

The "Suitcase Hypothesis" – can eddies provide a pathway for gene flow between Madagascar and KwaZulu-Natal?

by

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Thesis submitted in fulfilment of the requirements of for the degree Master of Technology: Oceanography in the Faculty of Applied Science at the Cape Peninsula University of Technology

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> Cape Town Date submitted: November 2016

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DECLARATION

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ABSTRACT

Similarities in marine fauna found off the coasts of southern Madagascar and KwaZulu-Natal (KZN, South Africa) led to the development of the "Suitcase Project", with the aim of establishing whether eddies that form off southern Madagascar may package and transport biological material, as if in a suitcase, across the Mozambique Channel. In pursuit of this question, sampling was conducted on the southern Madagascan shelf and along a transect across a cyclonic eddy which originated off the southern tip of Madagascar, between the 15th and 23rd of July 2013. Bongo nets (300 and 500 µm-mesh) and a neuston net (900 µmmesh) were used to collect zooplankton within the upper 200 m and at the surface, respectively. Samples were sorted for meroplankton (larval stages of fish and benthic invertebrates) under a stereo microscope, particularly seeking species known to be common to both the east coasts of Madagascar and South Africa and, thus potential indicators of connectivity between these regions. Larvae of crabs, rock lobster, and fish were used for DNA barcoding. Zooplankton biovolume and abundance were compared between the eddy core, eddy periphery and outer regions of the eddy, as well as stations from the Madagascan shelf. Mean neuston biovolume on the Madagascan (0.08 mL m⁻³) was not significantly higher than that in the eddy (0.06 mL m⁻³). Mean bongo biovolume in the upper 200 m was much higher on the Madagascan shelf (0.62 mL m⁻³) than in the eddy (0.16 mL m⁻³) although only 2 stations were sampled on the shelf. Highest biovolume in the eddy was recorded in the west eddy zone (0.25 mL m⁻³) and west outer zone (0.23 mL m⁻³), which was not statistically significantly higher than the eddy core (0.12 mL m⁻³) and east eddy zone (0.17 mL m⁻³). Meroplankton was comprised of coastal origin taxa and was most abundant on the shelf and in the eddy perimeters. Larval goat-fish, Parupeneus fraserorum was identified, a newly described mullid, and has been recorded on both the coasts of Madagascar and KZN, SA. Larvae of coastal invertebrate species identified, include the squat lobster Allogalathea elegans and camel shrimp Rhynchocinetes durbanensis. Other larval fish identified, but not found in high abundance include the families of reef associated fishes, for example: Apogonidae, Labridae, Pomacentridae, Priacanthidae, Serranidae and Sparidae. Higher zooplankton biovolumes, larval abundances and reef-associated larval assemblages found on the Madagascan shelf and in the periphery of the cyclonic eddy compared to the core in this study provide support for the suitcase hypothesis that planktonic organisms are entrained within eddies as they propagate south-westwards of the Madagascan shelf. However, further studies are required to determine whether planktonic larvae are able to cross the Mozambique Channel and reach the KZN coast in time to settle.

ACKNOWLEDGEMENTS

This project is part of the African Coelacanth Ecosystem Project (ACEP) and was funded by the South African National Research Foundation (NRF), and the Departments of Environmental Affairs (DEA) and Science and Technology (DST).

I would like to thank my supervisors, Dr Jenny Huggett, Dr Gavin Gouws and Dr Conrad Sparks for their support and guidance throughout the completion of this project.

A warm thanks to Bob Ward (CSIRO) and Kevin Sarvanen (MOI) for providing me with unpublished data, to complete my analysis.

Lastly, I am thankful to my family and friends for their support and encouragement for the duration of my MTech project.

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LIST OF ACRONYMS

AC (Agulhas Current)

- ACEP (African Coelacanth Ecosystem Programme)
- ANOVA (Analysis of Variance)
- ASCLME (Agulhas and Somali Currents Large Marine Ecosystems Programme)
- KZN (KwaZulu-Natal)
- BOLD (Barcode of Life Data Systems)
- COI (cytochrome *c* oxidase subunit I)
- CTD (Conductivity Temperature Depth)
- DNA (Deoxyribonucleic acid)
- EACC (East African Coastal Current)
- K2P (Kimura 2-parameter distance)
- MC (Mozambique Channel)
- MEGA (Molecular Evolutionary Genetics Analysis)
- MESOBIO (Influence of mesoscale dynamics on biological productivity at multiple trophic
- levels in the Mozambique Channel)
- NEMC (North East Madagascar Current)
- NJ (Neighbour joining)
- PCR (Polymerase chain reaction)
- PLD (Pelagic larval duration)
- SA (South Africa)
- SEC (South Equatorial Current)
- SEMC (South East Madagascar Current)
- SICC (South Indian Countercurrent)
- SST (Sea Surface Temperature)
- SSHA (Sea Surface Height Anomaly)
- Sv (Sverdrup): Measurement of volume transport i.e. $15 \times 106 / m^3 = 15 Sv$
- SWIO (South West Indian Ocean)
- WBC (Western Boundary Currents)
- WIO (Western Indian Ocean)

CHAPTER 1: INTRODUCTION

1.1 Introduction

Mesoscale eddies are features of ocean circulation, with horizontal spatial scales of 10 – to 1000 km and time scales of 1 to 3 years, which may entrain planktonic organisms, influencing their distribution and acting as vectors of transport (Rodriguez *et al.* 1999, Mackas and Galbraith 2002, Batten and Crawford 2005, Holliday *et al.* 2011). Through the clockwise rotation of cyclonic eddies in the southern hemisphere, a vertical upwelling flow is caused in their interiors which causes a divergence (outward flow) of surface waters and subsurface nitrate-rich water is pushed upwards into the euphotic zone (Bakun 2006), resulting in increased primary production in the cores of eddies (Yentsch and Phinney 1985, Falkowski *et al.* 1991, McGillicuddy and Robinson 1997, McGillicuddy *et al.* 1998). In anticyclonic eddies, the opposite occurs; anticlockwise rotation and convergence cause surface waters to be pushed downwards (downwelling) (Bakun 2006). Eddies both cyclonic and anticyclonic may also entrain productive water of coastal origin and, as a consequence, eddies can function as nursery grounds for organisms such as fish larvae (Rodriguez *et al.* 1999, Govoni *et al.* 2010).

