east Australian commercial scallop population has a genetically homogeneous single population which largely allows for a uniform harvest strategy to be adopted across all three jurisdictions. However, there was some evidence of population structure within Bass Strait. Significant, but slight differences in genetic structure between beds do occur in the Strait, which has significant implications for management of apparently genetically-linked populations that occur in separate management jurisdictions.

Objectives 2 & 3:
Development and implementation of a risk-based assessment approach to the rotational fishing harvest strategy, which minimises the risks to adult spawner stock and scallop communities.

With a view to development and implementation of a risk-based assessment approach to the rotational fishing harvest strategy, this study explored the effect of dredging activities on the benthic community within the fishing grounds of the BSCZSF. Abundance of all captured species (commercial scallop and all by catch) comprising the communities did not differ significantly between fished and non-fished areas in the regions examined. The total number of species and species richness did not differ significantly either. This suggests that the rotational fishing harvest strategy has a relatively low short- to medium-term impact on the benthic communities within the fishing grounds of the BSCZSF.

In accordance with research in other benthic molluscs we found a strong indication that the density of recruits is related to the density of adults in the previous year. In the areas studied, recruit density increased by between 2 and 10 times for every single unit of adult density prior to spawning. The density of adult spawners also has an impact on the level of synchronicity between spawning adults. This study showed a difference in spawning intensity and synchronisation between sites of high and low densities, and suggests that maintaining dense areas of adult scallops may increase the probability of recruitment, through increased spawning intensity. As such, development and implementation of a best-practice risk-based approach to the rotational fishing harvest strategy, which minimises the risks to adult spawner stock, would incorporate the protection of high density scallop beds in some

manner.

Project results have been communicated to stakeholders through a number of presentations throughout the project at the Tasmanian Scallop FAC and RAG and the Commonwealth Scallop RAG and MAC.

11.CONCLUSION

The original objectives were well met during the successful completion of this project.

Objective 1. Determine the broad- and fine-scale population linkages and stock status of commercial scallops (*P. fumatus*) in SE Australia.

Our findings showed the south east Australian commercial scallop population has a genetically homogeneous single population. There was however some evidence of population structure within Bass Strait. Significant but slight differences in genetic structure between beds do occur in the Strait on a relatively fine scale (several hundred km), which may have significant implications for management of apparently genetically-linked populations that occur in separate management jurisdictions.

Evidence from this study proposes that these differences may be due the effect of ocean gyres that exist in the Bass Strait and may force self-recruitment of certain beds and genetic separation from the general population of the scallops in the Strait.

Objective 2. Evaluate the effects of intensive rotational dredge fishing on scallops beds and scallop recruitment events.

Industry-based dredge surveys were conducted in several areas of the Bass Strait before and after the areas were opened to fishing. Abundance of all captured species comprising scallop bed communities did not differ significantly between fished and non-fished areas within the fishing grounds of the BSCZSF. The total number of species and species richness did not differ significantly either. This demonstrates that scallop dredging has a relatively low medium-term impact on the benthic communities within the fishing grounds of the BSCZSF. There was no recruitment in either fished or unfished sites examined in this portion of the study, so it is not possible to determine if fishing had any influence on recruitment.

Objective 3. Examine the importance of scallop density (spawner biomass) on synchronisation of spawning and recruitment success.

In accordance with research in other benthic molluscs we found a strong indication that the density of recruits is related to the density of adults in the previous year. In the areas studied recruit density increased by between 2 and 10 times for every single unit of adult density prior to spawning. The density of adult spawners does have an impact on the level of synchronicity between spawning adults. This study showed a difference in spawning intensity and synchronisation between sites of high and low densities, and suggests that maintaining dense areas of adult scallops may increase the chances of recruitment, through increased

spawning intensity and synchronisation.

Overall, the results of this study have significant implications for the sustainable management of south east Australian commercial scallop fisheries and greater continuity between jurisdictional harvest strategies.

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13. APPENDIX 1 – Intellectual property claim

No commercially valuable or intellectual property prevention public dissemination of the results arose from the research in this project.

14. APPENDIX 2 – Personnel involved in this project

Staff involved in the FRDC 2008/022 Project:

IMAS
Jayson Semmens (PI)
Nicholas Jones
Tania Mendo
Sean Tracey
Ed Forbes
Klaas Hartmann
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15. APPENDIX 3 – Characterisation and summary of 15 genetic loci

Appendix 3A

Characterisation of fifteen polymorphic microsatellite loci for *Pecten fumatus.* Engineered sequences (i.e. 'tails') on forward and reverse primers are in upper case. Shaded loci were later excluded due to the occurrence of null alleles at frequencies greater than 0.05 across the 1124 samples. Annealing temperature was 57ºC; size indicates the size range in base pairs of observed alleles in base pairs.
Note: Repeat motif sequences will be deposited in GenBank and the Genbank number will be quoted.

Locus	Primer sequence 5'→3'	Repeat motif	Locus Sequence 5'→3' (repeat motif highlighted)	Size (bp)
A09 Genbank name PeFu01	Forward: CAGTCGGGCGTCATCAATCCTGAATCCCGAGAACC Reverse: GTTTGAGGAAGCGTACAAGGGAAA	$(CTGT)_6$	CGTAGGCGTATATTAACAGTCACTAAATAGATATACTGCACGTAA CTTTAATTGGGATGATTGATATGAATTGGTACTGTCTGATAAAAC ATATTAAGAGCCTATCCGTAGACTTTGCATACCCAGCCAAGAATT CACAATATACCTCACCGTCCAAGGTCATTTGGCTAAATGAATTGT TTTCTTATAATCATGCAAATATTTCAAATGGCATGGTGTAAAATG TGTTACATATCAAGATCAGGTAATGGCATGCTGTAAAAGTTGGA ATTATGTATACTATTCAATCCTGAATCCCGAGAACCATGCAAAAT CGTTAGCATATACTCGTGATAAGTAACGATTGAACGTCTGTCCG GCCGGTATGCAAATCTGTCTGTTTGTCAGTTTTTCTGTCTGTCTG TATGT**CTGTCTGTCTGTCTGTCTGTCTGT**TTGTCTGTCTGTCT GTTTGTCTGCTTGTCTGTCCTCCCTTTAACGATTTCATATTATTTC CCTTGTACGCTTCCTCAATGTTAGGTATAGACCTGATGGAATTCT TCAAAGAATTCGAACTGATCTGTAAATACAAAATTCAGAACTGT CGCATAATCATCATAACACCCATGGTTTTATTATCACTATCACACT TTAACTAAATGTCCTATCTGCTTTGGATCCTTATGTTCAGTTGTG TCATATGGTTTTTCTCATTATTGAACCCCGGGACTCATTATAGNN GNTCGTTTTGTKNCAATATCAGAAAA	192-327
PeFu_P1_B05 Genbank name PeFu02	Forward: CAGTCGGGCGTCATCACCCCATACCCTTTTTACG Reverse: GTTTGTGGAACGCTTTGGTGAACT	$(AGGT)_4$	CGTGGGATCTTAGTGTGGAAGAAAACCGGTGAACACGGGGAA AGTCCAAGTTGTCGGGCAGATCACCCCATACCCTTTTTACGTCC GATCGGAGAACTACGAGTGTGTTACCACTGCGCCATTCGACCAA TAGTTAGTTAGTTAGTGTTAGTTAGTGAGATAGGTGT**AGGTAGG** **TAGGTAGGT**AGGAAGGGTGGGGTAGCTAGTTAGGTAGGAAAG GAGTAAACCGTAGTAGCTAAGGTCATTTTATGTTCAAATACCTAC GGTTCTTGCATCATGAAACAAGTATAGTTCACCAAAGCGTTCCA CAACCCTCTATGCTGAGTAGAGTAATGCACGTTCCGTCTGTCCT GAGTACAGAGGAAATGGCACGGAATT	200-289

PeFu_P1_E12 Genbank name PeFu03	Forward: CAGTCGGGCGTCATCAGTTCTTCTAAATCAGAGGTGTCC Reverse: GTTTGTTCCTCCGAGCTATTGACG	$(AGTT)_{15}$	NCCGCTTGTAACAGTGCGGACAAATTCCACCGACTCTCTTGTTT TCGAGGTTGTTAATACATTGATAATTAATTTCATGGCGTTTCGGG TTCCTCCGAGCTATTGACGTAATTAATTAATCGTTTTTTTCGCTTC ATATACAAATGAATTATCCGACATAACGATATTCATAAATGCAAA CCAAATAAACATTATAAACGTCAAATGACAATCAGATAACATTT GATGAATAGCAAAT**AGTTAGTTAGTTAGTTAGTTAGTTAGTTA** **GTTAGTTAGTTAGTTAGTTAGTTAGTTAGTT**ATTGTTGTGTCC GAGTGAGCTAGGGACACCTCTGATTTAGAAGAACTGTCTGATAT ACTTAAGTCATGTATAGACGGTCAAATATAACAGCAAATAAAGA AAAGCATAAATTGTGAACCCCAACAAAGAGTTGTTACCCTTAG ACAATATTTCGTTAGGAAATATTCAAGAGGATTTTAAAATGATTA AGATAAATACCAGAGAAGAACAAACTTCATCCGGATGATCTTTG ACAAGTTGCCGAAGT	242-380
PeFu_P2_C12 Genbank name PeFu04	Forward: CAGTCGGGCGTCATCATGTTATCGTAGGTGGCACGA Reverse: GTTTCCGCCATATTTCATGTTCC	$(AAC)_5GAC(AAC)_5$	NGACAGTAAAAACGTCAATATTTCACCAATACACATCCCATACAT ATCTCCCCAACAATCGTGTGCATTCCTGCAGATATTTAACGCTGT TTTACTGAAGAGCAAGATATCTTTAACGGATTCATATCACACGTT CTTTGGAATGTTTCAACTTGAAACTGGAAATATCTTTTATTTGAG ATAATGATATCAATTCTTGTCTTTATTACCTGGAGAGCTATCTATT ATTCATTTCCCATAGTTAGCATTTAGTTTCAAAGTTATATATTTTTT AAATTTCGGAATGTCAGTTTACAAAAGGATAGGCACAGCATAAC ATGATCTTTTGCTATTTGAAACCATGTTTCTGACATTATCGAAAT TCCCAGTTTGATATTTGTCAAATGTTATCGTAGGTGGCACGAGA CATTTAATTGTAATTTCCCACCACCATCTCCACCGCAACAAAAC AACAACAGCAGCAGC**AACAACAACAACAACAAC**GAC**AACAACAA** **CAACAAC**ATAGTTTTTTAACATTTAAAATATAAAGTATGGCCGTT TCATACAATTGAAATATAAAGTATGGCGGTTTTAAACACAAGAA ATATAAATATGGCGGTTTTAAACACATAAAATATAAAGCATGACG TTTTTAAACGTTTGAAATATAAAGTATGGCGGTTTTAAACATTTG AAATATAAAGTATGGCGGTTATAAACATTTGAAATATAAAGTATG GCGGTTATAAACACATGGAACATGAAATATGGCGGATTAACTCA GGATGTATTCAATGCATAAACTACCTCGATTTCAAACTGCATTTG CGTGTTGTATATGTATATAAAAGGATGCAATTGGTTGAGTTTTATT NGAAGNGNNGAAAN	337-421
A06 Genbank name PeFu05	Forward: CAGTCGGGCGTCATCACCTGAGCTATGGACAATCATCA Reverse: GTTTGGTTTTAGCACATTTCGTGGA	$(GATT)_{8}...(GATT)_{16}$	AATTCTGTCCAGACTTCAGACAAGTTTTTTCAAGTGTTTCATATC GTATTGGACAAAGTTTTTGGTCTACAATCGAGATTACCGTCTTTT GTATATCTCGCTTTTCATGAATACCACAAAAATGTCAATATTCTG TCGTACAGTGTGGTAACTAGGAACTCAGCAACATCAATTCTCAG TATGACAATTATTATCCTGAGCTATGGACAATCATCAAATAAAAG CAACGTTGTTTTGGCCGGGTCTTTATTATTTT**GATTGATTGATT** **GATTGATTGATTGATTTATT**GATTGATTGATTGATTGATTGAT **TGATTGATTGATTGATTGATTGATTGATTGATTGATTG**	144-270

			ATTGATCGCTAGTATAGATAATCCACGAAATGTGCTAAAACCAC AAAATTTGAGCCCG	
PeFu_P1_C01 Genbank name PeFu06	Forward: CAGTCGGGCGTCATCACGAATGCTAGCCCTCATGTT Reverse: GTTTGACAGGCGACTCTCTTCCAC	$(GTTT)_6$	CGATTTGTATGCCTATACATAATGGACTAATTATATACAATATCCT GAATCAGACATCGAAGGAAGTCTTACAAGTTCCCGGAAACAAA AATAAAGCTCTAGTACTTAAATTAACCATTTACGACTGACATCAG GTCCGTCTGATAGGACTTGAAATGGTGTCCCGTGAGAATGTGTA ACTTACACGATAAAGATCCCTCGGCGGTCTTTTGGTGTGATAAC GCCGGCCCAGATGATAGGATATTTTTAGGCTGATATTTAATATTTC TTATTGTTGAAGTGTTTAGATGGACGTCAAAAATCTTGATAAAC CAAATCCACAGGATAGGGTCTTCTCTCTTCTCCCTTCTTAGGGTA AACGTAACTGCTACTTAATAGTGCTAGGTTAGGGCCCATTCGAA TCTGGGGGTCGCTTTCAAAAATTAATCACACCATCAATTAGACA GGCGACTCTCTTCCACCCCTATTTCTTTTTTCATTCTATACTGTTC CCATTCTACTCAATTTTCTATCTATTCCCGTCCGCTGAAAGGCAA CAAGGCGATAATA**GTTTGTTTGTTTGTTTGTTTGTT**TTTTTTC AAAGAGATACAGGTACAAAAATATCCTCAAACATGAGGGCTAG CATTCGCCATGCTACTTTCTTCCTATTGCGATGAATT	198-227
PeFu_P1_E04a Genbank name PeFu07	Forward: CAGTCGGGCGTCATCAGGTAGGATTATCTGTTGAAGCA Reverse: GTTTAAAAAGTAGGCAATGGGATTGA	$(AAC)_{15}$	CGGGTATCTGTACCCACTACGGACATGAGCTATTATCTAGATTCT ACTTCAGGTAAACGAGGTTCCCTTACTACATGNACTAGAAATAC AATTTGTCTATACTGAACTTTGACCTCTTTCTGACAGAAGGAAT GCTTTGACAGGTATGACCTACCTAAGGATAGTACAAACGTCAGG TAGGATTATCTGTTGAAGCACTTAAAATTTACCCACACTTTAAAT ATTTTGCGTACCTAGTAAATCCTTTCGTTTATCTTCGACAAGGTC AACAGAGATTGAC**AACAACAACAACAACAACAACAACAACA ACAACAACAACAACAAC**TATATTACAATTCTTATTGTATGTTTTT TCTTGATTTTCTTGGRATTCAATCCCATTGCCTACTTTTTTGTCAA CAAAACAGTTTGCGATAGAACACGGAGAATA	190-328
PeFu_P1_H11 Genbank name PeFu08	Forward: CAGTCGGGCGTCATCAGAAATGATGCGAGAAGAACG Reverse: GTTTGGATCCCGTGCTCCATAAC	$(GT)_{10}$	TNTTCTCCCTGAAACTTTATCGAGTTTGGTTATTTTTAGATAAAA AGATTACCGTTGTCACTGACAAATTAATTATTTTCAAGATTTATAT TTTAACCATTAAAAAATCAAGAAGACTACATATTTGCATACCTAT ATGCATGCTGATATTTTAACTACCATATTACGTTATGGCTGTTAGT ATGACAAATGAAAAAGAATCAAAAACCAAAAGAAGCTTTAGCA AACACTGATTTTGTACAAACTTGCCTAAGTGTACCACCAAAAAG AACGGGATCCTGTGGAATCGACGATAAATTGGAACGCAGAAGT TTCCGGGATATACTCCCAATTTCGACGTTATCAATAGTCACGTGA CCACCCGATAGGTCGGTCAGTCTAAACAGCGCAGCTGCCAGTG ATGATTTTCCTGTATACATAGCCAAAGTTAACTAGAGATGCATGC ATTATCAAAATTGTAAAATGATTTGGTTATGATGTTTTAAAAAAA TGTTTAGTTTAACTTTGTACATGCATAACATAGAAATGATGCGAG AAGAACGTTACATATAAATTCACTGAACAT**GTGTGTGTGTGTG**	218-244

			TGTGTGTTTTGTTCAAAGCAATAATTAAGGTTTATACTTATTTGA TAAGTCTTCCTCTGATTGAGTTTTATCCTACCTGCTCCCGTGCGG CCAACAATGCCGACCTTTTGTTTAGGAAGGATATCGAAACTGAT GTTATGGAGCACGGGATCCATGTCAACG	
PeFu_P2_D07 Genbank name PeFu09	Forward: CAGTCGGGCGTCATCAGCTACATTCTGCCGCTCTTC Reverse: GTTTGAATGCTTACCCGTCAAT	$(AATG)_{12}$.. .$(AATG)_4$	CGGCTACATTCTGCCGCTCTTCAGGGAATCACCTGTTTTGTATG AATGAATGAATGGAAACATTAAGGAATGGACGAATGAATAGAG GTATTT**AATGAATGAATGAATGAATGAATGAATGAATGAATG AATGAATGAATGA**AAAGG**AATGAATGAATGAATG**AACGAATG AAGGAAGGAGTTTAATAGGATAACCCACTTATAATTCAACATTT AATATAATTATTGACGGGTAAGCATTCAATATATCATACACCCACT GAACA	225-299
PeFu_P2_E11 Genbank name PeFu10	Forward: CAGTCGGGCGTCATCACTGTTGCCGATAAACTAATCAA CCT Reverse: GTTTCCAGTGGTTCGCTAACGTATT	$(AT)_4$...$(GAT)_6$	AGTTCAGAGTTTGTACGTATAGCCAGGATCTTATTGGCTTCGAA AATAAGATTTGCATGATACAATTCACTGACATAAGTTATATTAAAT ATAAAAGTCATGTACTATTGGTTACATATAATATTGATATAATAAC GGGATGGACAAAACAGAATGGTCGATATATGTAACAGAAAATAT GCAATTATTGTTGTTTTGTCTGAAGTGGAGATGTAGTCTGTATAT GTCAACGTTTACATTTTGGCAAAACTAGTTCTTTCCCCCGTGGAT ATAAAATCTTCAACTTTCTAATTAAATACGTCTACAACTAAATGA TTCATACATGCACTGCAATAACTAGTACTCGGCGCCATGTCAGG AATCAAGCTTTTATTCCTGGNTTATCGATAGAATATCAAAATAAT GGTTTTAACAAATTAGCACACACCGATCGGATACCAAAGTTTGT GTAGAAGTGTCTGTCCGTTGACTATTGAAAATAATTCAATGGTAT TTTTCTGTTGCCGATAAACTAATCAACCTACTTTTATGTAAGACT TTTTAGGCGTGAAATTATTTGCGGAATTCAGTTTAAATATTGACT GAATTGTTGTTACAGATAACCATTACAGTAAATACGATACATTTT AGTTTGAG**ATATATATAT**AGAAATTATAATGCGTGAAGTCAGTTTC AACCCGTATTTGTATTACTTTTACGT**GATGATGATGATGATGAT** GCTCGTACAACAGACTATCACTAGAATCCCTTGTCATATTAAGAT CTAACTGTAATACGTTAGCGAACCACTGGCTGTACTCGTGTCAG TTTCGATAGAGACCTGAGGCGCACGGACACGGGTNNCGGGTAG TGGACG	304-350
PeFu_P1_A11 Genbank name PeFu11	Forward: CAGTCGGGCGTCATCATGTGCAGATGGTTTGTGAGG Reverse: GTTTCGTCAATGTTAAGGTAGCTCGT	$(AAAC)_6$	CGTGCTTTATCATCCCTGTAAAGTAATTACAGTAATTGTGGCGAT AGATAGGTCTACACGGTATATAGGTCTACACGGTATATATGTGAA CTTTGTATTATAGTCCTTCATTTCTTCATTAACATCAAATAATAGC TTATGTTACCGATATCCCAAGTTTTAATGTAAATGTGCAGATGGT TTGTGAGGTTTTCTATTGATTCTGCTGGAAACTCTATTTCAAATA AAAATACGAAAACAAACAAACAAACAAACAAACAAAAGCA**AA AACAAAACAAAAAAACAAAAACAAAAAAC**AACTGACATTTAA TTTCGGATCCTGTTTCGGAATTCATTAAAATTCATTTCAAAATTG AATATTGCTCCTTTTATTTGACAACGAGCTACCTTAACATTGACG	235-258

			TCATGACAAACACAGAATTTAATGGTAGATATCAATATATGCTGT CCACACCGCAAGGTCAGGAGTCCTGTCCCTGTTTTTTCCAGGCT GGTTTTAATGTTGATATTTTGTATATTTCAGTATGTAAAGACAAA CATCCCCGGTCCCGGTTGTGACATGGACGAATTCGAAACCCAA ATCCTCGGCTGTCAGTGTGACAACAACATTTGTCTTGAAATGTG TCCATGTATCGTCAGATATGGCAGGATTTATGAAGACGGGAAAA TTATTCCGTCACGCATTGACGGTAAAAACATGGTGCCCATATTTG AATGCAATATTCGGTGTAAATGTCCATCCGACTGTCAAAACAGA TTGATTCAGAGAGGAATATCTATCAAAANGGAATT	
PeFu_P1_F02 Genbank name PeFu12	Forward: CAGTCGGGCGTCATCAATGTTTCCCCAATATGCAG Reverse: GTTTCAGAATGAGTCAAATGGAACAG	$(GAT)_8$	CGCCTAAGTGATGTGAAATAAGATATGTTACTCAGAATGAGTCA AATGGAACAGATCAGATGTGATTCTTAATCACGATGTACCGTTA ACGTTATAATTCAATGTAATTATGTCCATTTCAATTTAACTTCTTT TTCTTTTCTTCCTTTTGTACTCTCAAATTTTGAGGAATAAAGAAT **GATGATGATGATGATGATGATGAT**CTGTGCTGTGAGGGAAATA CGCTGAAATCTGTTATGTAATCAGAAGTGTTTTTTTAATTCTGCA TATTGGGGAAACATTCTATTGTTCCAGGAACAACTTTGCAATTT GGATATTAGTACGTGGTCTTGACAATAATCACATAATTACCGTAT CTGCTATTGCAGCCTCCATGTTCTACCAAAAATATCGTTTCCCGT GCGTAATTTACACCGTGTTCTGAGCGCAATCAGCGGAGACCGG TCGGTACACGATGTTATGCTTGTTCAAGAAAAAACGAAATGGG CGACAGGCGGCCATCCTGGATTTTTTCTCATATTTTCAGAAATTA TCTTTCTCAAATTCCATAATGATTAACGCATTGTTATCTTGGATTT CAATAATTCATTGCTATTACCGTCACCCGTCACTTCTTCTTCAAC GTGCTTATGATATTGATATAATTTAATACTACTTCTGTTAAAAAAC CACGAACA	241-330
PeFu_P2_C07 Genbank name PeFu13	Forward: CAGTCGGGCGTCATCAACGGATGCAGTATTGAGGA Reverse: GTTTCAACATCTCTACATGTGCATACTGA	$(GTTT)_5$	GATTCCAGGTATCAAAAACATTTACAACATCTCTACATGTGCATA CTGATTTTTCCAATAAATGAATTTTAAGTGTATTAACAAAAGTAT TAACAAAAGTGAAATTGTTGTGTTTTATACTAGGTAATAC**GTTT** **GTTTGTTTGTTTGTTT**GTGTTTTAGATATATTGATACAACAAGT ATAATACATGAAGTTGACTGGCTATATTTCTTTTAATATTCGACAC ATGAACTATCCTCAATACTGCATCCGTTACTCTCACTTTCGCTCT CTGCACCTCTGGGATACGTCATGTGAAAATCGTAGACTCGGTCA CCACGCCAACATCTGTTGATAAATAAGAAAGACTAGTTTTATCC TTTGATATGCATGGAACGAATCACGAGATCGCCATACCGTTATTT TGACTGGATTGGATCTTCGTTGTCGTTCCCCTGCTATCTTCGAAT GAAACACAAACTTAACGAGTGTTCAGGTTTTTTCCCATGTGCGA ATCAGATAGCTACCTAGCGATGTAAAAATATGAACCTAGCCACT GAAATATCGAGGATGAAGTGAATGTAAGCCCCGAAGTATAGAA GATGACATGTACATGAACCTAGCCCGAAATGNAAGATGTACATA CG	214-265

PeFu_P2_C09 Genbank name PeFu14	Forward: CAGTCGGGCGTCATCATGGAAGGTTTGTGGAGTGTG Reverse: GTTTGCTCATTTGTTGAGGAATAGCA	$(GTTT)_{11}$	ATTTCGCTAACGTGTGACTCCACTTATATAACAACTTTATCGTCG TGATGATTTGATTACAATTTTATCGTCGTAATGGTTTGTTTACAAA TTAATTTTCACTTCAAGTACATGTAACAACTAATAATAGACTTAC GTCACCACAAAATCTGAAAAGTACGCATGACAGCTTTGAATTCC TTGCAATCGACAATTCTTTGAAACAGACCAGTCGGTCTTGAAAA TACATTTGGAATTTAAAGAAGGATTTATTTTTCCCTTTTGTATGA AACAGAAGGAATATATGTGAAATCAACTTATTATCTTCAGTCTTT TTGTAAGCTAGCAGTAACAGATCAATTTGGGGAAAAGATGATAA TAAAAATAAAATGGTCATATTTTTTAAAGGTGAGAATTGCTCATT TGTTGAGGAATAGCAAGAGGATTCGTATCTCAAATGAGAGGCAT T**GTTTGTTTGTTTGTTTGTTTGTTTGTTTGTTTGTTTGTTTG** **TTT**GCTTGTTTGTTTGTTTGTTGGTTGGTTTGTTTGAATACCCTT TATGCCCTGGTATTATTGTGTCTGAATTTACCTAAAAGCATATCA ACATTCACACTCCACAAACCTTCCAGTCATCAAGTGGTCAAGA GATAGGAGACCTTTGACCTTTAACCTTGACAACTAGTCACAAAA ATCG	179-235
PeFu_P2_F01 Genbank name PeFu15	Forward: CAGTCGGGCGTCATCAGCGCCTATTGGCATATCTTT Reverse: GTTTCACGTCCCTTAATAATGACACA	$(CATT)_5$	CGATGGAGTTTTAAGAAATATTACAGGACATTTTCAAATCTTCTA AATAGTCGTACTTTTTTCTTGAATATCTTTCCCGGGCCCCATTCT GTTGCTTCCTCATGGTGATCCTATAGCGCCTATTGGCATATCTTTT TTATTCAGTAAATCTAATCTGATTTAGCTACAGGTAGTATATTCAT TTTATGTAATATGATTAATTGATTGATTGTTTGTTTGTTTGATTGTT TAGTTGTCTAATT**CATTCATTCATTCATTCATT**CGTTCTCTCATT CATTCAGGTCTTTGTTTACTGCAATAACGCACGAGATCATATGTG TTATATAAAACCCGAAATNGAATGTGTCATTATTAAGGGACGTG AAATCGTGACGGGGTTGATTTTATGGTGTTAACATAACAACATT GTCCCGTTTTNATTGAAAT	253-297

Appendix 3B.

Summary of genetic variation at 15 microsatellite loci for 18 populations of *Pectin fumatus*, including sample size (N), number of alleles (Na), number of effective alleles (Ne), Shannon's information index (I), observed heterozygosity (Ho), expected heterozygosity (He), unbiased expected heterozygosity (UHe) and fixation index (F_{IS}).

Location	Locus														
	A09	PeFu_P1_B05	PeFu_P1_E12	PeFu_P2_C12	A06	PeFu_P1_C01	PeFu_P1_E04a	PeFu_P1_H11	PeFu_P2_D07	PeFu_P2_E11	PeFu_P1_A11	PeFu_P1_F02	PeFu_P2_C07	PeFu_P2_C09	PeFu_P2_F01
Satellite Island															
N	28	32	32	25	32	32	32	32	30	32	32	32	30	31	32
Na	6	7	25	10	16	7	23	5	13	10	4	8	5	10	8
Ne	1.463	3.644	12.962	6.757	6.919	2.096	6.585	2.459	10.000	3.835	1.645	2.837	3.214	5.539	4.258
I	0.723	1.518	2.863	2.080	2.292	1.146	2.566	1.085	2.392	1.708	0.781	1.375	1.306	1.966	1.589
Ho	0.321	0.781	0.938	0.800	0.844	0.500	0.844	0.500	0.600	0.594	0.281	0.656	0.367	0.742	0.844
He	0.316	0.726	0.923	0.852	0.855	0.523	0.848	0.593	0.900	0.739	0.392	0.647	0.689	0.819	0.765
UHe	0.322	0.737	0.938	0.869	0.869	0.531	0.862	0.603	0.915	0.751	0.398	0.658	0.701	0.833	0.777
F_{IS}	-0.016	-0.077	-0.016	0.061	0.014	0.044	0.005	0.157	0.333	0.197	0.283	-0.014	0.468	0.095	-0.103
Gordon - Channel															
N	59	59	59	54	59	59	59	59	59	59	59	56	46	56	59
Na	6	8	30	12	16	8	26	5	16	10	6	18	5	11	7
Ne	1.857	4.559	16.116	4.930	6.605	1.725	5.797	2.572	8.308	3.916	1.548	4.015	3.201	5.158	4.739
I	0.932	1.638	3.044	1.906	2.232	1.005	2.457	1.145	2.330	1.686	0.788	1.890	1.283	1.940	1.640
Ho	0.356	0.780	0.915	0.741	0.831	0.390	0.729	0.508	0.542	0.712	0.339	0.732	0.435	0.857	0.661
He	0.462	0.781	0.938	0.797	0.849	0.420	0.827	0.611	0.880	0.745	0.354	0.751	0.688	0.806	0.789
UHe	0.465	0.787	0.946	0.805	0.856	0.424	0.835	0.616	0.887	0.751	0.357	0.758	0.695	0.813	0.796
F_{IS}	0.229	0.001	0.024	0.071	0.021	0.073	0.119	0.168	0.383	0.044	0.042	0.025	0.368	-0.063	0.162
Great Bay 10															
N	42	42	42	41	41	42	42	42	40	41	42	42	40	42	42
Na	9	7	27	11	16	10	22	5	14	9	8	14	5	10	7

Ne	2.125	3.955	14.226	5.449	7.389	2.033	6.114	2.403	9.040	3.946	1.639	3.399	3.544	4.742	3.929
I	1.203	1.527	2.958	1.926	2.288	1.235	2.453	1.100	2.345	1.693	0.911	1.695	1.367	1.877	1.572
Ho	0.286	0.595	0.905	0.854	0.878	0.595	0.786	0.429	0.425	0.634	0.357	0.714	0.200	0.714	0.667
He	0.529	0.747	0.930	0.816	0.865	0.508	0.836	0.584	0.889	0.747	0.390	0.706	0.718	0.789	0.745
UHe	0.536	0.756	0.941	0.827	0.875	0.514	0.847	0.591	0.901	0.756	0.394	0.714	0.727	0.799	0.754
F_{IS}	0.460	0.203	0.027	-0.046	-0.015	-0.171	0.061	0.266	0.522	0.151	0.084	-0.012	0.721	0.095	0.106
Great Bay 25															
N	61	61	58	61	60	60	49	59	60	59	60	61	54	61	60
Na	14	7	32	17	15	12	21	7	13	10	8	20	5	15	8
Ne	1.899	3.931	14.046	5.892	7.243	1.749	3.743	2.640	8.889	3.426	2.048	3.370	3.253	6.427	4.746
I	1.180	1.526	3.010	2.133	2.235	1.094	2.103	1.241	2.328	1.616	1.160	1.828	1.294	2.188	1.651
Ho	0.410	0.639	0.948	0.787	0.850	0.450	0.592	0.593	0.417	0.712	0.550	0.738	0.407	0.852	0.700
He	0.473	0.746	0.929	0.830	0.862	0.428	0.733	0.621	0.888	0.708	0.512	0.703	0.693	0.844	0.789
UHe	0.477	0.752	0.937	0.837	0.869	0.432	0.740	0.627	0.895	0.714	0.516	0.709	0.699	0.851	0.796
F_{IS}	0.134	0.143	-0.021	0.052	0.014	-0.051	0.192	0.045	0.531	-0.005	-0.075	-0.049	0.412	-0.010	0.113
Great Bay															
N	112	114	114	111	119	119	114	118	113	116	104	119	114	119	119
Na	14	10	42	17	18	14	40	9	19	13	8	21	8	13	9
Ne	1.971	4.297	18.848	6.182	6.666	2.077	9.346	2.844	10.023	4.201	1.670	2.880	3.364	5.101	4.810
I	1.141	1.718	3.230	2.145	2.227	1.260	2.898	1.309	2.522	1.753	0.916	1.701	1.346	1.940	1.688
Ho	0.375	0.711	0.956	0.829	0.866	0.504	0.877	0.500	0.619	0.724	0.365	0.588	0.421	0.782	0.723
He	0.493	0.767	0.947	0.838	0.850	0.518	0.893	0.648	0.900	0.762	0.401	0.653	0.703	0.804	0.792
UHe	0.495	0.771	0.951	0.842	0.854	0.521	0.897	0.651	0.904	0.765	0.403	0.655	0.706	0.807	0.795
F_{IS}	0.239	0.074	-0.010	0.011	-0.018	0.027	0.018	0.229	0.312	0.050	0.089	0.099	0.401	0.028	0.088
White Rock															
N	84	81	84	84	88	85	86	84	81	88	88	88	87	88	88
Na	13	11	40	16	19	13	35	6	14	9	9	24	6	12	7
Ne	1.800	4.445	21.611	6.601	8.372	2.144	7.112	2.559	9.012	4.283	1.849	4.315	3.934	6.071	4.442
I	1.067	1.741	3.328	2.149	2.396	1.325	2.779	1.161	2.351	1.690	1.037	2.078	1.476	2.067	1.579
Ho	0.381	0.802	0.976	0.786	0.852	0.494	0.802	0.524	0.568	0.830	0.466	0.750	0.460	0.841	0.750
He	0.444	0.775	0.954	0.848	0.881	0.534	0.859	0.609	0.889	0.767	0.459	0.768	0.746	0.835	0.775
UHe	0.447	0.780	0.959	0.854	0.886	0.537	0.864	0.613	0.895	0.771	0.462	0.773	0.750	0.840	0.779
F_{IS}	0.143	-0.035	-0.024	0.074	0.032	0.074	0.066	0.140	0.361	-0.082	-0.014	0.024	0.384	-0.007	0.032
Eddystone Deep															

N	24	24	28	27	30	30	30	30	29	30	29	30	30	30	30
Na	3	10	24	11	14	13	25	5	13	9	5	13	6	12	6
Ne	1.341	4.204	12.959	5.586	7.930	3.197	10.909	2.956	7.897	3.681	1.991	3.285	3.719	5.714	4.467
I	0.475	1.715	2.889	1.962	2.305	1.739	2.816	1.249	2.250	1.572	1.033	1.615	1.434	2.047	1.584
Ho	0.208	0.750	0.893	0.926	0.900	0.700	0.967	0.500	0.586	0.867	0.483	0.733	0.500	0.833	0.667
He	0.254	0.762	0.923	0.821	0.874	0.687	0.908	0.662	0.873	0.728	0.498	0.696	0.731	0.825	0.776
UHe	0.260	0.778	0.940	0.836	0.889	0.699	0.924	0.673	0.889	0.741	0.506	0.707	0.744	0.839	0.789
F_{IS}	0.181	0.016	0.032	-0.128	-0.030	-0.019	-0.064	0.244	0.329	-0.190	0.030	-0.054	0.316	-0.010	0.141
Eddystone															
N	37	35	36	39	39	39	38	38	39	39	36	39	39	39	39
Na	10	7	27	12	21	11	17	5	14	9	6	16	5	12	7
Ne	1.746	3.781	15.521	5.613	7.124	3.328	7.912	2.547	7.141	3.875	1.976	3.705	3.591	5.290	4.202
I	0.996	1.487	2.996	1.980	2.424	1.688	2.438	1.138	2.218	1.585	1.060	1.859	1.358	1.960	1.568
Ho	0.378	0.686	0.917	0.949	0.769	0.641	0.921	0.474	0.359	0.769	0.500	0.641	0.513	0.795	0.821
He	0.427	0.736	0.936	0.822	0.860	0.700	0.874	0.607	0.860	0.742	0.494	0.730	0.722	0.811	0.762
UHe	0.433	0.746	0.949	0.833	0.871	0.709	0.885	0.615	0.871	0.752	0.501	0.740	0.731	0.822	0.772
F_{IS}	0.115	0.068	0.020	-0.154	0.105	0.084	-0.054	0.220	0.583	-0.037	-0.012	0.122	0.289	0.020	-0.077
Banks Strait															
N	104	104	108	106	102	106	109	108	103	106	109	109	105	109	103
Na	20	11	43	18	23	14	37	6	17	12	9	23	7	12	10
Ne	2.167	3.727	18.412	6.592	8.469	2.778	5.632	2.732	7.537	4.084	2.248	3.780	3.598	5.340	4.539
I	1.392	1.617	3.233	2.197	2.480	1.613	2.613	1.236	2.291	1.741	1.216	1.932	1.497	1.992	1.663
Ho	0.452	0.702	0.917	0.849	0.833	0.575	0.743	0.556	0.456	0.679	0.569	0.743	0.438	0.826	0.631
He	0.539	0.732	0.946	0.848	0.882	0.640	0.822	0.634	0.867	0.755	0.555	0.735	0.722	0.813	0.780
UHe	0.541	0.735	0.950	0.852	0.886	0.643	0.826	0.637	0.872	0.759	0.558	0.739	0.726	0.816	0.783
F_{IS}	0.161	0.041	0.031	-0.001	0.055	0.101	0.096	0.124	0.474	0.101	-0.025	-0.010	0.393	-0.016	0.191
Babel Island															
N	90	93	90	90	85	87	92	91	84	88	92	93	93	93	93
Na	13	10	40	15	18	12	29	7	16	12	9	22	7	13	12
Ne	1.955	3.786	18.728	6.391	8.032	2.329	6.733	2.605	6.746	4.475	1.833	4.747	3.417	6.309	4.485
I	1.153	1.575	3.238	2.103	2.392	1.370	2.566	1.216	2.191	1.787	1.059	2.141	1.356	2.062	1.713
Ho	0.300	0.753	0.933	0.778	0.871	0.517	0.859	0.516	0.274	0.761	0.435	0.688	0.462	0.806	0.731
He	0.488	0.736	0.947	0.844	0.876	0.571	0.851	0.616	0.852	0.777	0.455	0.789	0.707	0.841	0.777
UHe	0.491	0.740	0.952	0.848	0.881	0.574	0.856	0.620	0.857	0.781	0.457	0.794	0.711	0.846	0.781