Mesoscale eddies are found in all oceans (Rhines 2001), but are particularly prominent at the ends of Western Boundary Currents (WBC). The Agulhas Current (AC) is the largest WBC in the global ocean (Bryden *et al.* 2005) and the only WBC with frequent mesoscale activity in its source region, generated by two zones of high mesoscale variability: the Mozambique Channel (MC) (Schouten *et al.* 2002) and the South East Madagascar Current (SEMC) (Siedler *et al.* 2009).

A number of recent studies conducted on mesoscale eddies in the MC (Barlow *et al.* 2014, Halo, *et al.* 2014a, Hancke *et al.* 2014, Huggett 2014, Lamont *et al.* 2014, Lebourges-Dhaussy *et al.* 2014, Marsac *et al.* 2014, Ménard *et al.* 2014, Potier *et al.* 2014, Ternon, Roberts, *et al.* 2014a) demonstrated the origins and importance of eddies in the largely oligotrophic system of the MC, where they provide mechanisms by which the physical energy of the ocean system can be converted to trophic energy to support biological processes and food webs (Bakun 2006, Godø *et al.* 2012).

The biota on the south-east coast of South Africa (SA) comprises species of both subtropical and tropical origin (Teske *et al.* 2011). The coastal environment on the south-east coast of SA is profoundly influenced by the warm, southward-flowing AC, which could explain the presence of tropical biota on the southeast coast of SA in this region (Figure 1) (Teske *et al.*

2011). The disjunct distribution of certain subtropical species on the coasts of both KZN and Madagascar is less easily explained. These species include several fishes of the family Sparidae (S. Fennessy, personal communication) as well as various, non-endemic invertebrates, including the brown mussel *Perna perna* (Berry 1978), the shallow water spiny lobster *Panulirus homarus* (Charbonnier and Crosnier 1961), the deep-water spiny lobster *Palinurus delagoae* (Gopal *et al.* 2006), the ghost crab *Ocypode madagascariensis* (Jackson *et al.* 1991), the estuarine crabs *Scylla serrata* and *Varuna litterata* (Petrocci and Lipton 1994), and the corals *Acropora austera* and *Platygyra daedalea* (M. Schleyer, ORI, unpublished data). Additionally, southern Madagascan gammarid amphipods (Ledoyer 1982) have striking similarities morphologically to coastal and marine amphipods found in northern KZN (F. Mackay, ORI, unpublished data).



Figure 1 Sea Surface Temperature (SST) of the South African coastal region. The coastal region is divided into four major marine biogeographic provinces (cool temperate, warm temperate, subtropical and tropical) by the two major boundary currents: the cold Benguela Current on the west coast and the warm Agulhas Current on the south-east coast. Each of these provinces has its own characteristic assemblages of species (Source: Teske *et al.* 2011).

There is no distinct westward-flowing ocean current, nor an eastward-flowing one linking South Africa and Madagascar in the opposite direction, which could possibly explain this similarity in fauna and the distributions of these species. One possibility is that these populations could have been common to both Madagascar and South Africa before the splitting up of the two landmasses over geological times (McLoughlin 2001). However, several studies on mesoscale turbulence from the southern Madagascan coast (Lutjeharms et al. 1981, Gründlingh 1995, Biastoch and Krauss 1999, Chapman et al. 2003, Schouten et al. 2003, Quartly and Srokosz 2004, Quartly et al. 2006, Siedler et al. 2009) led to an alternative explanation - that westward-propagating eddies could provide oceanic connectivity between the south-east coast of Madagascar and the east coast of South Africa. This gave rise to the suitcase concept (Marsac et al. 2014), which proposes that eddies could provide a mechanism to transport planktonic larvae of the above-mentioned species from Madagascar across the Southwest Indian Ocean (SWIO) Mozambique Basin to the KZN coast. The analogy used was that of biological material of Madagascan shelf origin being "packed up" in an eddy, like clothes in a suitcase, which is then transported across the SWIO to the KZN coast, where the contents of the suitcase are subsequently released.

Once planktonic larvae are incorporated within the cyclonic eddies, the physical processes within the eddies influence the biological characteristics, with cyclonic eddies characterised by the upwelling of cooler water from depths, and subsequent nutrient and phytoplankton enrichment (Bakun 2006). Eddies may also modify the biological environment with regard to food availability, larval prey and predators within the eddy (Muhling et al. 2007). Landry et al. 2008 recorded higher zooplankton biomass within a cyclonic eddy in response to elevated primary production. (Mullaney and Suthers 2013) also recorded greater biomass within an eddy compared to the adjacent shelf in the East Australian current, with enhanced growth rates found in the larval fish Sardinops sagax in the eddy ~ 5 mm longer and ~ 10 days older. Retention time of planktonic larvae within an eddy is also an important factor to consider. For example, using a particle-tracking model, Condie and Condie 2016 found that eddy retention times of plankton ranged from 5 to 67 days, with plankton residing near the surface experiencing shorter retention times than those residing in the same eddy at depth. Thus plankton undergoing vertical migration have longer retention times compared to plankton that do not undergo vertical migration. Eddies clearly have the potential to retain and support planktonic larvae.

Should eddies make the journey across the MC, how would they release their biological contents onto the KZN coast? (Braby 2014) found that eddies dissipate upon reaching the KZN coast, with more eddies near the coast than in the open ocean. It was further suggested that eddies interact with the AC and the continental shelf, which could cause

eddies to become weak and dissipate. This could provide a mechanism for biological material entrained within an eddy to be released onto the continental shelf. Braby (2014) further shows how the interaction of a cyclonic eddy with the KZN coast causes the eddy to become elongated and to progress down the AC. This was also recorded by (Morris *et al.* 2013) and suggests another way in which biological material could be released onto the KZN coast.

The Suitcase Project is a registered project under ACEP (African Coelacanth Ecosystem Programme) and is divided into two components, the oceanography component and shorebased component. The oceanography component includes several sub-projects focussing physical parameters, primary productivity, phytoplankton pigments and zooplankton in coastal waters of southern Madagascar and in a cyclonic eddy in the Mozambique Basin. This thesis fits within the oceanography component, testing whether mesoscale eddies are potential vectors of gene flow between KZN, South Africa and Madagascar. The shore-based component focussed on the population genetics of organisms common to both regions. Seaweeds, limpets, barnacles, corals, mussels, prawns, lobsters and fishes from estuaries, rocky shores and reefs in the region of Fort Dauphin, the main town in south-east Madagascar were collected. Equivalent biological material from South African fauna has also been collected to enable scientists to start determining whether there is a genetic connection between the two areas.

1.2 Hypothesis

It is hypothesised that eddies are able to entrain fish and invertebrate larvae from the southeast Madagascan coast and transport these westwards across the MC to the east coast of SA. This hypothesis will be explored by examining the following questions:

- Can eddies entrain planktonic larvae of fish and invertebrate species from the southeast Madagascan coast?
- Would eddies be able to transport planktonic larvae to the east coast of Africa within a reasonable time before they undergo metamorphose/settle/swim away/sink/die?

1.3 Objectives of the research

The aim of this thesis is to investigate the "suitcase hypothesis", proposed by Marsac et al. (2014) whereby meroplankton (invertebrate and fish larvae) may be entrained by mesoscale eddies and transported across the Mozambique Channel. The objectives are as follows:

- To investigate the abundance and taxonomic composition of meroplankton along the southern Madagascan shelf.
- To investigate the abundance and taxonomic composition of meroplankton within the eddy core, annulus and outer regions.
- To compare the abundance and taxonomic composition of meroplankton along the southern Madagascan shelf to meroplankton within the eddy.
- To use DNA barcoding to identify key species which can be linked to adult species found on both the KZN and Madagascan coasts.

CHAPTER 2: LITERATURE REVIEW

2.1 Circulation of the Southwest Indian Ocean

The circulation of the SWIO is characterised by high variability with frequent mesoscale activity, which largely results from the interaction between the South Equatorial Current (SEC) and the Madagascan landmass (Penven *et al.* 2006). The SEC flows from east to west and, as it approaches Madagascar at 20°S, then bifurcates into the North East Madagascar Current (NEMC) and South East Madagascar Current (SEMC) (Ridderinkhof *et al.* 2010). The NEMC flows north and around Cape Amber, the northern tip of the island, contributing to the northward East African Coastal Current (EACC), as well as flowing into the MC (Figure 2) (Swallow *et al.* 1988). The SEMC flows southward and retroflects when it reaches Cape St. Marie, casting off eddies which become entrained within the Agulhas Current (AC) (Lutjeharms *et al.* 1981, Lutjeharms 1988a, Di Marco et al. 2000, Lutjeharms and Machu 2000, Quartly and Srokosz 2004). Furthermore, the mesoscale variability of the AC is related to flow through the MC (Schouten et al. 2002) and from the SEMC (Stramma and Lutjeharms 1997).



Figure 2 Bathymetry and major circulation features of the Southwest Indian Ocean (Source: Ridderinkhof *et al.* 2010).

2.2 The South East Madagascar Current

The SEMC is a narrow WBC, 120 km in width, reaching as deep as 1100 m with typical velocities of 1.1 m.s⁻¹ (Nauw *et al.* 2008), which are approximately half that of the fast flowing AC at 2 m.s⁻¹ (Lutjeharms 2006a) Early studies depicted the SEMC as flowing directly westwards into the AC (Gründlingh 1985, 1987, 1993, Lutjeharms 1988b), but subsequent studies found that the SEMC retroflects as it reaches the southern tip of Madagascar, shedding off eddies (Lutjeharms 1988a). Quartly *et al.* (2006) concluded that no persistent retroflection exists and that the SEMC alternates between periods of retroflection and no retroflection.

The area south-east of the SEMC near 25° S is characterised by strong disturbances in the flow field, propagating from east to west across the South Indian Ocean until they arrive at the eastern side of Madagascar (Siedler *et al.* 2009). Schouten *et al.* (2002) detected these disturbances to be Rossby waves, whereas Quartly *et al.* (2006) considered them more likely to be a train of propagating eddies. Using altimetry data Morrow *et al.* (2004) observed that anticyclonic eddies generated south of 25°S in the Leeuwin Current off Australia head in a west-north-westward direction (towards Madagascar), which could be a source of eddies in this region. Another large-scale oceanographic feature just south of the SEMC is the South Indian Ocean Countercurrent (SICC), described by Siedler *et al.* (2006) and Palastanga *et al.* (2007). The SICC is a shallow, eastward-flowing current, transporting ~10 Sv (1 Sv = 1 Sverdrup = $10^6 \text{ m}^3.\text{s}^{-1}$) down to 800 m (Siedler *et al.* 2006), compared to the AC transporting ~ 70 Sv (1 Sv = 10^6 m^3) in the upper 2000 m (Lutjeharms 2006a) It lies above the deepreaching, westward-flowing SEC around the latitude of the high variability band at 25°S (Palastanga *et al.* 2007) (Figure 3), and is an essential component of the near-surface subtropical circulation in the South Indian Ocean (Siedler *et al.* 2006).

Siedler *et al.* (2009) identified two branches in the SEMC, using satellite observations and numerical model data. South of Madagascar, the SEMC separates into one branch toward the AC and into a second branch, retroflecting and connecting to the SICC, contributing 40% of the volume. This interpretation is not supported by recent *in situ* hydrographic data (Ridderinkhof *et al.* 2013). Halo *et al.* (2014b) suggested that a connection exists between the SEMC and SICC through the shedding of anticyclonic eddies. *In situ* hydrographic observations and satellite altimetry data revealed that, after the SEMC separates from the Madagascan coast, it propagates south-westwards and breaks into a series of contrarotating eddies, known as dipoles (Ridderinkhof *et al.* 2013). Anticyclones are generated south-west of Madagascar, caused by the interaction of the SEMC with the Madagascar

Ridge, leading to an anticyclonic recirculation, whereas cyclones are generated as lee eddies inshore of the SEMC as it separates from the southern Madagascan shelf (de Ruijter *et al.* 2004, Ridderinkhof *et al.* 2013).