F_{IS}	0.386	-0.023	0.014	0.078	0.006	0.094	-0.008	0.162	0.679	0.020	0.043	0.128	0.346	0.042	0.059
West Flinders 2															
N	86	88	71	81	90	85	88	89	86	90	90	90	87	90	90
Na	15	11	38	18	23	14	35	7	16	11	9	25	7	14	14
Ne	1.912	3.811	21.870	7.616	8.012	2.681	6.095	2.535	6.346	3.692	2.030	4.745	3.450	5.973	4.813
I	1.172	1.626	3.318	2.273	2.456	1.531	2.663	1.174	2.180	1.621	1.147	2.208	1.391	2.116	1.771
Ho	0.372	0.739	0.958	0.778	0.922	0.659	0.807	0.483	0.372	0.678	0.589	0.789	0.402	0.800	0.800
He	0.477	0.738	0.954	0.869	0.875	0.627	0.836	0.606	0.842	0.729	0.507	0.789	0.710	0.833	0.792
UHe	0.480	0.742	0.961	0.874	0.880	0.631	0.841	0.609	0.847	0.733	0.510	0.794	0.714	0.837	0.797
F_{IS}	0.220	-0.001	-0.004	0.105	-0.054	-0.051	0.035	0.202	0.558	0.070	-0.160	0.000	0.433	0.039	-0.010
Commonwealth sth eastern															
N	47	47	40	45	47	47	47	44	46	46	47	46	43	47	46
Na	12	8	28	13	17	10	36	8	14	10	8	17	5	13	9
Ne	2.182	3.691	14.414	6.418	6.634	3.064	9.360	2.698	9.004	4.502	2.045	3.208	2.764	5.247	4.236
I	1.286	1.554	2.978	2.130	2.230	1.559	2.956	1.267	2.374	1.800	1.141	1.740	1.200	1.936	1.642
Ho	0.511	0.638	0.950	0.822	0.745	0.723	0.936	0.614	0.348	0.739	0.489	0.739	0.395	0.787	0.587
He	0.542	0.729	0.931	0.844	0.849	0.674	0.893	0.629	0.889	0.778	0.511	0.688	0.638	0.809	0.764
UHe	0.547	0.737	0.942	0.854	0.858	0.681	0.903	0.637	0.899	0.786	0.517	0.696	0.646	0.818	0.772
F_{IS}	0.057	0.124	-0.021	0.026	0.123	-0.074	-0.048	0.025	0.609	0.050	0.043	-0.074	0.381	0.027	0.232
Commonwealth western															
N	48	49	47	48	49	48	48	48	48	49	49	48	41	49	49
Na	8	6	33	14	16	11	29	6	12	10	12	18	7	12	7
Ne	2.146	3.586	19.812	7.035	6.386	3.076	5.703	2.695	6.330	4.377	2.512	4.603	3.923	5.744	4.797
I	1.096	1.453	3.228	2.186	2.234	1.626	2.571	1.197	2.092	1.794	1.367	1.988	1.538	2.023	1.645
Ho	0.458	0.776	0.830	0.917	0.857	0.688	0.875	0.625	0.417	0.694	0.612	0.813	0.415	0.837	0.735
He	0.534	0.721	0.950	0.858	0.843	0.675	0.825	0.629	0.842	0.772	0.602	0.783	0.745	0.826	0.792
UHe	0.540	0.729	0.960	0.867	0.852	0.682	0.833	0.636	0.851	0.780	0.608	0.791	0.754	0.834	0.800
F_{IS}	0.142	-0.075	0.126	-0.069	-0.016	-0.019	-0.061	0.006	0.505	0.101	-0.017	-0.038	0.444	-0.013	0.072
Commonwealth nth eastern															
N	45	46	43	44	46	46	46	45	46	46	46	46	42	46	45
Na	7	9	31	13	18	13	28	5	15	10	10	19	7	12	7
Ne	1.617	4.215	18.677	5.957	6.972	3.019	4.436	2.295	5.142	3.518	2.208	4.077	3.607	5.244	3.955
I	0.860	1.649	3.159	2.012	2.300	1.688	2.363	1.024	2.112	1.674	1.260	1.987	1.442	1.971	1.480
Ho	0.356	0.870	0.977	0.818	0.913	0.739	0.870	0.511	0.261	0.630	0.543	0.783	0.429	0.783	0.667

He	0.382	0.763	0.946	0.832	0.857	0.669	0.775	0.564	0.806	0.716	0.547	0.755	0.723	0.809	0.747
UHe	0.386	0.771	0.958	0.842	0.866	0.676	0.783	0.571	0.814	0.724	0.553	0.763	0.731	0.818	0.756
F_{IS}	0.069	-0.140	-0.032	0.017	-0.066	-0.105	-0.123	0.094	0.676	0.119	0.006	-0.037	0.407	0.033	0.108
Victoria_1															
N	28	27	28	28	27	21	27	26	22	28	16	21	8	19	8
Na	10	7	26	11	15	13	18	6	9	7	6	14	6	8	5
Ne	1.995	3.787	16.505	6.374	7.554	4.220	6.658	2.551	5.232	4.170	3.580	3.835	4.414	5.270	3.879
I	1.206	1.526	3.013	2.054	2.286	1.972	2.382	1.177	1.865	1.620	1.466	1.838	1.635	1.856	1.461
Ho	0.464	0.852	0.929	0.786	0.778	0.810	0.815	0.462	0.409	0.679	0.500	0.762	0.125	0.684	0.750
He	0.499	0.736	0.939	0.843	0.868	0.763	0.850	0.608	0.809	0.760	0.721	0.739	0.773	0.810	0.742
UHe	0.508	0.750	0.956	0.858	0.884	0.782	0.866	0.620	0.828	0.774	0.744	0.757	0.825	0.832	0.792
F_{IS}	0.069	-0.158	0.012	0.068	0.104	-0.061	0.041	0.241	0.494	0.107	0.306	-0.031	0.838	0.156	-0.011
Victoria_2															
N	32	35	35	32	34	34	35	29	32	35	25	21	20	24	25
Na	14	7	27	12	14	12	22	6	9	9	8	15	6	13	7
Ne	2.674	3.746	16.443	5.737	9.102	2.919	5.373	2.803	4.258	4.139	2.381	6.391	3.463	5.565	4.630
I	1.610	1.545	3.032	1.960	2.371	1.619	2.367	1.284	1.702	1.700	1.291	2.246	1.435	2.036	1.658
Ho	0.500	0.800	0.943	0.844	0.912	0.676	0.800	0.448	0.313	0.800	0.560	0.905	0.350	0.708	0.680
He	0.626	0.733	0.939	0.826	0.890	0.657	0.814	0.643	0.765	0.758	0.580	0.844	0.711	0.820	0.784
UHe	0.636	0.744	0.953	0.839	0.903	0.667	0.826	0.655	0.777	0.769	0.592	0.864	0.729	0.838	0.800
F_{IS}	0.201	-0.091	-0.004	-0.022	-0.024	-0.029	0.017	0.303	0.592	-0.055	0.034	-0.073	0.508	0.137	0.133
Victoria_3															
N	106	99	111	95	118	109	118	108	105	115	121	121	119	120	74
Na	20	9	47	18	22	17	38	8	16	12	12	28	7	13	7
Ne	1.846	3.616	21.335	6.248	9.101	3.718	6.978	2.719	8.507	4.664	2.574	4.989	3.064	5.978	4.494
I	1.216	1.556	3.396	2.121	2.473	1.847	2.775	1.257	2.414	1.865	1.340	2.247	1.340	2.029	1.596
Ho	0.368	0.768	0.937	0.821	0.864	0.752	0.788	0.546	0.381	0.757	0.628	0.818	0.471	0.800	0.649
He	0.458	0.723	0.953	0.840	0.890	0.731	0.857	0.632	0.882	0.786	0.612	0.800	0.674	0.833	0.777
UHe	0.461	0.727	0.957	0.844	0.894	0.734	0.860	0.635	0.887	0.789	0.614	0.803	0.676	0.836	0.783
F_{IS}	0.197	-0.061	0.017	0.022	0.029	-0.029	0.080	0.136	0.568	0.037	-0.027	-0.023	0.301	0.039	0.166
Port Phillip Bay															
N	32	32	29	30	30	32	25	31	29	29	23	30	25	31	31
Na	9	8	25	14	16	6	20	5	13	6	4	15	5	9	7
Ne	1.449	3.220	12.552	6.923	8.654	3.587	8.224	1.909	7.751	4.280	1.704	6.228	2.847	5.045	4.309

I	0.806	1.455	2.874	2.184	2.376	1.472	2.544	0.926	2.237	1.600	0.762	2.194	1.211	1.809	1.602
Ho	0.219	0.625	0.793	0.833	0.933	0.719	0.880	0.419	0.655	0.793	0.304	0.800	0.560	0.774	0.742
He	0.310	0.689	0.920	0.856	0.884	0.721	0.878	0.476	0.871	0.766	0.413	0.839	0.649	0.802	0.768
UHe	0.315	0.700	0.936	0.870	0.899	0.733	0.896	0.484	0.886	0.780	0.422	0.854	0.662	0.815	0.781
F_{IS}	0.294	0.093	0.138	0.026	-0.055	0.003	-0.002	0.119	0.248	-0.035	0.263	0.047	0.137	0.034	0.034

16.Appendix 4 -2012 Victorian Scallop Fishery Survey Report

2012 Victorian Scallop Fishery Survey Report

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TABLE OF CONTENTS

1 Executive Summary

An industry-based scallop survey was conducted in the Victorian Scallop Fishery during January 2012. The survey covered a relatively large area of the fishery, which overlapped the traditional fishing grounds and largely repeated the survey conducted in 2009. Only 3 of the 297 sample tows conducted contained greater than 10 kg scallops per 1000 m^2 standardised sample tow (40, 16 and 12 kg scallops per 1000 m^2). These catches approximately equate to catch rates of 484, 193 and 138 kg scallops per hour commercial fishing. However, the average abundances within the survey grids were less than 1 kg scallops per 1000 m^2 sample tow (or approximately 10 kg scallops per hour commercial fishing). In general, very low abundances of scallops were located throughout the survey region, with abundances similar to those encountered in 2009.

Scallops located within the survey area ranged between 33 mm and 120 mm in size, with the peaks in the size distribution falling within the 69-75 mm and 87-98 mm size ranges. The small tail of scallops less than 70 mm suggested that there has been some recruitment in the past two years, although at relatively limited levels. This suggests that although new cohorts of scallops will be available to the commercial fishery in the next two years, they are unlikely to be available in commercial quantities.

A poor survey result in the 2009 Victorian survey resulted in a TAC of zero being set for 2010 and 2011, as continued fishing of depleted stocks was determined as likely to inhibit their recovery. As such, there is a need for Fisheries Victoria to again carefully consider 2012/13 management arrangements, as there has not been a significant recovery of stocks in the two years of zero TAC.

2 Introduction

In late 2011, the Institute for Marine and Antarctic Studies (IMAS) were approached by Fisheries Victoria to co-ordinate a survey within the Victorian scallop fishery, which followed up on that conducted by IMAS (then known as TAFI) in 2009 (see Appendix 1).Vessels with several years experience in surveying were contacted by Fisheries Victoria, with only one vessel able to conduct the survey in the required time-frame in January, the FV Panagia. The survey subsequently commenced on the 14th of January 2012.

The primary goal of the survey was to revisit the areas surveyed in 2009 to determine if there had been any recovery of stocks. A secondary objective was to sample any new sites deemed important by the participating Victorian industry member. Specific sample tow locations, however, were left to the discretion of the participant. It is important to note that the *FV Panagia* had participated in the 2009 survey and as such was well placed to undertake this repeat survey.

The overall task of organising and implementing the 2012 survey was given to IMAS. This report provides the results of the industry-based fishery survey conducted during January 2012 within the Victorian scallop fishery. The report provides detailed information concerning the abundance and size distribution for sample tows conducted.

3 Materials and Methods

3.1The Survey

The survey was conducted during January 2012. The vessel that participated in the survey *FV Panagia* is based in Lakes Entrance. In total, 297 dredge tows were conducted during approximately 84 hours of combined survey time. Specific sample tow locations were left to the

discretion of the participant, who used their long-running experience in the fishery and their experience of the 2009 survey to select individual dredge shot locations. All survey activities were conducted within Victorian waters.

The *FV Panagia* departed from Lakes Entrance (Vic) on the 14th of January 2012. They initially conducted survey tows in a southwest direction, after which they headed northeast past Lakes Entrance towards Point Hicks. On the 21st of January the final sample tows were conducted during the return trip southwest to Lakes Entrance. Figure 1 shows the location of all sample tows conducted during the survey, as recorded by the skipper of the *FV Panagia* on the data sheets provided.

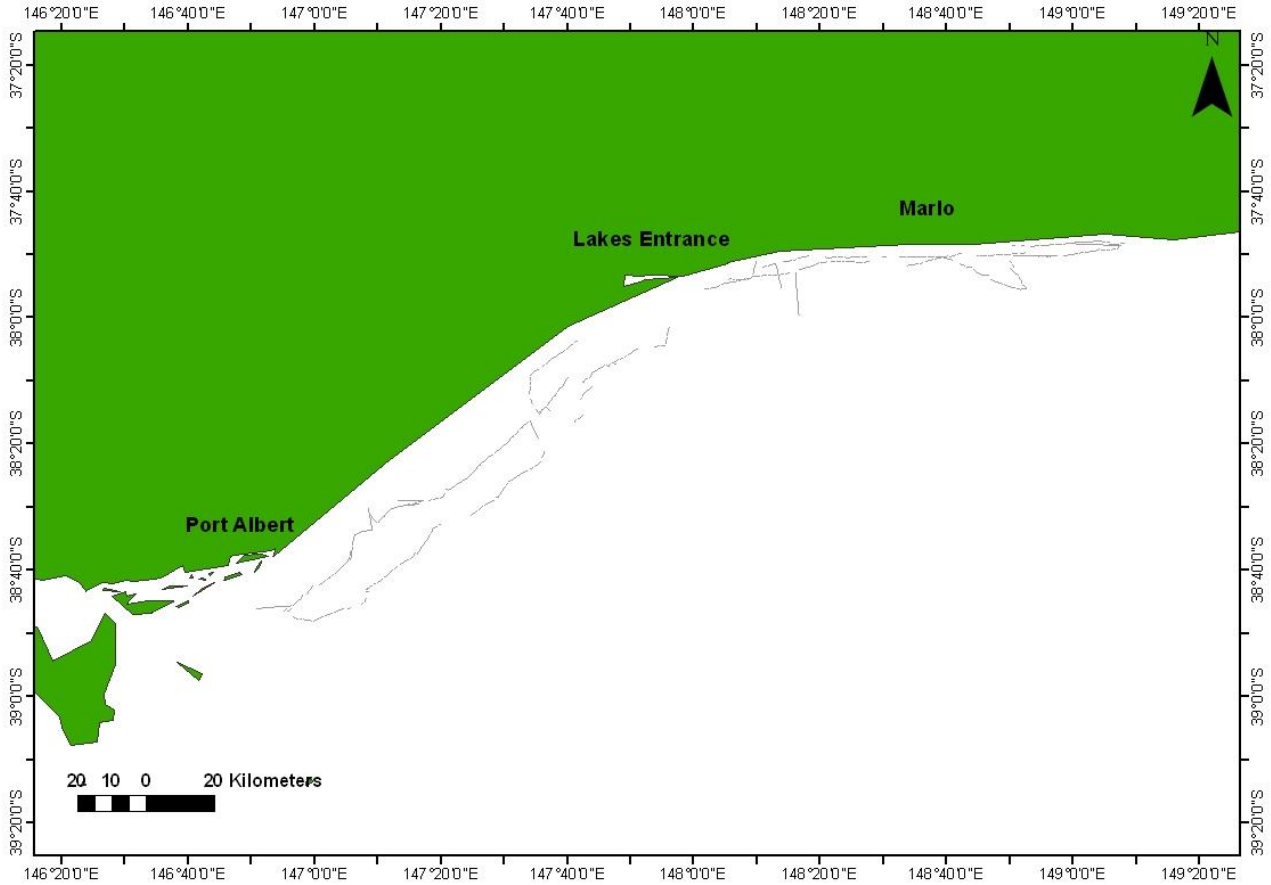

Figure 1: Overview of sample tows conducted during the 2012 Victorian scallop survey.

3.2 Data Collection

The *FV Panagia* conducted seven days survey time (~ 84 hours survey time). For each sample tow conducted, the skipper and crew recorded the start and finish latitude and longitude, depth and an estimation of the total scallop catch. Total catch was estimated either as the kilograms of scallops caught or the number of individual scallops caught. Electronic measuring boards were used to measure the shell width of all scallops caught or a randomly selected subsample (50 scallops was suggested) of scallops when the catch was larger.

3.3 Stratification

To align with Fisheries Victoria scallop catch record returns / historical catch data and the 2009 survey, a grid system consisting of 10’ latitude x 10’ longitude (approximately 10 x 10 nm) was used to analyse and interpret the data. Each grid will be referred to using the letter and number coding used by Fisheries Victoria (see Figure 2).