Figure 3 Schematic of the South East Madagascar Current (SEMC) and surface currents in the South West Indian Ocean (SWIO). MOZ_CH is the Mozambique Channel, MOZ_B is the Mozambique Basin, MAD_P is the Madagascar Plateau, MAD_B is the Madagascar Basin, WIL_R is the Wilshaw Ridge and MAS_P is the Mascarene Plateau. Thin solid arrows indicate currents and thick open arrows indicate the subtropical gyre. Eddies are indicated by rotating arrows. (Source: Siedler *et al.* 2009)

2.3 Mesoscale variability off southern Madagascar

Sea surface temperature (Di Marco et al. 2000), ocean colour (Lutjeharms and Machu 2000) and hydrographic data (Machu et al. 2002) have shown the southern coast of Madagascar to be a very productive area with year-round coastal upwelling events, which are mainly wind driven. Using satellite altimetry and hydrographic data, both cyclonic and anti-cyclonic eddies have been observed to form south of Madagascar, which then propagate into the northern AC (De Ruijter et al. 2004, Ridderinkhof et al. 2013). These mesoscale eddies are generated at two regions on the southern Madagascan coast, the south-east and southwest, with distinctly different mesoscale activity and eddy characteristics (Halo et al. 2014b). Formation of eddies is seasonal, with more eddies formed in winter than in summer, and with mesoscale activity highly impacted by seasonality in the southeast region but only slightly affected in the south-west region (Halo et al. 2014b). The south-east region eddies are formed in the upper ocean (0-300 m) and the south-west region eddies at intermediate depths (800-2000 m) (Halo et al. 2014b). Cyclonic eddies tend to form directly south and southwest of the Madagascan coast, whereas anticyclonic eddies form slightly offshore (Halo et al. 2014b). De Ruijter et al. (2004) and Ridderinkhof et al. (2013) recorded between four and six mesoscale eddies per annum originating south of Madagascar, while Halo et al. (2014b) reported between six and thirteen mesoscale eddies per annum in this area. The latter study used more precise algorithms to identify mesoscale eddies, hence obtaining higher estimates.

Using a numerical model and observational data, Halo *et al.* (2014b) showed that nearly all eddies to the south of Madagascar were highly nonlinear, suggesting that they can trap and transport biological material over considerable distances (Robinson 1983), and are thus potential vectors of planktonic larvae between Madagascar and Africa. The nonlinear properties of these mesoscale eddies was also observed by Quartly and Srokosz (2004), where chlorophyll *a* features (indicative of the phytoplankton community) were visualised using ocean colour data, and the eddies were shown to propagate in a south-westerly direction from southern Madagascar towards the African coast, carrying chlorophyll *a* rich waters offshore away from the Madagascan coast (Quartly and Srokosz 2004) (Figure 4).



Figure 4 Cyclonic eddies southwest of Madagascar made visible by high chlorophyll *a* concentration around their peripheries. One chlorophyll *a* feature (pink circle) appears and propagates in a southwesterly direction towards Durban (4a-4i). The second chlorophyll *a* feature (orange circle) can be seen (4c-4i) and also proceeds in a south-westerly direction. The second series (4j-4o) shows images of a cyclonic eddy heading south-westwards. (Source: Quartly and Srokosz 2004).

2.4 The role of mesoscale eddies in retention and transport of plankton

Plankton comes from the Greek "planktos", meaning that which is passively drifting or wandering (Lalli and Parson 1993), and refers to marine organisms that live in the water column and are incapable of swimming against a current, i.e. are passively transported by currents in the sea. There are two types of plankton, phytoplankton, the microscopic plants and zooplankton, the microscopic animals of the ocean. Zooplanktons are capable of movement, but not capable of making their way against a current and are thus zooplanktons are subject to ocean currents and oceanographic processes.

Oceanographic processes influence larval distribution and transport, which are vital for recruitment dynamics and variability in marine populations (Nakata *et al.* 2000, Hare *et al.* 2002, Werner and Quinlan 2002, Govoni 2005). Plankton studies associated with mesoscale eddies in the SWIO are scarce, with only few studies recorded in the MC. Recently Huggett, (2014) described zooplankton biomass and composition associated with mesoscale eddies in the MC, while Lebourges-Dhaussy *et al.* (2014) investigated the size composition of zooplankton associated with these eddies.

On a global scale, the importance of mesoscale eddies in relation to retention (Sale 1970, Hamner and Hauri 1981, Lee et al. 1994) and transport (Limouzy-Paris et al. 1997, Yeung et al. 2001) of planktonic larvae has been widely reported. For example, the retention mechanism of eddies enhanced survival rates of sardine larvae in the California Current, where sardine larvae distributions in relation to environmental conditions were investigated (Logerwell and Smith 2001). Observations indicated more 'survivor' sardine larvae offshore associated with mesoscale eddies than inshore, where chlorophyll biomass and zooplankton were highest. On the Great Barrier Reef, tidal eddies occurring in close proximity to One Tree Island retained reef fish larvae in the vicinity of the reef, increasing their chances of returning to their natal reef (Burgess et al. 2007). In the Florida Current, eddies retained fish larvae of snappers and groupers, and also provided a source of food for survival of these larvae (Lee et al. 1994). Short-lived eddies (2 to 4 weeks) increased recruitment of fish larvae in the East Australian Current where fish larvae were retained in eddies for a sufficient time to complete their larval cycle and return to the coast (Mullaney and Suthers 2013). Furthermore, zooplankton were retained within an eddy of coastal origin in the North Pacific, avoiding predation by not undergoing diel vertical migration during the day (Mackas and Galbraith 2002, Mackas et al. 2005).

With respect to transport of plankton, mesoscale eddies in the Gulf of Alaska (Shelikof Strait) have been shown to be important for retention and transport of larval fish during their pelagic

phase, whilst providing a nursery ground and subsequently enhancing recruitment success of walleye pollock (Canino *et al.* 1991, Bailey *et al.* 1996, Hermann *et al.* 1996, Kendall *et al.* 1996). Mesoscale eddies propagating along the continental shelf of the Gulf of Alaska influenced larval fish growth, survival and subsequent recruitment, with implications for the timing and extent of larval distribution in this region (Atwood *et al.* 2010). Limouzy-Paris *et al.* (1997) demonstrated how spin-off eddies of the Florida Current act as a transport mechanism, where eddies transported fish larvae back to their inshore settlement sites across a strong frontal boundary.

2.5 Importance of the pelagic larval phase and dispersal

Most marine animals have a planktonic larval stage (Riginos *et al.* 2011), which increases the opportunities for long-distance dispersal. Dispersal varies among marine organisms, with the majority of marine species spawning planktonic eggs from which larvae hatch, but there are a few marine invertebrates, as well as fish, that do not have a pelagic larval phase at all (Riginos and Victor 2001). Dispersal of planktonic larvae plays a fundamental role in structuring the populations of fish and invertebrates (Kinlan and Gaines 2003). (Shanks *et al.* 2003) initially suggested that pelagic larval duration (PLD) may be a strong predictor of dispersal distances. However, subsequent research showed that PLD is in fact a weak indicator of dispersal distances and that other factors such as larval behaviour and mesoscale oceanography can influence larval dispersal considerably (Shanks 2009, Weersing and Toonen 2009).