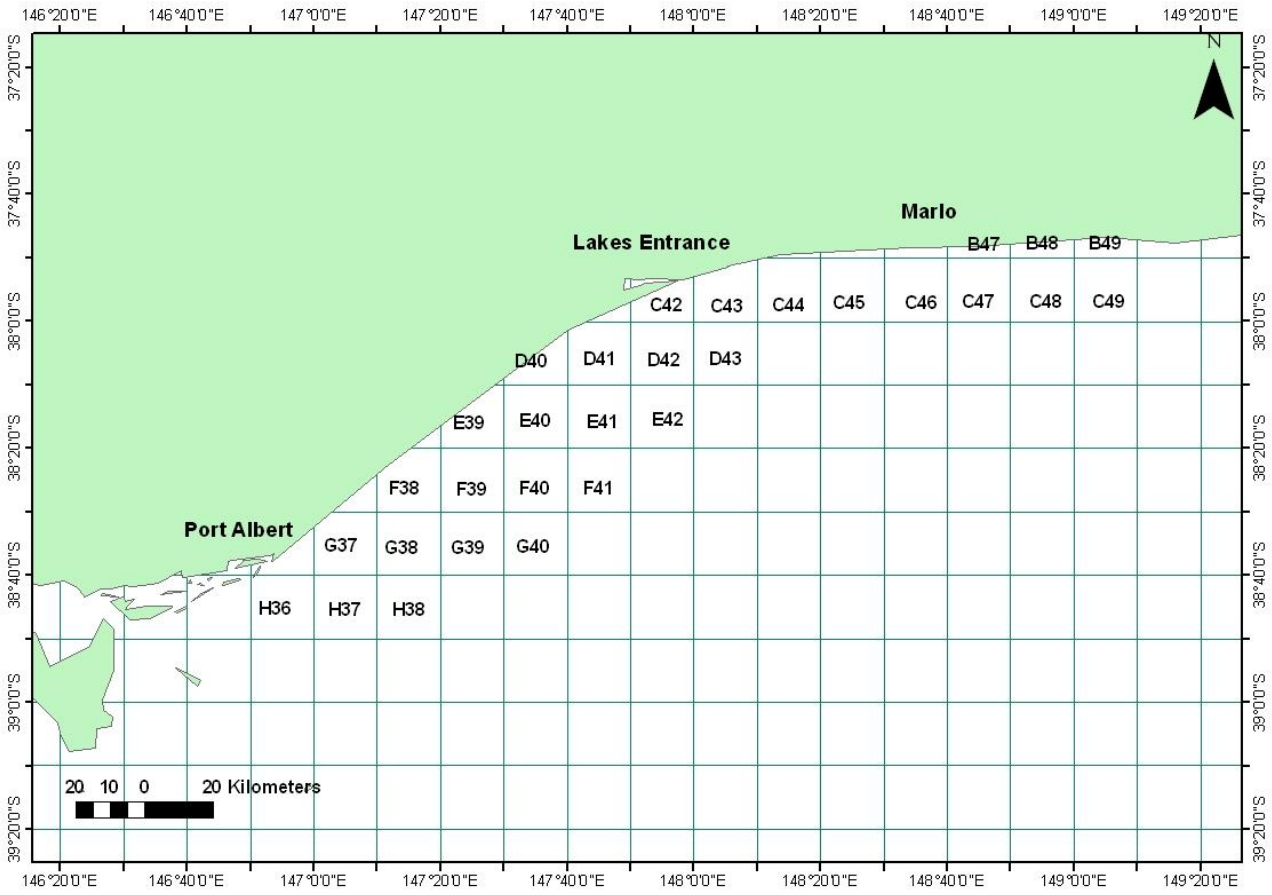

Figure 2: The 10’ latitude x 10’ longitude grid and grid cell codes used by Victorian scallop fishers to record catches. These cells overlap the regions where the vast majority of scallop catches have been taken since 2000 and those surveyed in 2009.

3.4 Data Analysis

3.4.1 Scallop Abundance

Scallop abundance estimates were standardised. The distance of each sample tow was calculated from the start and finish tow locations. The area swept (A) during each sample tow was then calculated by multiplying the tow distance (L) by the width of the dredge used (W).

$$A = L \times W$$

The estimated kg of scallops per $1000m^2$ standardised tow ($C^{Standardised}$) was then calculated by dividing the estimated catch in a sample tow (C) by the area swept (A) (note this equals the kg of scallops per m^2) and multiplying by 1000.

$$C^{standardised} = (C / A) * 1000$$

3.4.2 Approximate Commercial Catches and Catch Rates

Although $C^{standardised}$ provides a means of comparing scallop abundances between survey tows and regions, it does not provide any indication of potential catches and catch rates. Advice from fishers suggests that commercial tow durations of 10 minutes are not unrealistic, and many fishers try to conduct four commercial tows per hour of fishing. Survey data collected by IMAS since 2000 shows that the distance covered by a 10 minute tow is approximately 750 m. Given a standardised $1000m^2$ sample tow covers approximately 250 m tow distance, the approximate catch per 10 minute commercial tow (C^{tow}) can be calculated by multiplying the catch per standardised $1000m^2$ tow ($C^{standardised}$) by three.

$$C^{tow} = C^{standardised} \times 3$$

Furthermore, an estimate of the commercial catch per hour fishing can be made by multiplying the catch per commercial tow (C^{tow}) x four (i.e. four 10 minute tows per hour).

$$C^{hour} = C^{tow} \times 4$$

3.4.3 Size Frequencies

Length – frequency plots were used to compare the population structure of scallops caught within different grids of the survey region. Because the larger catches were sub-sampled for size frequency (i.e. not all scallops from a particular sample tow were measured), the ratio of the sub-sample to total catch was used to scale the numbers in each size class to total catch. To characterise the properties of the resulting size distributions the length frequencies were plotted as histograms, with data grouped into 2 mm size classes to reduce noise.

4. Results

4.1 Overview

Overviews of scallop abundance (kg per standardised 1000m^2 sample tow) and size frequency distribution are illustrated in Figures 3 and 4 respectively.

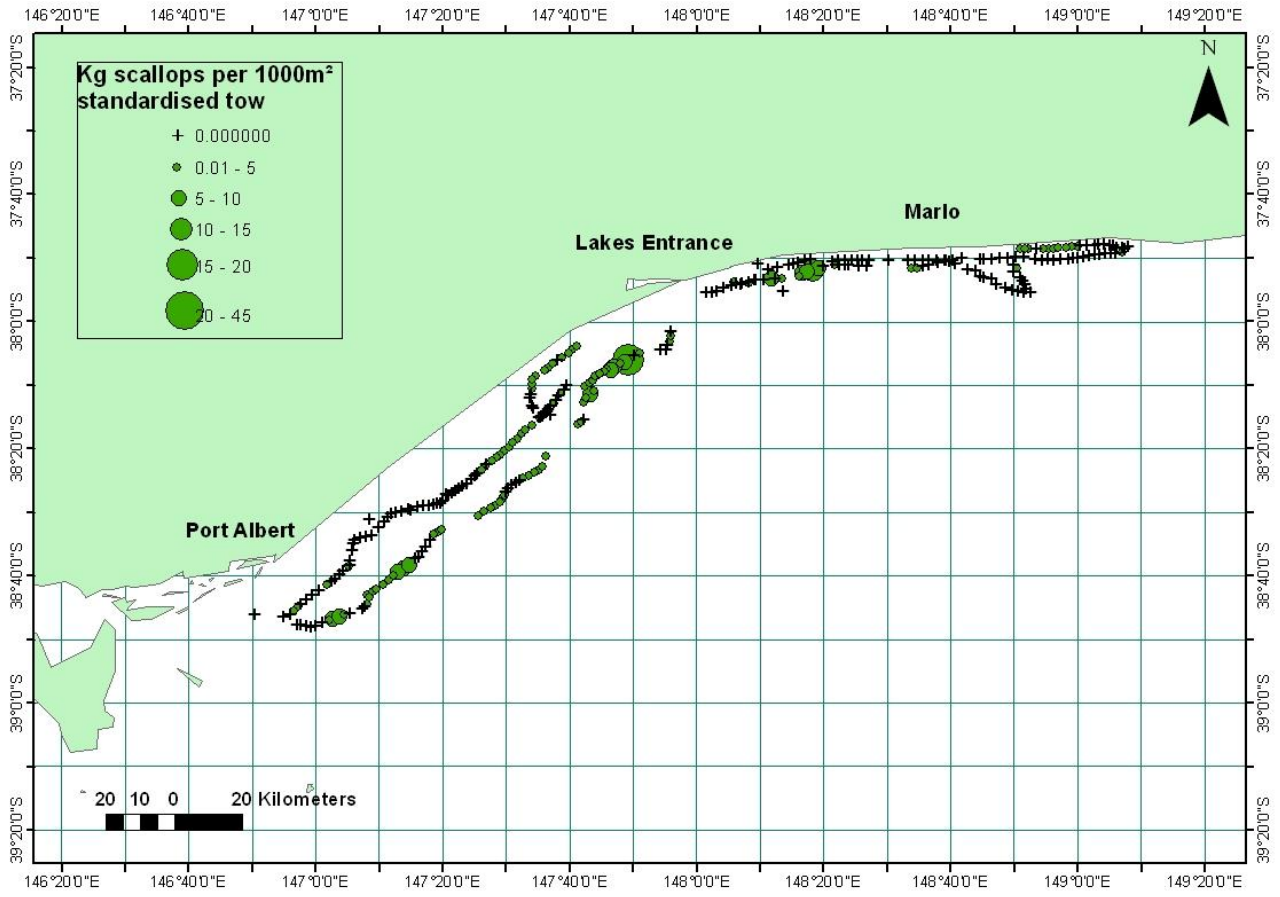

Figure 3: Scallop abundances (kg scallops per 1000m^2 sample tow) for tows conducted during the January 2012 Victorian scallop survey. The 10' latitude x 10' longitude grid is shown as a reference for later results.

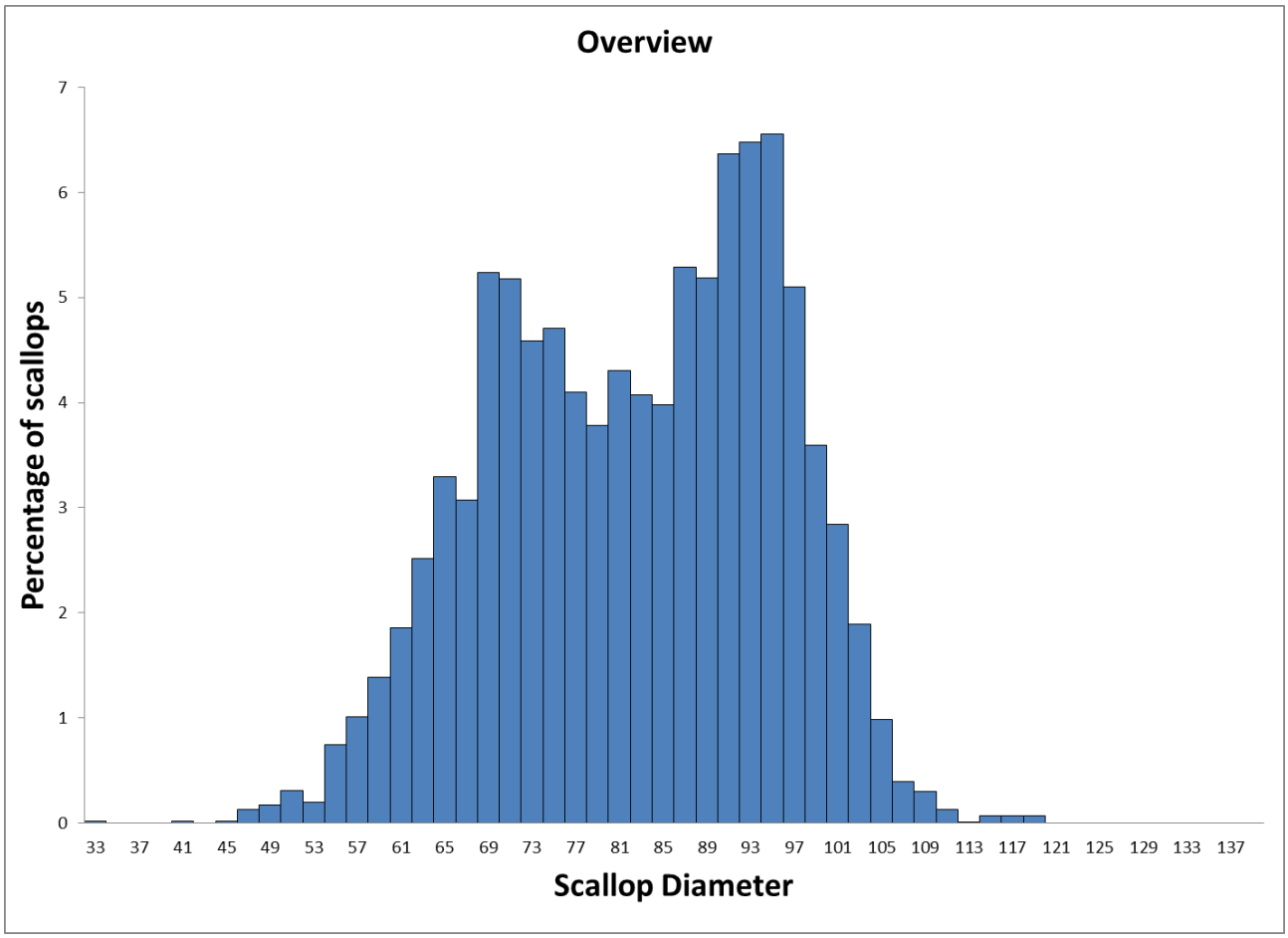

Figure 4: The length frequency distribution for all scallops measured during the 2012 survey

4.2 South West Survey Region (Grids F38 to H38)

The highest average abundance for any grid within this region was 2.3 kg scallops per 1000 m^2 (H38). Extrapolation of this standardised abundance suggests very low catch rates of approximately 27.6 kg per commercial fishing hour (Table 1). The mean abundance for the region was 0.7 kg scallops per 1000 m^2 or approximately 10 kg per commercial fishing hour. The maximum catch for an individual sample tow within this survey region was 9.9 kg scallops per 1000 m^2 (Figure 5). This abundance of scallops would provide an approximate commercial catch of 118.8 kg of scallops per hour commercial fishing.

Scallops located within these survey grids ranged between 45 mm and 120 mm in size (Figure 6), with the peaks in the size distribution falling within the 63-66 mm, 69-72 mm and 87-98 mm size ranges (Figure 6). The tail of scallops less than 70 mm suggested that there has been some recruitment in the past two years, although at relatively limited levels.

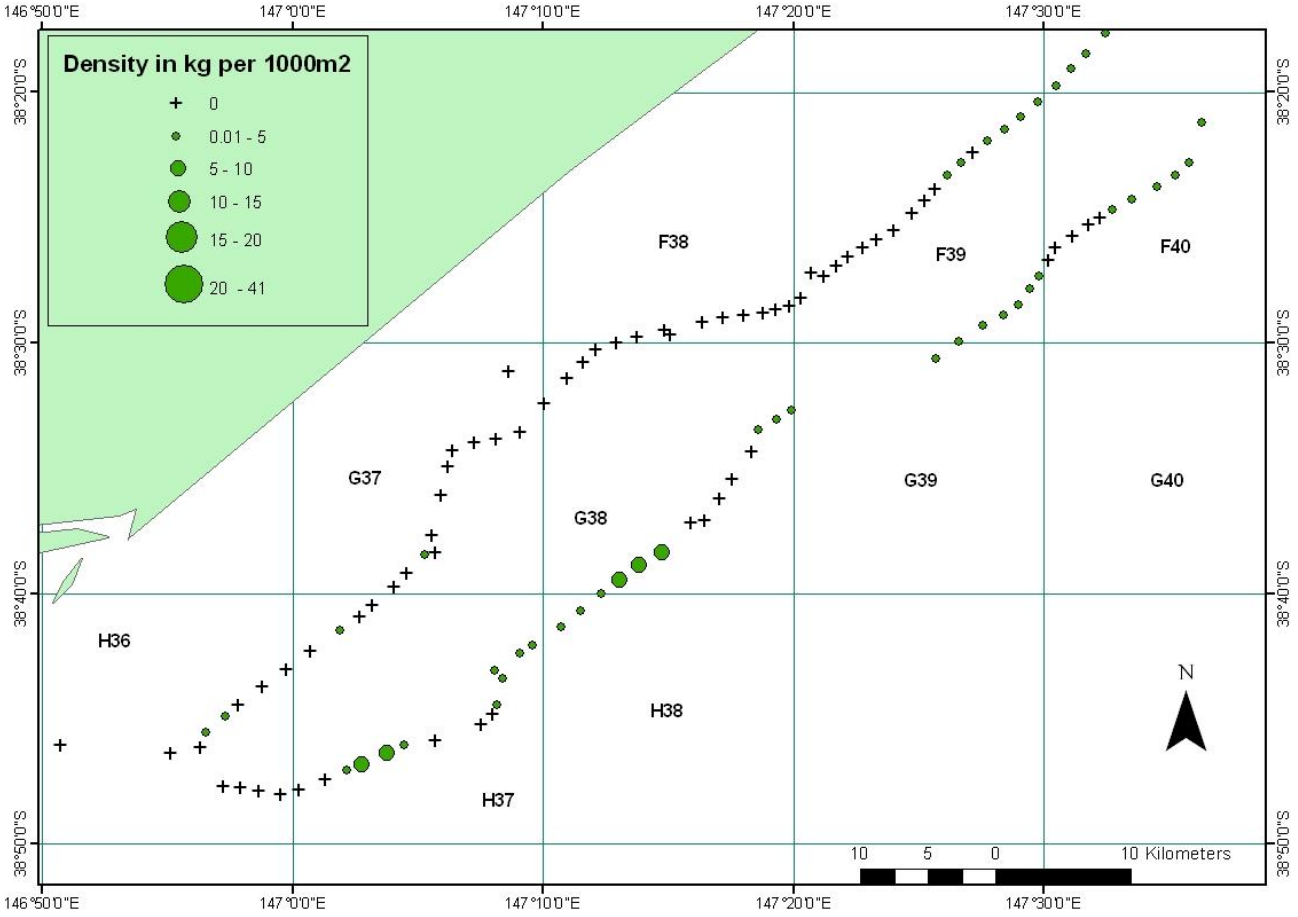

Figure 5: Scallop density (kg per 1000m^2 sample tow) for tows conducted within the southwest survey region (survey grids F38 to H38).

Table 1: Summary of survey effort, catch, abundance and estimated commercial catch for survey grids F38 to H38.