Dispersal of marine species over long distances is not unusual and is aided by lengthy planktonic larval phases (Shanks 2009). In the SWIO, studies on gene flow and ocean connectivity are limited, with only few studies documented in this area. Spiny lobsters (Palinuridae) have a flat-bodied crystalline larval phase, the phyllosoma, which is adapted for dispersal in oceanic waters (Booth and Phillips 1994, Palero and Abello 2007), making them excellent models for studying the influence of ocean processes on gene flow. The rock lobster *Panulirus homarus* occurs off both the SA east coast and the southern Madagascan coast (Berry 1974). *P. homarus* has a phyllosoma larval stage lasting up to 6 months, making it an ideal species to survive being transported across the Mozambique Channel. Interestingly, the scalloped spiny lobster *Panulirus homarus rubellus* appears to have distinct lineages for the southeast coast of Africa and Madagascar, suggesting an absence of contemporary gene flow across the Mozambique Channel (Reddy *et al.* 2014). It is also shown that the African lineage appears to be ancestral, and the source population for the

Madagascan clade, which would negate the likelihood of eddies in facilitating genetic connectivity between the modern South African and Madagascan populations.

The giant mud crab *Scylla serrata* is widely distributed throughout mangrove habitats in the Indo-West Pacific region (MacNae 1969). These crabs would also be good candidates to survive the channel crossing as they also have a long larval stage. For example, a larval stage duration of 62 days (roughly 2 months) at a water temperature of 25°C has been recorded for *Scylla serrata* (Nurdiani and Zeng (2007).

The brown mussel *Perna perna* is widely distributed in the tropical and subtropical regions of the Indian and Atlantic Oceans and also extends into the Mediterranean (Berry 1978). *Perna perna* also has a long planktonic larval phase of around 15 to 20 days with two stages: a dispersal stage (the actively swimming veliger) and a recruitment stage (the pediveliger), (Hicks and Tunnell 1995). However, settlement can be delayed by three months, depending on food availability and (low) water temperatures (Teske *et al.* 2007). Just like the above mentioned crustaceans, *P. perna* has a long-lived planktonic stage ranging from 1-3 months, which makes the brown mussel a possible candidate for surviving the journey across the MC.

As with invertebrates, a long larval phase for fish would be required for cross-channel eddy transport. However, in fish other factors, such as larval behaviour and distribution (Leis 1991), swimming speeds and orientation (Stobutzki and Bellwood 1994, 1997, Leis and Carson-Ewart 1997), should be considered along with larval duration. In the Western Indian Ocean (WIO), only a few studies on genetic connectivity in fishes have been conducted. In one study, a prolonged pelagic larval phase (30 days) and strong swimming ability enhanced larval dispersal for the snapper *Lutjanus kasmira* over distances up to 4000 km, suggesting high gene flow within the WIO (Muths *et al.* 2012). The parrot fish *Scarus ghobban* was shown to have a high dispersal range of at least 2500 km (Visram *et al.* 2010), and a study on the genetic structure of the grouper *Epinephelus merra* revealed high gene flow in the WIO (Muths *et al.* 2015). A hydrodynamic model revealed that reefs in the WIO are connected by larval dispersal, which is mainly driven by ocean currents (Crochelet and Lagabrielle 2012). Given the above examples of reef fish species showing high gene flow in the WIO, it should be possible for larvae of some fish species to survive the journey across the MC.

2.5 DNA Barcoding as an identification tool

Traditionally, microscopic analysis has been used to identify plankton. Using morphological characteristics only, it can be difficult and sometimes impossible to identify the early stages of species, for example, larval phases such as the zoea and megalopa of decapods (Bucklin et al. 2011). It also becomes difficult when dealing with cryptic species (species that are morphologically similar but genetically distinct) (Hebert et al. 2004a) and species where the larvae have not been identified, characterised or described yet (Bucklin et al. 2011). For a long time, molecular systematists have been able to identify species based on DNA sequences or genetic data (Avise 1994), but it was Hebert et al. (2003a) who popularised this in terms of (and established the phrase) "DNA-barcoding". DNA barcoding uses a single mitochondrial cytochrome c oxidase subunit I (COI) gene fragment (for most animal taxa) to accurately identify known taxa and assign unknown individuals to species, thus enhancing the discovery of new species (Hebert et al. 2003a, Stoeckle 2003). Hebert et al. (2003a) proposed the compilation of an online library of DNA barcodes that would be linked to named specimens, and in 2004 the Barcode of Life Data Systems (BOLD) (Ratnasingham and Hebert 2007) was launched. The goal of this online library was to develop DNA barcoding as a global standard for the identification of biological species (Savolainen et al. 2005).

DNA barcoding studies at a global scale have shown this method to be effective in identifying meroplanktonic taxa such as decapods. For example, a barcoding study on megalopa larvae of three sympatric crab species in the southeastern Pacific Ocean resulted in the identification and description of diagnostic characters, which now allow species to be distinguished (Pardo et al. 2009). This method has been particularly effective with fish species that undergo ontogenetic changes during the larval phase, which makes identification difficult to achieve and requires high levels of expertise (Caterino and Tishechkin 2006, Pegg et al. 2006). DNA barcoding has also been a successful tool in identifying fish larvae, and linking adult and larval fish. For example, DNA barcoding was used to identify fish larvae in Antarctica (Webb et al. 2006), and fish eggs and larvae off the Great Barrier Reef (Pegg et al. 2006). In other studies, it proved an effective tool for matching young stages and adults of fish (Valdez-Moreno et al. 2010, Baldwin et al. 2011). Bivalve larval stages are not easily distinguishable due to their similar appearance during their early development (Garland and Zimmer 2002). However, molecular techniques showed 92 % overall accuracy when used to identify commercially important bivalve species in New England (Hare et al. 2000).

The COI gene is the barcoding standard fragment for most animal taxa (Hebert *et al.* 2003a). It can be used to identify a species across all larval and life stages (e.g., eggs and larvae of marine fishes) (Savolainen *et al.* 2005), and to distinguish between cryptic species. Furthermore, universal primers for this gene are robust and have proven to be useful for species from a broad range of metazoan phyla (Folmer *et al.* 1994). In comparison to other genes, COI appears to possess phylogenetic signal that is useful over a broad range of taxonomic levels (Folmer *et al.* 1994).