Grid	Mean depth (m)	All tows	Tows that caught scallops	Total number of scallops	Average scallops per sample tow	Average scallop abundance (kg/1000m^2)	Abundance range (kg/1000m^2)	Estimated commercial catch (kg) per hour fishing
F39	37	24	12	327	13.6	0.225	0 - 1.767	2.704
F40	43	11	6	635	57.7	1.019	0 - 3.493	12.233
G37	24	13	1	1	0.1	0.001	0.017	0.016
G38	38	14	6	1570	112.1	2.049	0 - 9.902	14.591
G39	40	1	1	27	27.0	0.29	0.29	3.481
H36	28	12	2	2	0.2	0.003	0 - 0.025	0.04
H37	37	18	10	926	51.4	1.025	0 - 6.681	12.298
H38	42	3	3	504	168	2.303	1.752 2.820	27.633
Region	-	105	41	3066	29.2	0.676	0 - 9.902	8.115

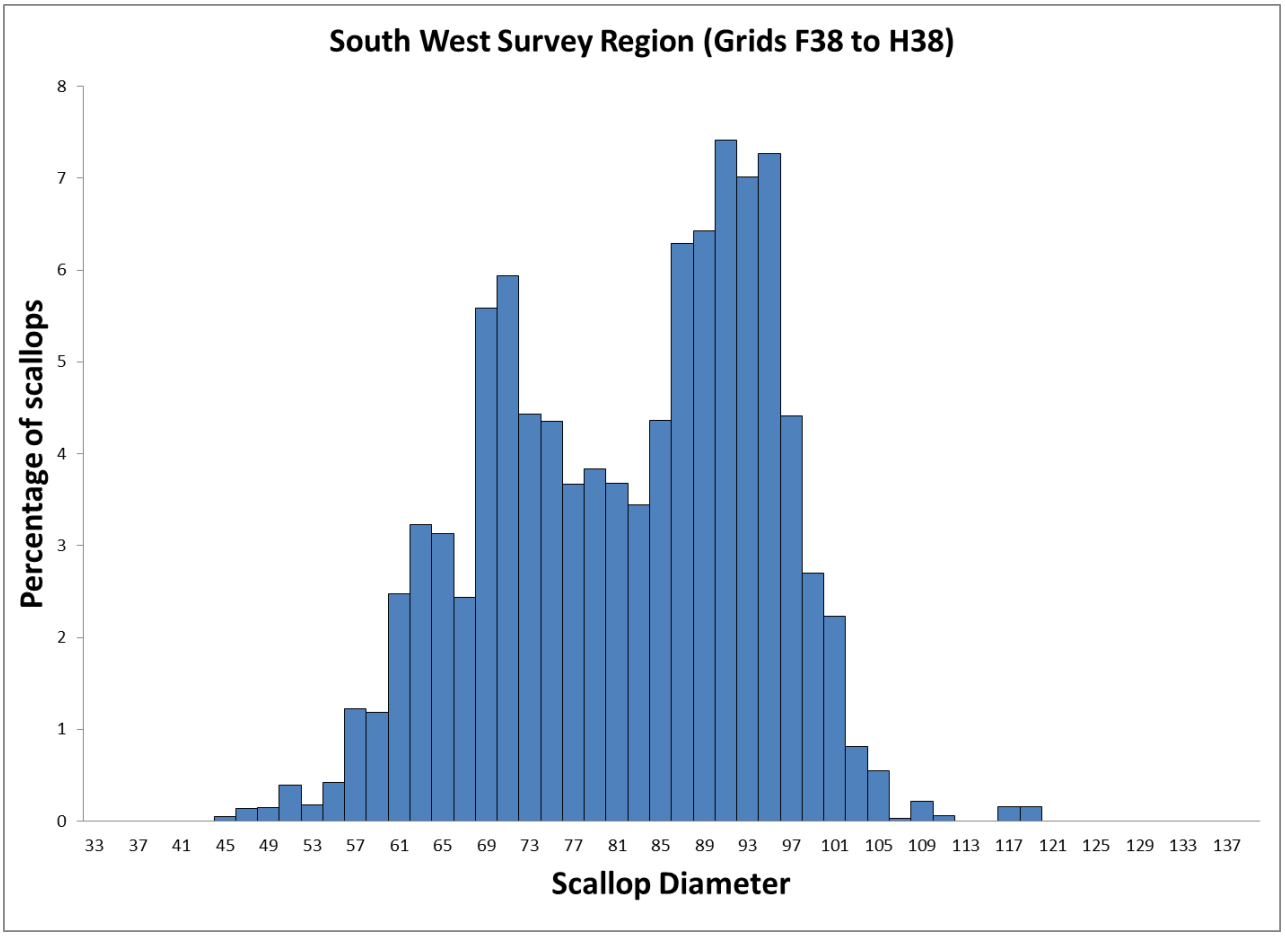

Figure 6: The length frequency distribution for scallops measured within grids F39 to H38. A total of 1170 scallops were measured in this region.

4.3 Central Survey Region (Grids D40 to E41)

The highest average abundance for any grid within this region was 3.7 kg scallops per 1000 m^2 (D41). Extrapolation of this standardised abundance suggests very low catch rates of approximately 44.7 kg per commercial fishing hour (Table 2). The mean abundance for the region was 1.3 kg scallops per 1000 m^2 or approximately 15.5 kg per commercial fishing hour. The maximum catch for an individual sample tow within this survey region was 16.1 kg scallops per 1000 m^2 (Figure 7). This abundance of scallops would provide an approximate commercial catch of 193.1 kg of scallops per hour commercial fishing.

Scallops located within these survey grids ranged between 33 mm and 116 mm in size (Figure 8), with the peaks in the size distribution falling within the 65-97 mm size range (Figure 8). The tail of scallops less than 70 mm suggested that there has been some recruitment in the past two years, although at relatively limited levels.

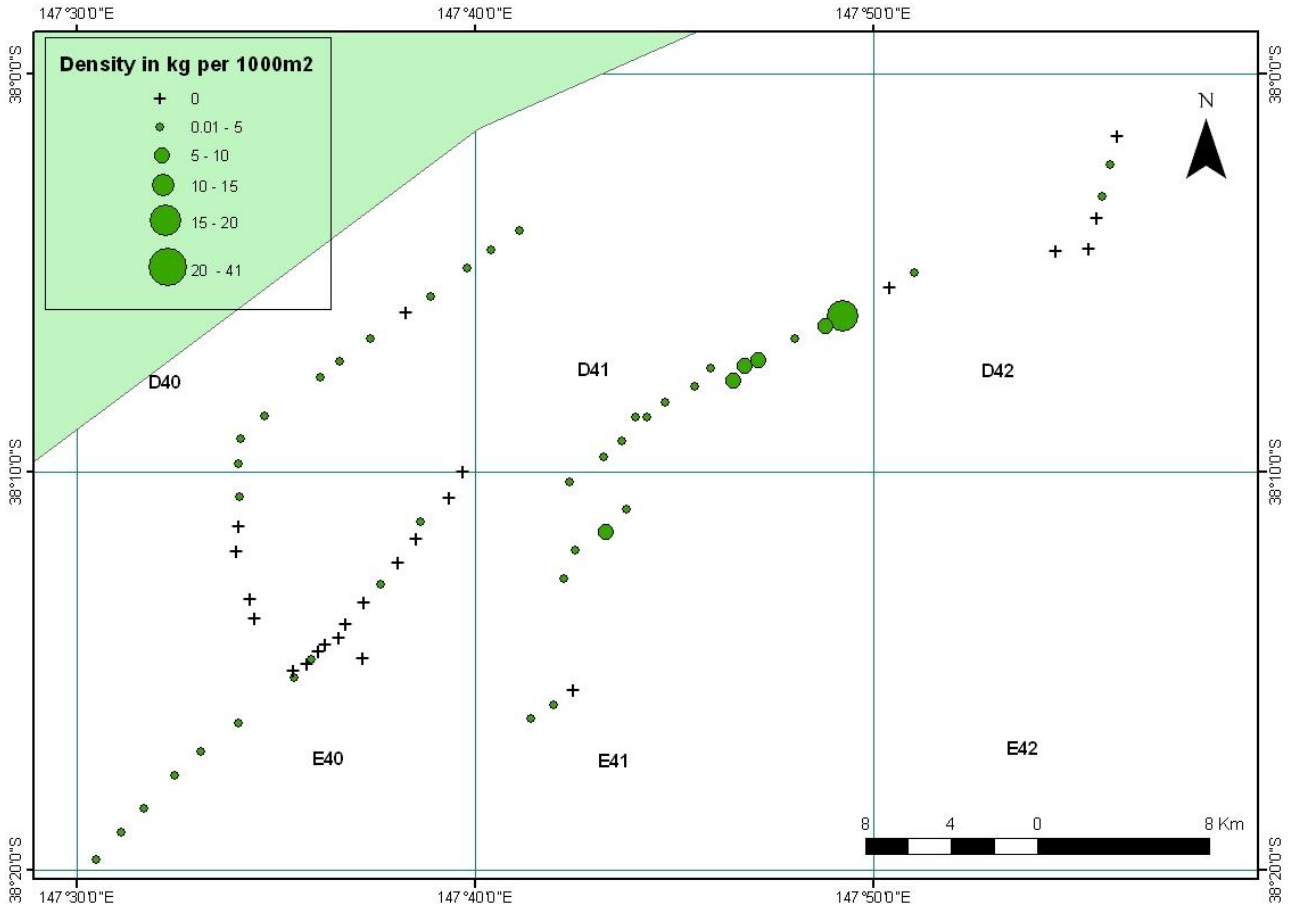

Figure 7: Scallop density (kg scallops per 1000m^2 sample tow) for tows conducted within the central survey region (survey grids D40 to E41).

Table 2: Summary of survey effort, catch, abundance and estimated commercial catch for survey grids D40 to E41.

Grid	Mean depth (m)	All tows	Tows that caught scallops	Total number of scallops	Average scallops per sample tow	Average scallop abundance (kg/1000m^2)	Abundance range (kg/1000m^2)	Estimated commercial catch (kg) per hour fishing
D40	24	10	8	37	3.7	0.076	0 - 0.194	0.919
D41	40	15	15	2303	153.5	3.721	0.134- 6.094	44.652
D42	46	8	3	205	25.6	0.792	0 - 2.171	3.652
E40	36	26	11	559	21.5	0.619	0 - 2.109	3.141
E41	44	8	7	1463	182.9	2.985	0 - 7.607	31.343
Region	-	67	44	4567	68.2	1.969	0 - 16.094	15.519

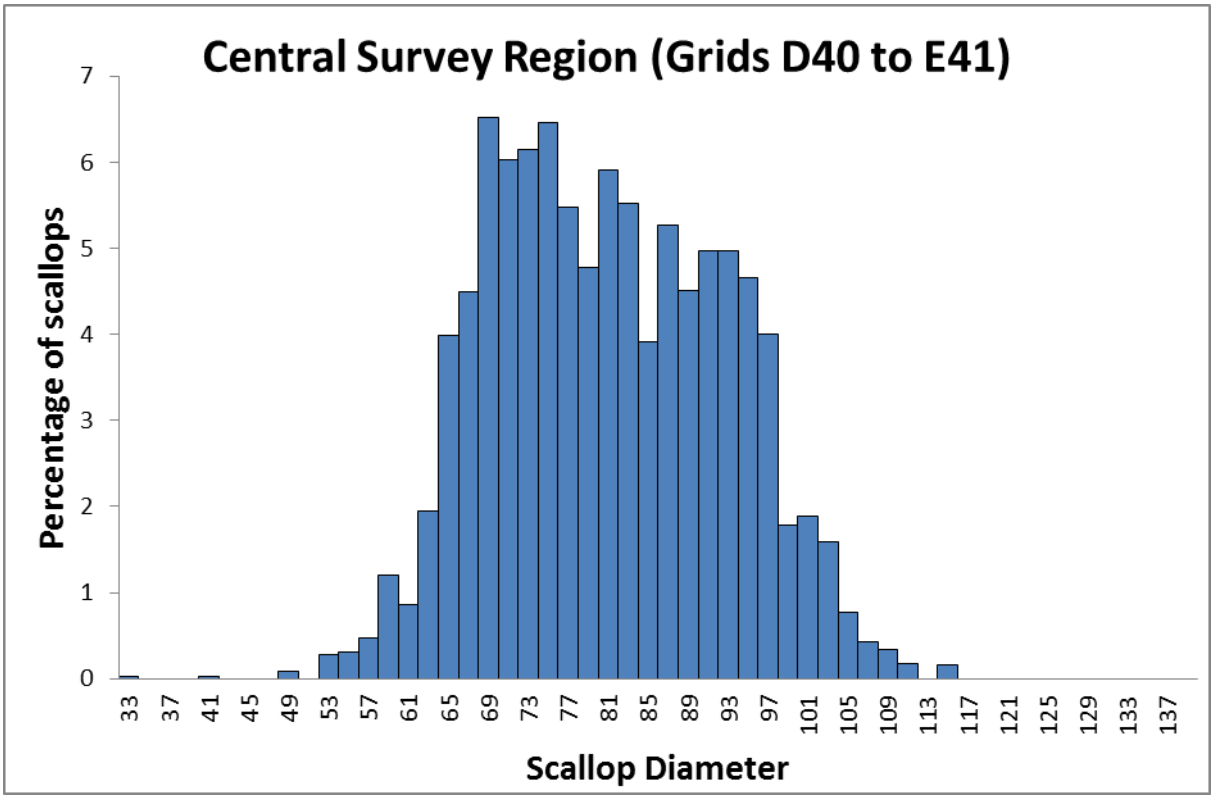

Figure 8: The length frequency distribution for scallops measured within grids D40 to E41. A total of 1259 scallops were measured in this region.

4.4 Eastern Survey Region (Grids B47 to B49 and C43 to C48)

The highest average abundance for any grid within this region was 4.7 kg scallops per 1000 m^2 (C44). Extrapolation of this standardised abundance suggests very low catch rates of approximately 56.1 kg per commercial fishing hour (Table 3). The mean abundance for the region was 0.8 kg scallops per 1000 m^2 or approximately 9.9 kg per commercial fishing hour. The maximum catch for an individual sample tow within this survey region was 40.3 kg scallops per 1000 m^2 (Figure 7). This abundance of scallops would provide an approximate commercial catch of 483.8 kg of scallops per hour commercial fishing.

Scallops located within these survey grids ranged between 47 mm and 114 mm in size (Figure 10), with the peaks in the size distribution falling within the 55-62 mm and 93-99 mm size ranges (Figure 10). The tail of scallops less than 70 mm suggested that there has been some recruitment in the past two years, although at relatively limited levels.

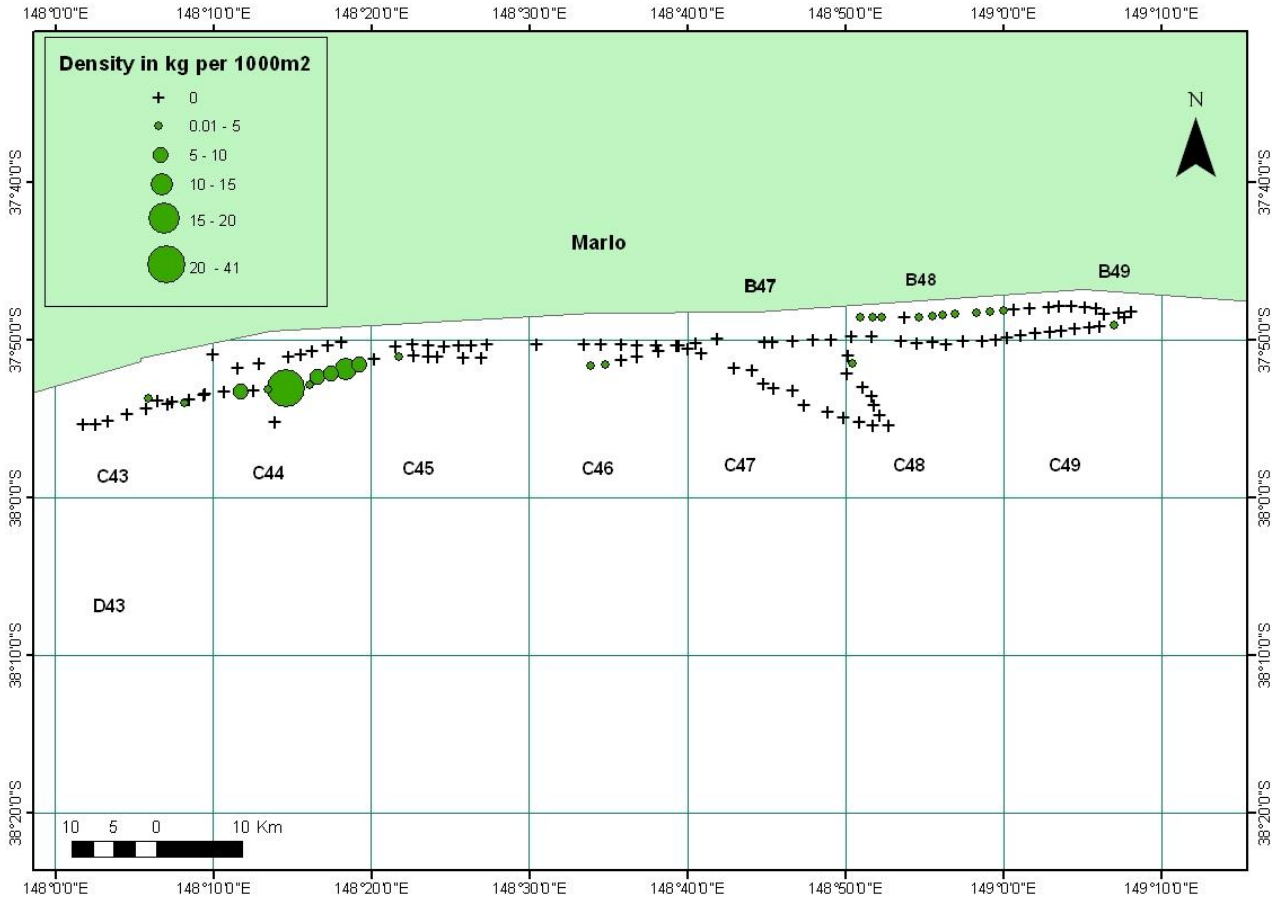

Figure 9: Scallop density (kg scallops per 1000m^2 sample tow) for tows conducted within the eastern survey region (survey grids B47 to B49 and C43 to C48).

Table 3: Summary of survey effort, catch, abundance and estimated commercial catch for each survey grids B47 to B49 and C43 to C48.

Grid	Mean depth (m)	All tows	Tows that caught scallops	Total number of scallops	Average scallops per sample tow	Average scallop abundance (kg/1000m^2)	Abundance range (kg/1000m^2)	Estimated commercial catch (kg) per hour fishing
C43	33	14	2	32	2.3	0.0592	0 - 0.786	0.711
C44	36	18	8	4187	232.6	4.676	0 - 40.316	56.106
C45	37	14	1	5	0.4	0.007	0 - 0.107	0.092
C46	35	13	2	323	24.8	0.372	0 - 2.746	4.461
C47	45	15	0	0	-	-	-	-
C48	48	17	1	13	0.8	0.0158	0 - 0.269	0.19
B47	36	1	0	0	-	-	-	-
B48	27	13	9	20	1.5	0.029	0 - 0.089	0.345
B49	32	20	1	13	0.7	0.013	0.265	0.159
Region	-	105	24	4593	36.7	0.826	0 - 40.316	9.909

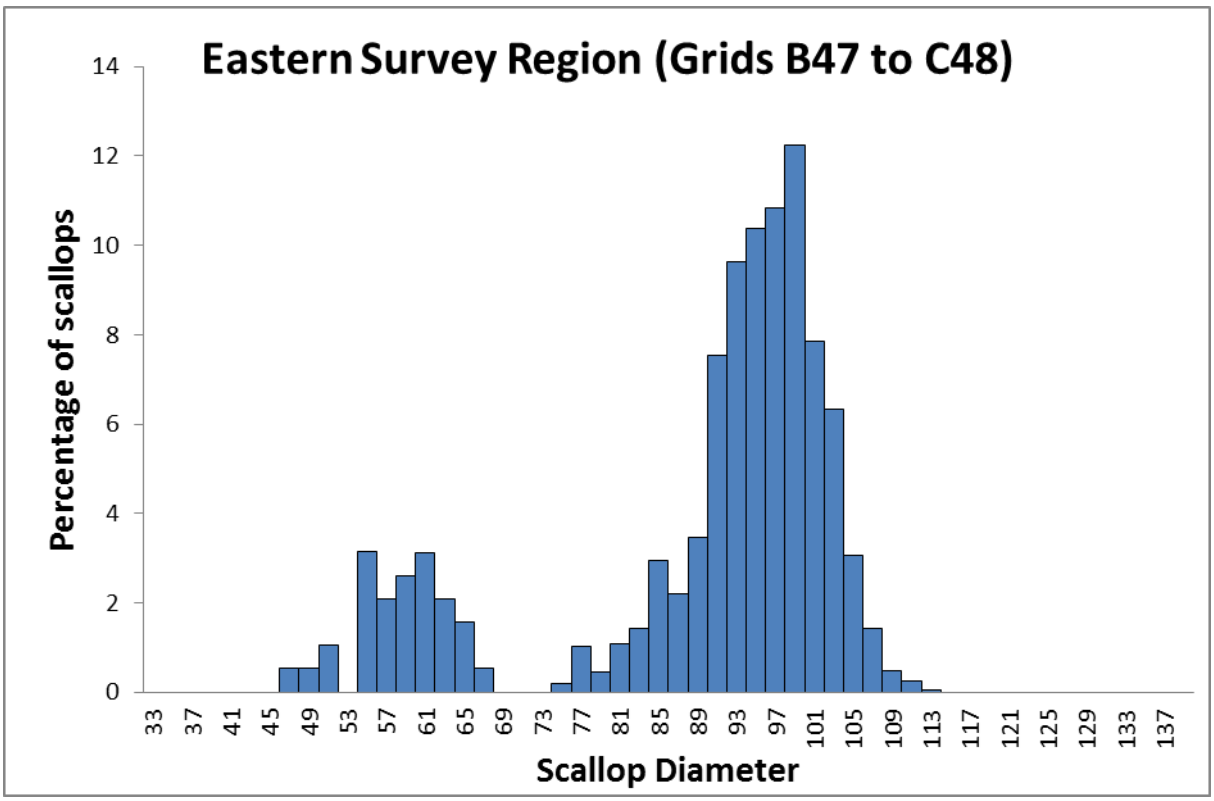

Figure 10: The length frequency distribution for scallops measured within grids C43 to C48 and B48 and B49. A total of 583 scallops were measured in this region.

5 Discussion

1 Despite only the *FV Panagia* participating, there was excellent spatial coverage of the key traditional fishing grounds within the Victorian scallop fishery and those areas surveyed in 2009. Approximately 60% of the number of shots undertaken in 2009 (506) were completed by the *FV Panagia* (297) in 2012 and a very large number of scallops measured.

2 As per the 2009 survey, in general low abundances of scallops were located during the 2012 Victorian scallop survey, with only 3 of the 297 sample tows conducted containing greater than 10 kg scallops per 1000 m^2 standardised sample tow (40, 16 and 12 kg scallops per 1000 m^2). These catches approximately equate to catch rates of 484, 193 and 138 kg scallops per hour commercial fishing.

3 The average catches within the survey grids were less than 1 kg scallops per 1000m^2 sample tow (or approximately 10 kg scallops per hour commercial fishing).

4 On average, the abundances encountered during the survey were similar to those in 2009, although abundances in individual grids were both higher and lower than in 2009.

5 As was the case in 2009, the grids with the highest and most consistent catches were grids C44 (increase from 2009), D41 and E41 (decrease for both from 2009). Grid D42 also had a relatively high catch rate in 2009 (34.1 kg scallops per hour commercial fishing), but this had decreased significantly in 2012 (3.5 kg scallops per hour commercial fishing). However, this may be due to a reduced number of shots undertaken i.e. 21 in 2009 and 8 in 2012).

6 No survey regions were considered to constitute a commercially viable scallop bed, although there were several individual shots with good catches.

7 Scallops located within the survey area ranged between 33 mm and 120 mm in size, with the peaks in the size distribution falling within the 69-75 mm and 87-98 mm size ranges. The tail of scallops less than 70 mm suggested that there has been some recruitment in the past two years, although at relatively limited levels. This suggests that although new cohorts of scallops will be available to the commercial fishery in the next two years, they are unlikely to be available in commercial quantities. It should be noted, however, that scallops in the 20 – 40 mm size range are generally under-represented in a dredge, as they can fall through the mesh lining the dredge.

8 On a more positive note, however, scallops of a wide size range are still located throughout the spatial range of the survey, albeit in relatively low abundances.

9 Written and verbal comments provided by the survey participant suggested scallops were generally in good condition throughout the survey area and there was limited new dead shell.

10 To put these survey catches and predicted catch rates into an economically viable fishery perspective, we can make comparisons with the Tasmanian and Commonwealth scallop fisheries.

   a. Taking into account the cost of diesel / running a commercial fishing vessel, catch rates in the order of 200 kg per hour fishing has been considered the minimum economical level of catch within the Tasmanian commercial scallop fishery. This low level was only viable given the close proximity of the fishing grounds to a major unloading port (1hr 20min), the very large and healthy scallop size (110 – 120 mm and 60 – 70 meats / kg) and subsequent high price of product ($18 per kg).
   b. Average catch rates within the 2009 Commonwealth Bass Strait Central Zone Scallop Fishery were in the order of 630 kg scallops per hour fishing. Furthermore, comments from commercial fishers at a 2009 Commonwealth RAG meeting stated a minimum catch rate of approximately 400 – 500 kg of scallops per hour commercial fishing was the minimum required for an economical level of fishing within this fishery given current costs of running fishing vessels a significant distance from unloading ports and returns for the high quality scallop product being caught within this fishery.

11 A poor survey result in the 2009 Victorian survey resulted in a TAC of zero been set for 2010 and 2011, as continued fishing of depleted stocks was determined as likely to inhibit their recovery. As such, there is a need for Fisheries Victoria to again carefully consider 2012/13 management arrangements as there has not been a significant recovery of stocks in the two years of zero TAC.

6 Acknowledgements

We would like to thank the skipper Paul Anastos and the crew of the *FV Panagia* for their enthusiasm and support during the organisation and completion of this survey. It should be noted that the vessel conducted a very large number of tows, surveyed for more time than the minimum expected survey time and measured many more scallops than expected. Furthermore, Paul's vast experience and history in this fishery was invaluable.

7 Appendix 1: 2009 Survey Report

SURVEY FINAL REPORT

2009 Victorian Scallop Fishery Survey Final Report

Julian J Harrington, Stephen Leporati, Jayson M Semmens

February 2010

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1. Executive Summary

An industry-based scallop survey was conducted in the Victorian Scallop Fishery during December 2009. The survey covered a relatively large area of the fishery, which overlapped the traditional fishing grounds. Only five of the 506 sample tows conducted caught greater than 150 individual scallops per 1000m^2 standardised sample tow. Catches of 150 scallops per 1000m^2 approximately equate to catch rates of 180 kg scallops per hour commercial fishing. However, the average catches within the survey grids were less than 48 scallops per 1000m^2 sample tow (or approximately 58 kg scallops per hour commercial fishing). In general, very low abundances of scallops were located throughout the survey region.

The majority of scallops caught measured between 70 mm and 110 mm shell diameter. Very few scallops measuring less than 70 mm were caught during the survey. This suggests that no new scallop resource / cohort of scallops will be available to the commercial fishery in the next two years.

Similar poor survey results in the Commonwealth and Tasmania scallop fisheries have resulted in temporary closures to commercial fishing, as continued fishing of depleted stocks is likely to inhibit their recovery. As such, there is a need for Fisheries Victoria to carefully consider 2010/11 management arrangements.

2. Introduction

In early 2009, the Tasmanian Aquaculture and Fisheries Institute (TAFI) were approached by Fisheries Victoria to co-ordinate a survey within the Victorian scallop fishery. Nominations from interested Victorian scallop fishers were received by early August 2009. Although it was proposed to undertake the survey during late August / early September 2009, the three vessels selected to participate in the survey suggested that early December was a more suitable time to undertake the survey. This was due to the Bass Strait Central Zone Scallop Fishery being opened during this time, and the need for the survey participants to catch their quota from this fishery. The survey subsequently commenced on the 7th December 2009.

Consultation between TAFI and Fisheries Victoria determined that an industry-based survey, where vessels were paid in dollars for their time, was the best approach. Money was available for three vessels to survey for a maximum of four days each. This combined survey effort was deemed appropriate to cover the key areas within the fishery. The key survey areas were determined using historical scallop catch data from the Victorian fishery and information from the participating Victorian industry members. Specific sample tow locations, however, were left to the discretion of individual participants.

The overall objective of the survey was:

Objective 1:
Conduct a broad scale search for scallops within the Victorian scallop fishery. This search was to primarily target areas where industry believed that scallops may be located, and where historical catch records suggested scallops had been in the past.

A secondary objective of the survey was:

Objective 2:
Where time permitted, map, in greater detail, the spatial extent and size distribution of scallops within any scallop bed located within the Victorian fishery. It was agreed however, that minimal time was to be spent within any one scallop bed location in order to ensure the ultimate aim of maximising spatial survey coverage was achieved.

The overall task of organising and implementing the 2009 survey was given to TAFI. This report provides the results of the industry-based fishery survey conducted during December 2009 within the Victorian scallop fishery. The report provides detailed information concerning the abundance and size distribution for sample tows conducted.

3. Materials and Methods

a. *The Survey*

The survey was conducted during December 2009, with a TAFI scientist on board one of the vessels during the entire survey. The three vessels that participated in the survey: Northern Star, Panagia and Nea Artaky, were all based in Lakes Entrance. In total, 506 dredge tows were conducted during 144 hours of combined survey time. Specific sample tow locations were left to the discretion of individual participants, who used their long-running experience in the fishery to target areas they have fished extensively over many years. All survey activities were conducted within Victorian waters.

The vessels departed from Lakes Entrance (Vic) on the 7th of December 2009. They initially conducted survey tows offshore (deeper water) in a southwest direction. On the 8th of December, the three vessels moved inshore (shallower water) and heading northeast (back towards Lakes Entrance). By the 9th of December the vessels had passed Lakes Entrance and continued surveying east towards Pt Hicks. On the 10th of December the final sample tows were conducted during the return trip west to Lakes Entrance. Figure 1 shows the tracks the three vessels took during the survey, as recorded automatically by a GPS device fitted within the electronic measuring boards used to measure scallops. This device records position every 10 seconds, when in satellite range. Figure 2 shows the location of all sample tows conducted during the survey, as recorded by the participating fishers on the data sheets provided.

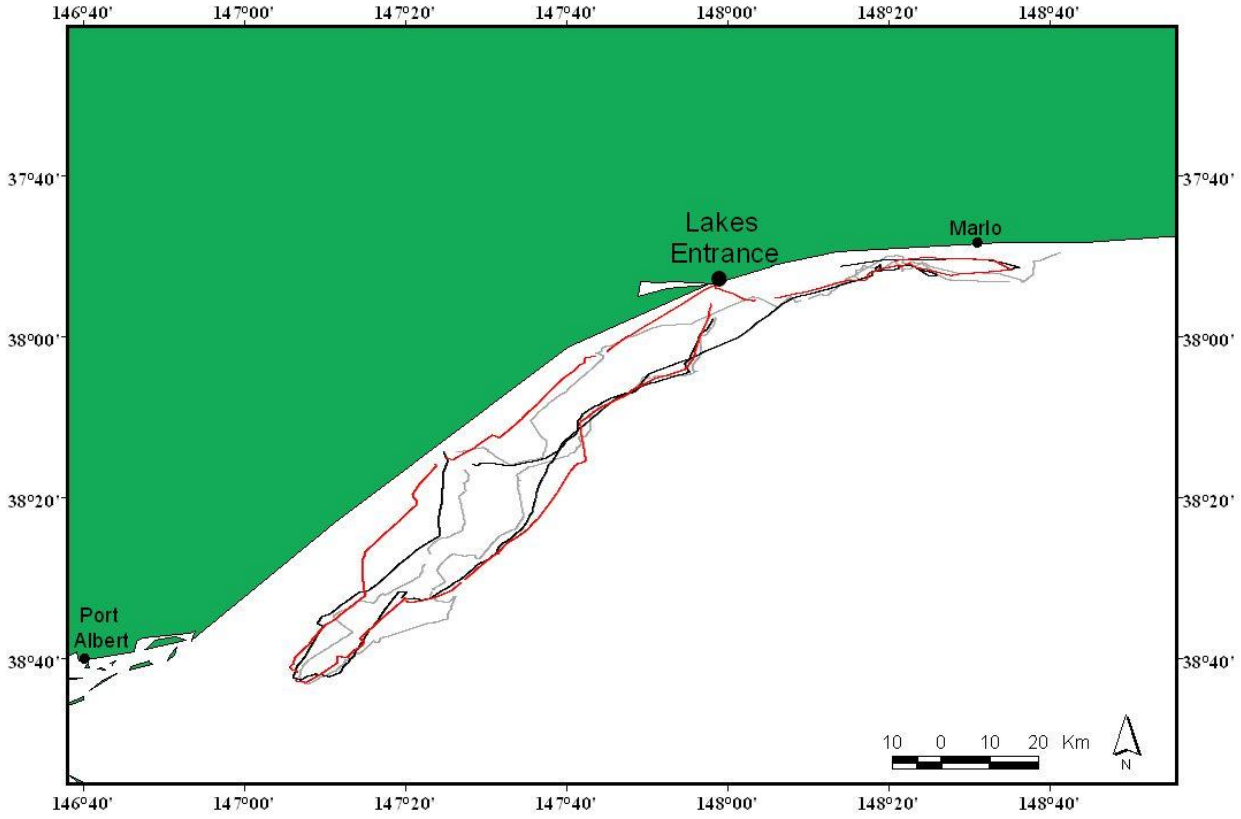

Figure 1: Overview of the tracks taken by each of the three vessels (three colours) participating in the December 2009 Victorian scallop survey.

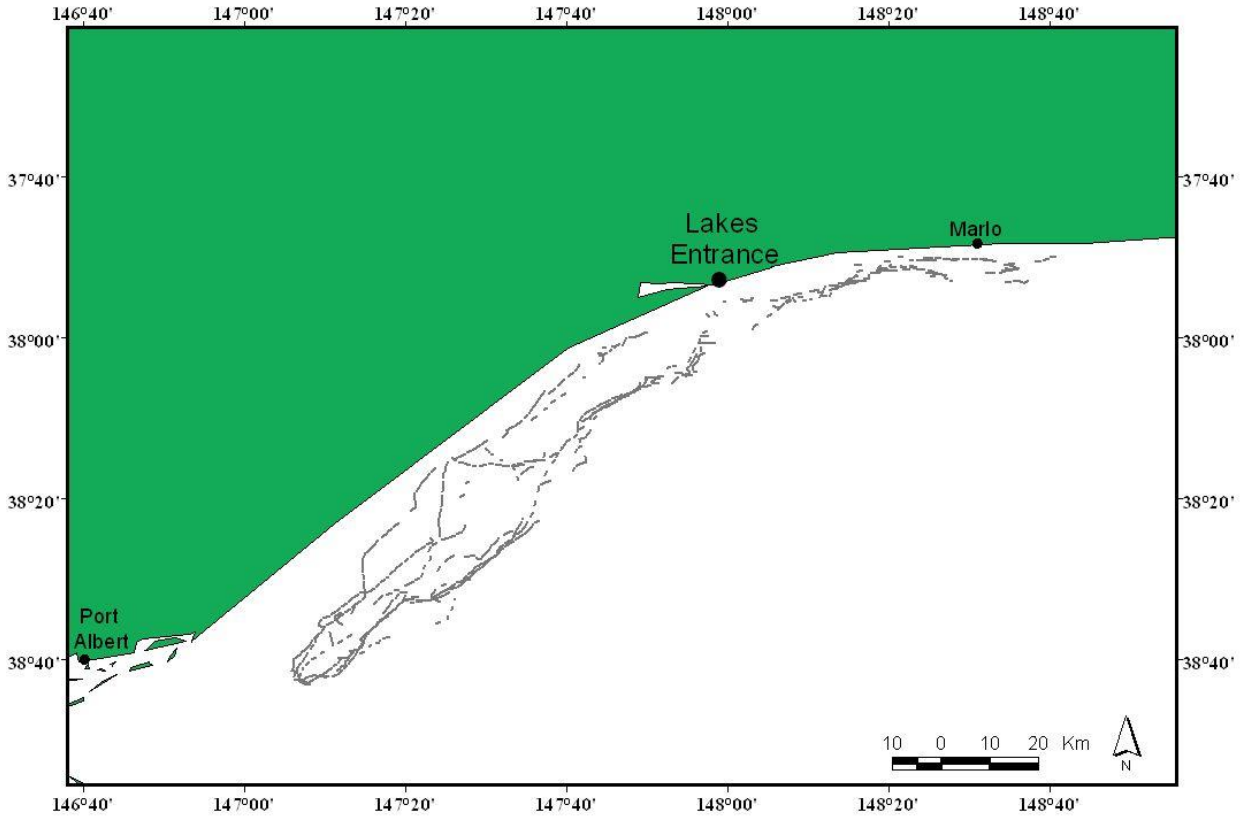

Figure 2: Overview of sample tows conducted by the three participating vessels during the Victorian scallop survey.

b. *Data Collection*

Each vessel conducted a minimum four days survey time (~ 48 hours survey time), however, the majority of the participating vessels completed more than the required minimum time. For each sample tow conducted, the skipper and crew of the survey vessel recorded the start and finish latitude and longitude, depth and an estimation of the total scallop catch. Total catch was estimated either as the kilograms of scallops caught or the number of individual scallops caught. Electronic measuring boards were used to measure the shell width of all scallops caught or a randomly selected subsample (50 scallops was suggested) of scallops when the catch was larger.

c. *Stratification*

To align with Fisheries Victoria scallop catch record returns / historical catch data, a grid system consisting of 10' latitude x 10' longitude (approximately 10 x 10 nm) was used to analyse and interpret the data. Each grid will be referred to using the letter and number coding used by Fisheries Victoria (see Figure 3).