CHAPTER 3: MATERIALS AND METHODS

3.1 Materials and Methods

Sampling was conducted during a 24-day cruise between the 16th and the 22nd of July 2013 on the RV *Algoa*, as part of the African Coelacanth Ecosystem Programme (ACEP). The RV *Algoa* sailed from Durban on Monday 8 July 2013 to undertake a study of a cyclonic eddy which had originated off the southern tip of Madagascar, and to collect comparative samples from the southern Madagascan coast. The eddy was first detected on the 16th of June 2013 as an enclosed, coherent eddy in the south-eastern Mozambique Channel and was a month old when it was sampled during this cruise (Figure 5). Eddy life-time from the SWIO region ranges from 90-183 days (Halo *et al.* 2014b) A more detailed description of the eddy formation and its movement is presented in Noyon *et al.* (in revision). En route to Fort Dauphin in Madagascar a series of stations was sampled along a transect running offshore to inshore towards the east of Fort Dauphin. On the southern Madagascan shelf a series of 24 stations was sampled from east to west. A course was then set to sail to the eddy (in the Mozambique Basin) and a set of 25 stations, 18.5 km apart along a transect from northeast to southwest was sampled (Figure 5).



Figure 5 Zooplankton sampling stations on the Madagascan shelf and along a transect through a cyclonic eddy in the Mozambique Basin. Station positions are superimposed on a real-time map of sea surface height anomaly (SSHA), where strong negative anomalies (in blue) indicate cyclonic features, and strong positive anomalies (in red) indicate anticyclonic features.

3.1.1 Environmental parameters sampling

CTD casts were conducted using a Seabird 911+ CTD-F (measuring conductivity, temperature, depth-fluorescence and oxygen), fitted with a 12-bottle Niskin (5L) rosette system. Physical parameters were sampled from the surface to a depth of 1000 m. Vertical fluorescence profiles were converted to chlorophyll *a* equivalents (mg m⁻³) by calibration against discrete chlorophyll *a* concentration of samples collected at several depths at each station (Noyon *et al.* in revision). Contour maps of sea surface temperature (°C) and chlorophyll *a* concentration (mg m⁻³) on the Madagascan shelf, as well as vertical profiles through the cyclonic eddy, and the horizontal distribution of zooplankton biovolume (mL m⁻³) were visualised using Surfer (Golden Software 2011).

3.1.2 Zooplankton sampling

Oblique bongos with 300 & 500 μ m mesh nets (0.25 m² mouth area) were deployed to a depth of 200 m to sample meroplankton (bivalve, echinoderm, decapod and fish larvae) in the upper 200 m or down to 5 m above the bottom at shallower depths (< 200 m). Bongo nets were towed obliquely through the water column at 2 knots to maximise the volume of water filtered and thus zooplankton catches. Volume filtered was calculated from flowmeters mounted in the mouth of the net. Only samples from the 500 μ m Bongo net were analysed in this study. A Neuston net fitted with 900 μ m mesh was towed at the surface for 15-20 minutes at 2 knots to collect neustonic plankton. Due to time constraints following a period of bad weather, only two Bongo net hauls (500 μ m) were made on the Madagascan shelf, one to the west (station 20) and one to the east (station 26) (Figure 6). Samples were preserved in ethanol (99%) for later extraction of meroplankton, as well as microscopic and genetic analysis.

3.1.3 Eddy Zonation

The approach used to divide the eddy into zones was derived from Noyon *et al.* (in revision), who considered chlorophyll *a* to be a better parameter than temperature to characterise the eddy structure. Vertical profiles of temperature indicated weak doming (elevation) of isotherms through the eddy, with no clear distinction between the eddy core and edges (Figure 7a). The chlorophyll *a* profiles indicated elevated chlorophyll *a* concentrations (>0.2 ug/l) in the eddy (stations 38 to 51), compared to the area outside the eddy (stations 30 to 37, and 52 to 54), with the highest concentrations in the eddy core (stations 44 to 47) (Figure 7b). From this, the different zones in the eddy were derived: namely, Outside Eddy (E-Out), East Eddy (E-Ed), Core, West Eddy (W-Ed) and West Outer (W-Out).

3.1.4 Microscope analysis

In the laboratory, samples from Bongo and Neuston nets were poured into a measuring cylinder, settled overnight and the volume was recorded. Biovolume (mL m⁻³) was calculated by dividing the settled volume (mL) by the volume filtered through the net (m³; Table 1). The whole sample was sorted under a stereo microscope and meroplankton were picked out and placed into vials for further microscope identification and later DNA barcoding. For this study a few selected stations were analysed from both the Bongo and Neuston nets. Stations were selected to represent the Madagascan shelf, the region outside of the eddy, and the different zones within the eddy. On the Madagascan shelf, stations were selected from both the east shelf (station 20) and the west shelf (stations 26 and 28). Along the eddy transect one station was selected from both the Bongo and Neuston nets respectively. Stations selected include: station 30, outside of the eddy (E-Out), stations 39 and 40 in the east eddy zone (E-Ed), stations 44 and 46 in the eddy core (Core), and stations 49 and 50 in the west eddy zone (W-Ed) (Figure 6).

Meroplankton were identified to the lowest taxonomic level where possible under a stereo microscope, using guides such as those of (Gurney 1942, Brownell 1979, Conway et al. 2003, Richards 2005). In particular, larvae of potential key indicator adult species, i.e. similar fauna that are known to occur on both the east coasts of Madagascar and South Africa, were sought. The extracted larvae were used for DNA barcoding to confirm microscopic identification. The abundance of meroplanktonic groups on the Madagascan shelf and through the cyclonic eddy was calculated and visualised using Microsoft Excel. The Pearson product-moment correlation was used to test for relationships between zooplankton biovolume and environmental parameters when variance was homogenous amongst samples and data were normally distributed. Otherwise, a Spearman's rank correlation was calculated. For the neuston net, near-surface environmental parameters (from the CTD) considered were temperature at 7 m, temperature at 100 m, temperature at the depth of maximum fluorescence, fluorescence at 7m and fluorescence at 100 m. To compare the zooplankton biovolume in the different zones (Madagascan shelf and along the eddy transect), a one-way Analysis of Variance (ANOVA) was used, followed by Tukey HSD post hoc tests when variance was homogenous amongst samples (Levene's test) and data were normally distributed, otherwise a Kruskal-Wallis test was performed. Statistical analyses were conducted using STATISTICA version 7.0.