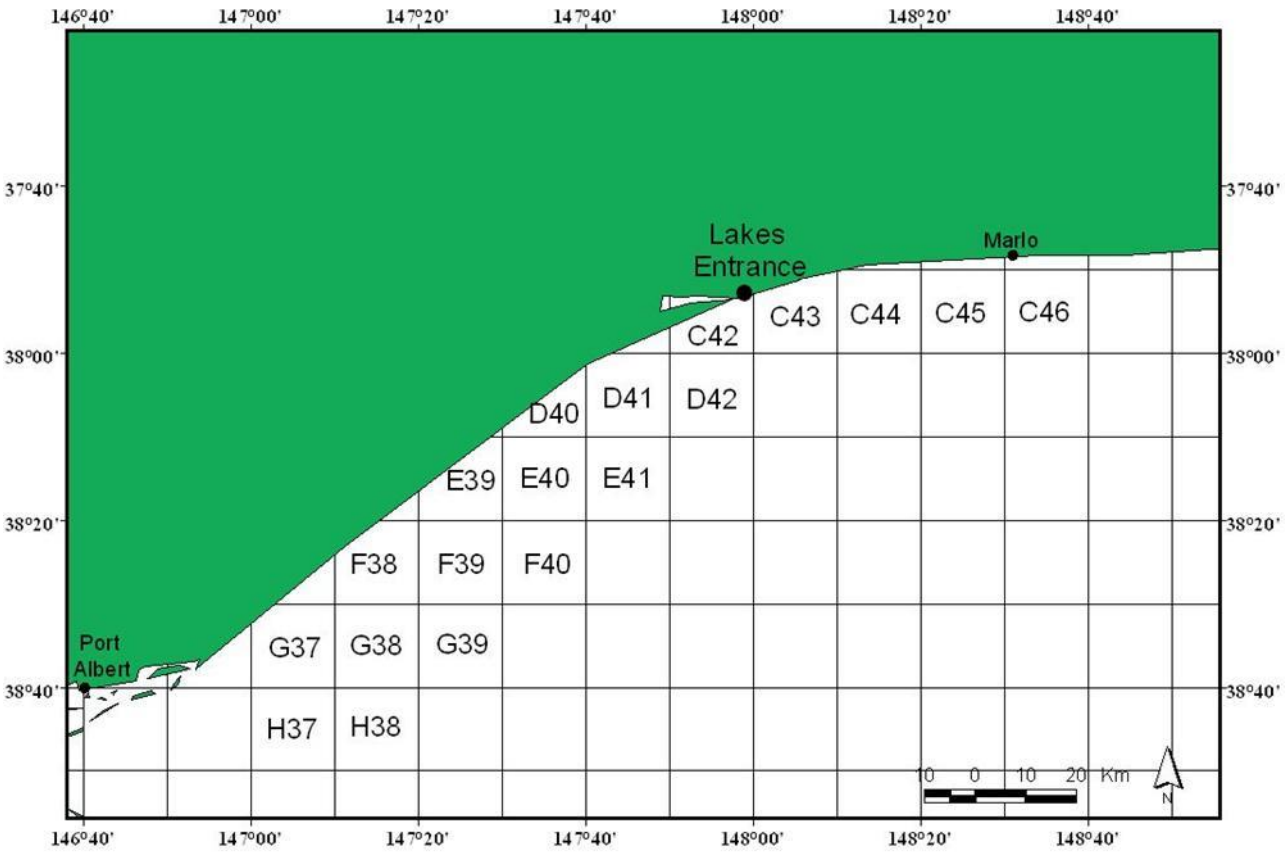

Figure 3: The 10' latitude x 10' longitude grid and grid cell codes used by Victorian scallop fishers to record catches. These cells overlap the regions were the vast majority of scallop catches have been taken since 2000.

d. *Data Analysis*

d.i. *Scallop Abundance*

The vessels participating in this survey used different dredge widths and conducted sample tows of different lengths / durations. Therefore, scallop abundance estimates needed to be standardised to allow a direct comparison of scallop catches between all survey vessels and tows. The distance of each sample tow was calculated from the start and finish tow locations. The area swept (A) during each sample tow was then calculated by multiplying the tow distance (L) by the width of the dredge used (W).

$$A = L \times W$$

The estimated catch of scallops per 1000m^2 standardised tow ($C^{Standardised}$) was then calculated by dividing the estimated catch in a sample tow (C) by the area swept (A) (note this equals the catch of scallops per m^2) and multiplying by 1000.

$$C^{standardised} = (C / A) * 1000$$

d.ii. Approximate Commercial Catches and Catch Rates

Although $C^{standardised}$ provides a means of comparing scallop abundances between survey tows and regions, it does not provide any indication of potential catches and catch rates. Advice from fishers suggests that commercial tow durations of 10 minutes are not unrealistic, and many fishers try to conduct four commercial tows per hour of fishing. Survey data collected by TAFI since 2000 shows that the distance covered by a 10 minute tow is approximately 750 m. Given a standardised 1000m^2 sample tow covers approximately 250 m tow distance, the approximate catch per 10 minute commercial tow (C^{tow}) can be calculated by multiplying the catch per standardised 1000m^2 tow ($C^{standardised}$) by three.

$$C^{tow} = C^{standardised} \times 3$$

Furthermore, an estimate of the commercial catch per hour fishing can be made by multiplying the catch per commercial tow (C^{tow}) x four (i.e. four 10 minute tows per hour).

$$C^{hour} = C^{tow} \times 4$$

d.iii. Size Frequencies

Length – frequency plots were used to compare the population structure of scallops caught within different grids of the survey region. Because the larger catches were sub-sampled for size frequency (i.e. not all scallops from a particular sample tow were measured), the ratio of the sub-sample to total catch was used to scale the numbers in each size class to total catch. To characterise the properties of the resulting size distributions the length frequencies were plotted as histograms, with data grouped into 2 mm size classes to reduce noise.

4. Results

a. *Overview*

An overview of scallop abundance per standardised 1000m^2 sample tow is illustrated in Figure 4.

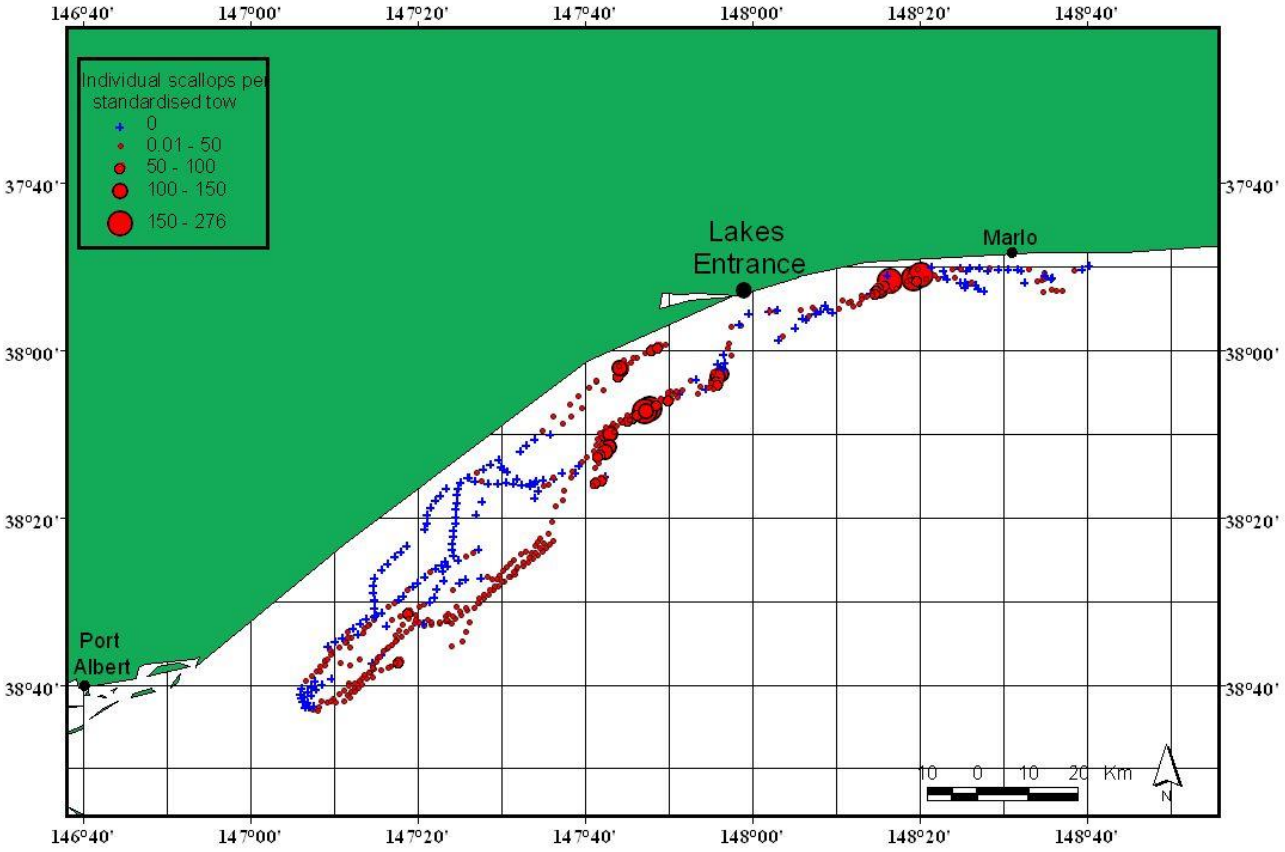

Figure 4: Scallop abundances (individual scallops per 1000m^2 sample tow) for tows conducted during the December 2009 Victorian scallop survey. The 10' latitude x 10' longitude grid is shown as a reference for later results.

b. *South West Survey Region (Grids F38 to H38)*

The maximum catch for an individual sample tow within this survey region was 70.3 scallops per 1000m^2 (Figure 5). This abundance of scallops would provide an approximate commercial catch of 84 kg of scallops per hour commercial fishing. Grid cells G38 and G39 had an average catch of 10.8 scallops per 1000m^2 (Figure 5; Table 1). Extrapolation of this standardised abundance suggests catch rates of approximately 13 kg per commercial fishing hour (Table 1). The majority of survey grids within this survey region, however, had

substantially lower average catches (see Table 1), with extrapolated catch rates for four of the surveyed grids being less than 6 kg scallops per hour commercial fishing (Figure 5; Table 1).

The bulk of scallops located within these survey grids fell within the 70 mm to 114 mm size classes (Figure 6), with the peaks in the size distributions falling within the 88 mm to 94 mm range (Figure 6).

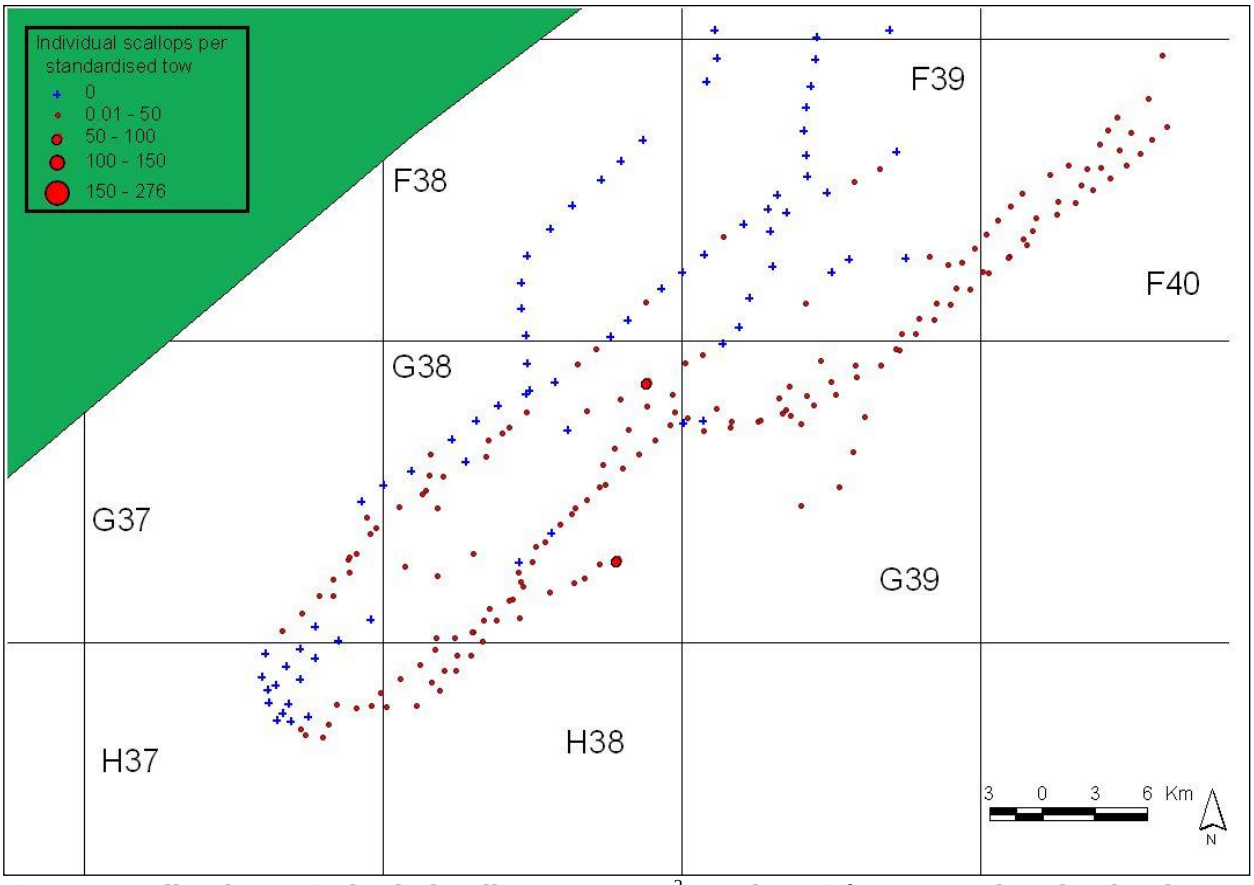

Figure 5: Scallop density (individual scallops per 1000m^2 sample tow) for tows conducted within the southwest survey region (survey grids F38 to H38).

Table 1: Summary of survey effort, catch and estimated commercial catch for each survey grids F38 to H38.

Grid	Number of tows	Average depth (m)	Total area swept (1000m^2)	Total number of scallops	Average scallops per sample tow	Average scallop abundance (1000m^2)	Estimated commerical catch (kg) per hour fishing
F38	14	26	60	25	1.8	0.5	0.6
F39	38	36	149	496	13.1	3.4	4.1
F40	33	44	128	1031	31.2	8.7	10.4
G37	16	33	63	302	18.9	5.1	6.1
G38	70	38	288	2632	37.6	10.8	13.0
G39	32	40	120	1262	39.4	10.8	13.0
H37	22	37	89	209	9.5	2.2	2.6
H38	12	44	43	482	40.2	10.7	12.9

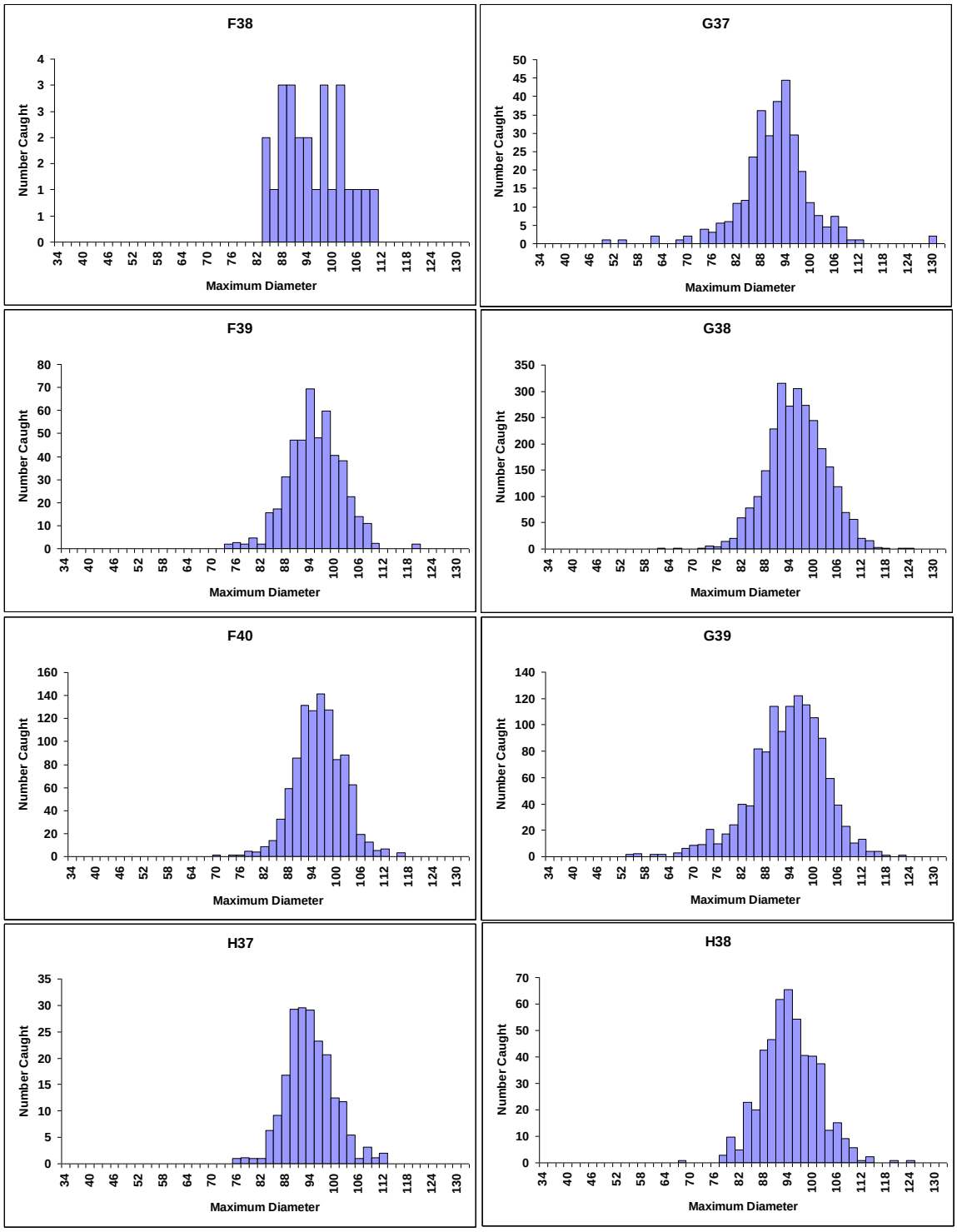

Figure 6: The length frequency distribution for scallops caught within grids F38 to H38.

c. *Central Survey Region (Grids D40 to E41 and C42)*

Very few scallops were caught within survey grids C42, D40, E39 and E40, with estimated abundances being below 1.2 scallops per 1000m^2 sample tow. This equates to a predicted catch rate of less than 1.4 kg scallops per hour commercial fishing (Figure 7; Table 2). Those scallops that were caught within these grids generally fell between the 74 mm and 108 mm size classes, however, a few individuals in the 46 mm to 66 mm size range were present within grid E42 and to a lesser extent grid D40 (Figure 8).