Figure 6 Stations (Bongo and Neuston nets) used for this study on the Madagascan shelf, station 26 and 28 on the west shelf and station 20 on the east shelf. Stations along the eddy transect: East Outer, station 30: East Eddy, stations 39 and 49; Core, stations 44 and 46; West Eddy, stations 49 and 50.



Figure 7 (a) Thermal structure, where grey vertical dashed lines indicate stations sampled, and (b) chlorophyll *a* concentrations (mg m⁻³) along the cyclonic eddy transect down to 200 m deep. The zones are indicated as East Outer (E-Out), East Eddy (E-Ed), Core, West Eddy (W-Ed) and West Outer (W-Out).

3.1.5 DNA Barcoding

A standardised gene region, a fragment of the mitochondrial DNA cytochrome *c* oxidase subunit I (COI) gene, was used to identify meroplankton to the lowest taxonomic level possible. The primary reason for the selection of the COI gene in this study is that it can clearly identify and delimit conspecifics, and thus distinguish between different species from the same genus (Hebert *et al.* 2003a).

3.1.5.1 DNA isolation

Total DNA was extracted from single individuals in a sample using a commercially-available kit. Initially, DNA was extracted from decapod and bivalve larvae, using the GeneJet Genomic DNA Purification Kit (ThermoScientific), according to the specifications of the manufacturer. Next, DNA from fish larvae was extracted using the "salting out" method (Sunnucks and Hales 1996). Attempts to extract DNA from bivalve larvae were unsuccessful using either extraction method.

3.1.5.2 Amplification and sequencing

The gene of interest was replicated by Polymerase Chain Reaction (PCR) using universal primers LCOI1490 (10 μ M) and HCOI2198 (10 μ M) (Folmer et al. 1994). These primers were successful with the prawn larvae, but failed to work with shrimp and crab larvae. In these cases, degenerate primers were used: dgLCO1490 (10 μ M) and dgHCO2198 (10 μ M) (Meyer 2003). Primers Fish F1 (50 μ M) and Fish R1 (50 μ M) (Ward *et al.* 2005) were initially used for the fish larvae, but when visualizing PCR success on 1% agarose gels, double bands were observed. A switch was made to primers (50 μ M) VR1-T1 and (50 μ M) VF2-T1 (Ivanova *et al.* 2007), which worked successfully for most fish larvae. For those that failed, the amplification was repeated using the degenerate (Meyer 2003) primers. For larvae such as the phyllosoma and fish larvae, which failed to work with above mentioned primers, the mitochondrial 16S ribosomal RNA gene was amplified using primers 16Sar (10 μ M) and 16Sbr (10 μ M) (Palumbi 1996).

The PCR consisted of a master mix of 12.9 μ L MilliQ H₂O, 2.5 μ l 10 x buffer, 3.0 MgCl₂ (25 mM), 2.5 μ L dNTP (10 mM), 0.5 μ L of each primer, 0.1 μ L Taq (5 U/ μ L) and 3 μ L of extracted DNA. PCR reactions were performed in a 96-well gradient thermal cycler (Applied

Biosystems Veriti cycler). Amplifications were made using a cycling profile that included an initial step of 2 min at 95°C, followed by 35 cycles of 30 s at 95 °C, 40 s at 48 °C and 1 min at 72°C, followed by 10 min at 72°C. The shrimp and crab larvae failed to be amplified initially with this thermo-cycling process, and, using optimization, the suitable annealing temperature was determined to be 46°C for the larvae of both groups. PCR products were visualized after electrophoresis in an 1% agarose gel, stained with ethidium bromide, under UV light and then purified using Exonuclease I - Shrimp Alkaline Phosphate (Exo/SAP ThermoFisher Scientific) (Werle et al. 1994). A reaction mixture of 10 µL, consisting of 0.5 µl Exonuclease I and 2 µI FastAP[™] Thermosensitive Alkaline Phosphatase/Shrimp Alkaline Phosphatase and PCR product, was incubated at 37°C for 15 minutes and the reactions were stopped by heating the mixture at 85°C for 15 minutes. Purified products were then sequenced using Sanger/Big Dye version 3.1 fluorescently-labelled terminator chemistry, using a 10 µL reaction with 1 µL BigDye reaction mix, 2 µL of 5X sequencing buffer, 1 µL of primer at 1 μ M, up to 3 μ L PCR product and ddH₂O to make up to 10 μ l. The thermocycling conditions were as follows: an initial step of 2 min at 95 °C and 25 cycles of 10 s at 95 °C, 5 s at 50 °C and 4 min for 60°C, and then maintained at 4 °C. These cycle-sequencing products were purified using EDTA/NaOAc/EtOH precipitation and frozen prior to sequencing. Purified products were then sequenced using SAIAB's in-house sequencer, an ABI 3500 Genetic Analyzer, following the manufacturer's instructions. There were initial attempts using this sequencer and the quality of some sequences was not good. Due to time constraints, samples were sent off to a commercial sequencing facility (Macrogen, Seoul, South Korea) for sequencing.

Sequences were edited and trimmed using software Chromas Lite version 2.1 (Technelysium PTY Ltd, South Brisbane, Queensland, Australia, 2012) and then submitted, for identification, to Barcode of Life Data Systems (BOLD: http://www.boldsystems.org). BLAST (Altschul *et al.* 1990) searches on GenBank (http://www.boldsystems.org). BLAST (Altschul *et al.* 1990) searches on GenBank (http://www.boldsystems.org). BLAST (Altschul *et al.* 1990) searches on GenBank (http://www.boldsystems.org). BLAST (Altschul *et al.* 1990) searches on GenBank (http://www.boldsystems.org). BLAST (Altschul *et al.* 1990) searches on GenBank (http://www.boldsystems.org). BLAST (Altschul *et al.* 1990) searches on GenBank (http://www.boldsystems.org). BLAST (Altschul *et al.* 1990) searches on GenBank (http://www.boldsystems.org). BLAST (Altschul *et al.* 1990) searches on GenBank (http://www.ncbi.nlm.nih.gov) were used to assign identities to unknown species which could not be matched using BOLD. COI DNA sequences generated in this study of fish larvae were aligned using ClustalX v.2.1 (Larkin *et al.* 2007) software. Sequence divergences were calculated using the Kimura two-parameter (K2P) distance model (Kimura 1980) and neighbour-joining (NJ) trees (Saitou and Nei, 1987) were constructed, based on K2P distances, in MEGA v.6 (Tamura *et al.* 2013) to provide a graphic representation of the divergence patterns and distance relationships. The analysis of genetic distances was complemented by downloading related sequences from BOLD/GenBank for comparison with unknown sequences. To test the reliability and robustness of the relationships depicted in the tree, it was b