The maximum catches for an individual sample tow within grids D41, D42 and E41 were 275, 128 and 134 individual scallops per 1000m^2 tow respectively (Figure 7). Extrapolation of these abundances suggests catch rates of 330 kg, 154 kg and 161 kg scallops per hour commercial fishing. It must be noted, however, that these catch rates are from a single sample tow conducted within these grids and only 5 sample tows during the entire survey had predicated catch rates greater than 180 kg scallops per hour commercial fishing. Conversely, when examining average catches, grid E41 had the highest average catch of only 48 individual scallops per 1000m^2 tow, and a predicted 58 kg scallops per hour commercial fishing (Table 2). This lower average is the consequence of the high number of sample tows containing zero and / or very low catches of scallops (Figure 7).

Those scallops caught within grids D41, D42 and E41 fell within the 76 mm to 106 mm size classes, with the peaks in the size distribution falling within the 88 mm to 94 mm range (Figure 8).

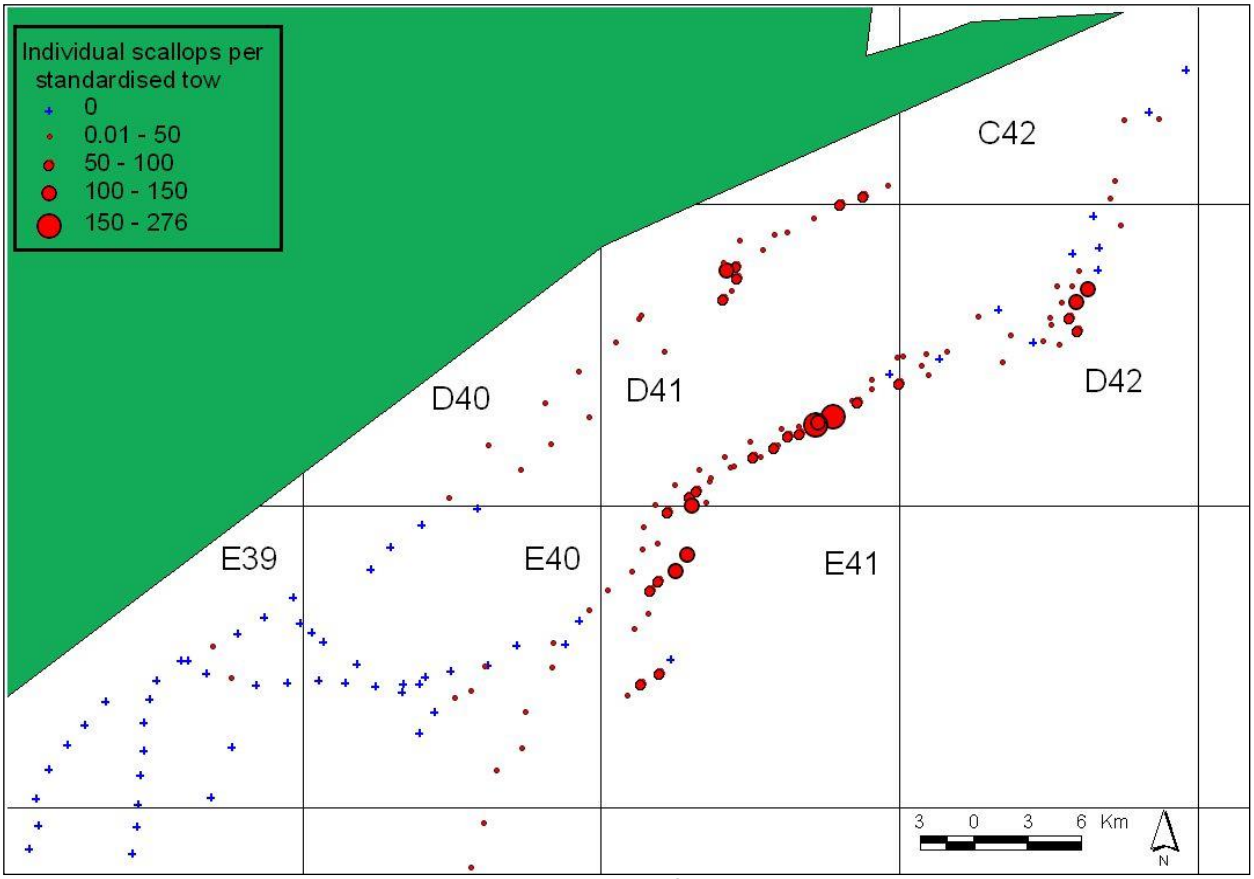

Figure 7: Scallop density (individual scallops per 1000m^2 sample tow) for tows conducted within the central survey region (survey grids C42 and D40 to E41).

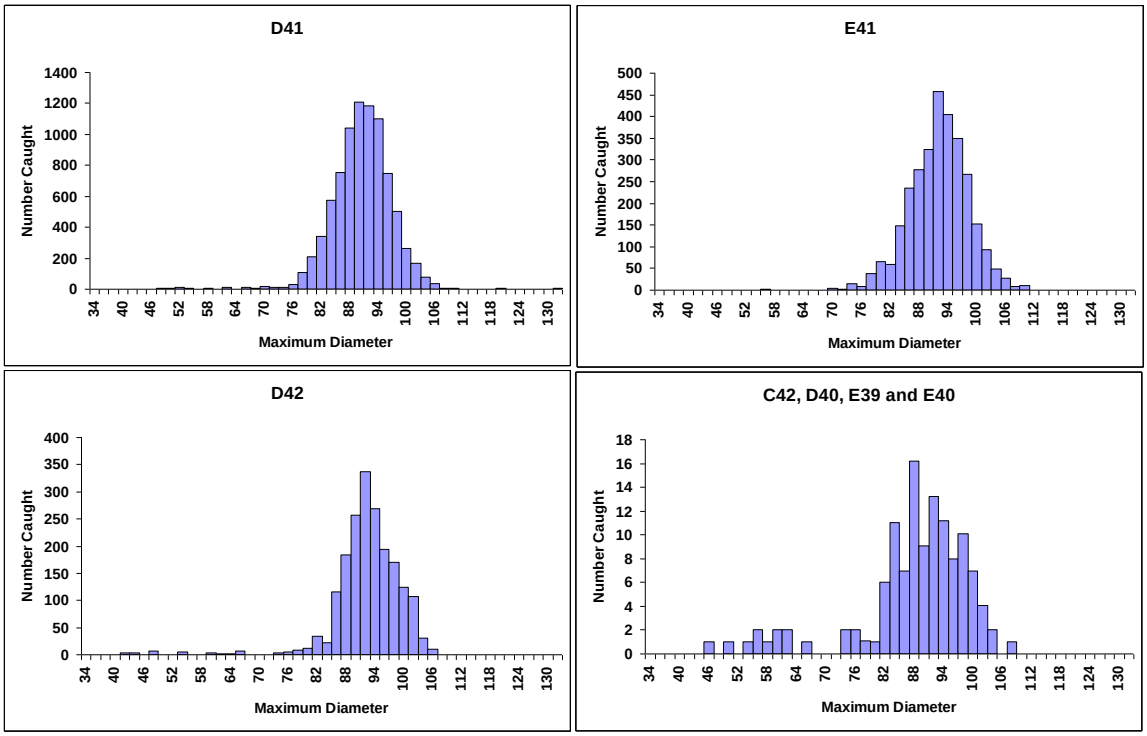

Figure 8: The length frequency distribution for scallops caught within grids D41, D42, E41 and grids C42, D40, E39 and E40 combined.

Table 2: Summary of survey effort, catch and estimated commercial catch for each survey grids D40 to E41 and C42.

Grid	Number of tows	Average depth (m)	Total area swept (1000m^2)	Total number of scallops	Average scallops per sample tow	Average scallop abundance (1000m^2)	Estimated commerical catch (kg) per hour fishing
C42	6	33	20	21	3.5	1.2	1.4
D40	7	27	49	24	3.4	0.6	0.7
D41	58	39	240	9237	159.3	43.8	52.6
D42	21	46	74	1920	91.4	28.4	34.1
E39	24	22	96	2	0.1	0.0	0.0
E40	30	36	127	72	2.4	0.5	0.6
E41	18	42	67	3022	167.9	48.0	57.6

d. *Eastern Survey Region (Grids C43 to C46)*

Very few scallops were caught within survey grids C43, C45 and C46, with the exception of one sample tow, which straddled the C44 – C45 boundary (Figure 9). Average abundances within these grids were 0.2, 11.7 and 2.3 scallops per 1000m^2 tows respectively (Table 3). These abundances equate to approximate commercial catch rates of 0.3 kg, 14.1 kg and 2.8 kg scallops per hour commercial fishing (Table 3).

The maximum catch for an individual sample tow within grid C44 was 262 scallops per 1000m^2 sample tow (Figure 9), or 314 kg scallops per hour commercial fishing. It must be noted, however, that this catch rate is from a single sample tow conducted within this grid

and only 5 sample tows during the entire survey had predicated catch rates greater than 180 kg scallops per hour commercial fishing. The average abundance per tow within grid C44 was 39.7 scallops per 1000m^2 tow, which equates to approximately 47.6 kg scallops per hour commercial fishing (Table 3). This lower average is the consequence of the high number of sample tows containing zero and / or very low catches of scallops (Figure 9 and Table 3). Scallops caught within grids C43 to C46 fell within the 72 mm to 104 mm size classes, with the peak in the size distribution falling within the 88 mm to 92 mm range (Figure 10).

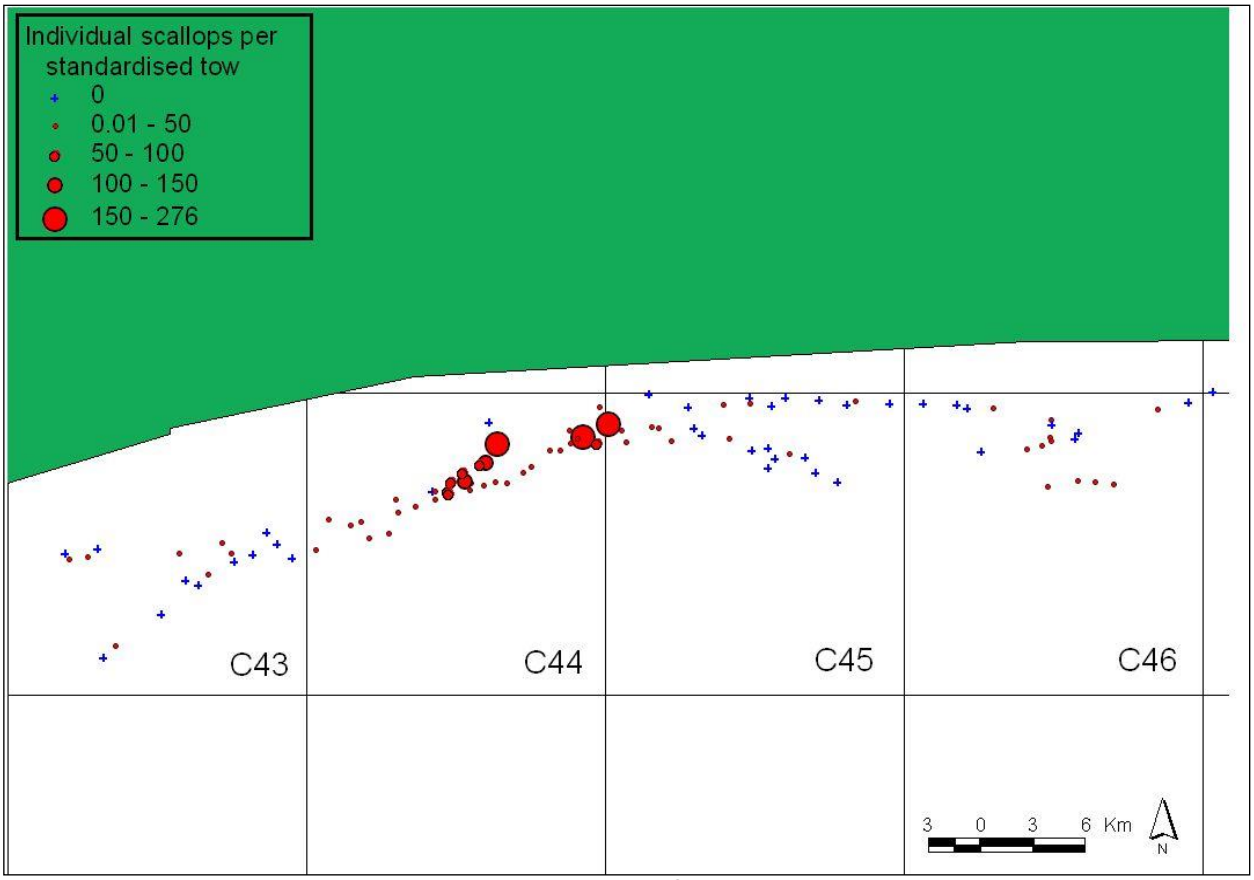

Figure 9: Scallop density (individual scallops per 1000m^2 sample tow) for tows conducted within the eastern survey region (survey grids C43 to C46).

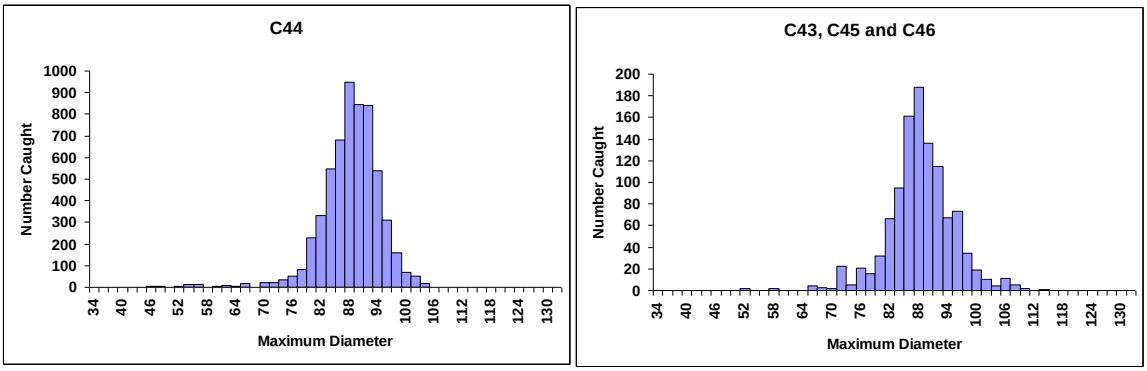

Figure 10: The length frequency distribution for scallops caught within grids C44 and grids C43, C45 and C46 combined.

Table 3: Summary of survey effort, catch and estimated commercial catch for each survey grids C43 to C46.

Grid	Number of tows	Average depth (m)	Total area swept (1000m^2)	Total number of scallops	Average scallops per sample tow	Average scallop abundance (1000m^2)	Estimated commerical catch (kg) per hour fishing
C43	18	40	70	15	0.8	0.2	0.3
C44	39	41	158	5846	149.9	39.7	47.6
C45	28	38	102	840	30.0	11.7	14.1
C46	20	39	87	221	11.1	2.3	2.8

5. Discussion

1. The three survey participants provided excellent spatial coverage of the key traditional fishing grounds within the Victorian scallop fishery.
2. Only low abundances of scallops were located during the December 2009 Victorian scallop survey, with only five of the 506 sample tows conducted having catches greater than 150 individual scallops per 1000m^2 sample tow (i.e. only 5 tows had predicated catch rates greater than 180 kg per hour commercial fishing).
3. The two grids with the highest and most consistent catches were grids D41 and E41. Average abundances within these regions were 45 scallops per standardised 1000m^2 sample tow (equivalent to a predicted catch rate of 54 kg scallops per hour commercial fishing).
4. No survey regions were considered to constitute a commercially viable scallop bed.
5. Majority of scallops caught during the 2009 Victorian scallop survey fell within the 70 mm to 110 mm size range. Very few scallops smaller than 70 mm were recorded, however, scallops in the 20 – 40 mm size range could easily go undetected as they may fall through the mesh lining the dredge. These results suggest that no new scallop resource will be available for commercial harvesting until at least 2 years time.
6. On a more positive note, however, scallops were located throughout the spatial range of the survey, albeit in low abundances.
7. Comments (both verbal and written on datasheets) provided by survey participants suggested scallops were in very poor condition within some survey regions, and may possibly be in their final stages of life. These comments, however, cannot be scientifically verified.
8. Further comments suggested high abundances of empty scallop shell were present within areas containing smaller scallops only 12 months previously. Again, there is no scientific knowledge of these small scallops, or a link to them ‘dying off’ over the last 12 months.
9. To put these survey catches and predicted catch rates into an economically viable fishery perspective, we can make comparisons with the Tasmanian and Commonwealth scallop fisheries.
    a. Taking into account the cost of diesel / running a commercial fishing vessel, catch rates in the order of 200 kg per hour fishing has been considered the minimum economical level of catch within the Tasmanian commercial scallop

fishery. This low level was only viable given the close proximity of the fishing grounds to a major unloading port (1hr 20min), the very large and healthy scallop size (110 – 120 mm and 60 – 70 meats / kg) and subsequent high price of product ($18 per kg).

b. Average catch rates within the 2009 Commonwealth Bass Strait Central Zone Scallop Fishery were in the order of 630 kg scallops per hour fishing. Furthermore, comments from commercial fishers at a 2009 Commonwealth RAG meeting stated a minimum catch rate of approximately 400 – 500 kg of scallops per hour commercial fishing was the minimum required for an economical level of fishing within this fishery given current costs of running fishing vessels a significant distance from unloading ports and returns for the high quality scallop product being caught within this fishery.

10. Continued fishing of this depleted stock is likely to inhibit recovery.
11. Similar survey results in the Commonwealth and Tasmania scallop fisheries have resulted in temporary closures to commercial fishing.
12. There is a need for Fisheries Victoria to consider 2010/11 management arrangements.

6. Acknowledgements

We would like to thank the skippers and crew of all participating vessels for their enthusiasm and support during the organisation of this survey. It should be noted that the participants conducted a very large number of tows and surveyed for more time than the minimum expected survey time. Furthermore, the vast experience and history in this fishery was invaluable. We would also like to thank Sonia Talman from Fisheries Victoria for her support of this survey.