CHAPTER 4: RESULTS

4.1 Environmental variables

Vertical sections of temperature along the eddy transect indicated weak doming of the isotherms with slightly cooler water ($22 - 22.5^{\circ}$ C) in the upper 100 m associated with the eddy, but could this not be used to clearly distinguish between the core and outer regions of the eddy (Figure 7a). Chlorophyll *a* concentrations along the eddy transect gave a clearer indication of the eddy structure, and were highest in the core ($0.5 - 0.7 \text{ mg m}^{-3}$) and intermediate in the eddy periphery ($0.3 - 0.5 \text{ mg m}^{-3}$) (Figure 7 b).

Cool near-surface water temperatures (<22 °C) were recorded inshore on the southwest shelf and southeast shelf of Madagascar, with warmer water of the SEMC (23-24°C) farther offshore off the southeast coast (Figure 8a). Near-surface chlorophyll *a* concentrations on the Madagascan shelf were highest at station 26 on the southwest shelf (1.08 mg m⁻³) and station 12 on the southeast shelf (1.06 mg m⁻³) (Figure 8b).

4.2 Zooplankton biovolume

Mean Neuston biovolume collected on the Madagascan shelf was 0.08 ± 0.04 mL m⁻³ (Table 1). Mean neuston biovolume in the eddy was 0.06 ± 0.03 mL m⁻³, with maxima in zones E-Ed (0.08 ± 0.03 mL m⁻³) and W-Out (0.07 ± 0.03 mL m⁻³). Mean Neuston biovolume in the eddy was not significantly different from that on the shelf (ANOVA; p>0.05). Using the bongo net, mean zooplankton biovolume in the upper 200 m was much higher on the Madagascan shelf (0.63 mL m⁻³) than in the eddy (0.16 ± 0.08 mL m⁻³) although only 2 stations were sampled on the shelf (Table 1). Highest mean biovolumes in the eddy were recorded in zones W-Ed (0.25 ± 0.07 mL m⁻³) and W-Out (0.23 ± 0.14 mL m⁻³)), but these were not significantly higher than eddy zones E-Ed (0.17 ± 0.06 mL m⁻³) and Core (0.12 ± 0.08 mL m⁻³) (ANOVA, p>0.05).

Highest neuston biovolume on the Madagascan shelf was associated with relatively cool water (<22°C), and with high chlorophyll *a* concentrations to the west (1.08 mg m⁻³), but not on the eastern shelf. In the eddy, there were no clear patterns, and highest neuston biovolumes were associated with intermediate chlorophyll *a* concentrations. A significant relationship was found between neuston biovolume and fluorescence at 7 m (Spearman rank r=0.42, p<0.05).



Figure 8 (a) Near-surface (7 m) temperature (° C) and (b) near-surface (7 m) chlorophyll a concentration (mg m^{-3}) on the southern Madagascan shelf.

Table 1 Mean (\pm standard deviation) of settled zooplankton biovolume (mL m⁻³) on the Madagascan shelf (east and west) and the eddy zones (E-Outer, E-Ed, Core, W-Ed, W-Out), collected with the Neuston and Bongo nets.

Zones	Neuston biovolume (mL m ⁻³)	n	Bongo biovolume (mL m ⁻³)	n
East shelf	0.07 ± 0.04	8	0.57*	1
West shelf	0.09 ± 0.05	7	0.68*	1
Mean shelf	0.08 ± 0.04	15	0.63*	2
E-Out	0.05 ± 0.03	7	0.12 ± 0.04	8
E-Ed	0.08 ± 0.03	6	0.17 ± 0.06	6
Core	0.05 ± 0.05	4	0.12 ± 0.08	4
W-Ed	0.06 ± 0.01	4	0.25 ± 0.07	4
W-Out	0.06 ± 0.03	3	0.23 ± 0.14	3
Mean eddy	0.06 ± 0.03	24	0.16 ± 0.08	25

* Only 2 stations sampled to east and the west on the Madagascan shelf with the Bongo net.


Figure 8 Contour plot of zooplankton biovolume (mL m^{-3}) on the southern continental shelf of Madagascar collected with the Neuston net.



Figure 9 Contour plot of zooplankton biovolume (mL m⁻³) along the eddy transect collected with the Neuston net.



Figure 10 Contour plot of zooplankton biovolume (mL m⁻³) along the eddy transect collected with the Bongo net (500 μ m).

4.3 Meroplankton communities

Morphological identification of decapod larvae was difficult given the lack of available reference data, especially for the SWIO. Thus, identification of invertebrate larvae was mainly to higher taxonomic groups. There were more resources available for the identification of fish larvae, which were used to identify them to family level.

Mean abundances of invertebrate larvae collected with the Neuston net was fairly low on the Madagascan shelf, with the highest recorded in the W-Ed zone (13.7 ind m⁻³; Table 2). Crab larvae were the most abundant group on the shelf, while prawn larvae dominated the eddy. Phyllosoma larvae were found on both the west and east Madagascan shelf in low numbers but not in the eddy larvae dominated in the eddy. Mean invertebrate larval abundances collected with the Bongo net was much higher compared to the Neuston net both on the shelf and in the eddy (Table 2). Highest abundances were recorded on the east (41.5 ind m⁻³) and west (55.6 ind m⁻³) Madagascan shelf and in eddy zone W-Ed (39.3 ind m⁻³). Shrimp larvae dominate the invertebrate meroplankton on the shelf and outside the eddy (E-Out), whereas prawn larvae dominated the eddy meroplankton. Phyllosoma larvae were found in low abundances in the west Madagascan shelf and in the outer eddy perimeter (W-Ed). Bivalve larvae were present in the eddy core and outside the eddy (E-Out), also in low numbers.

Low larval fish abundances was also recorded with the Neuston net on the Madagascan shelf, with the highest abundance in the eddy zone E-Out (6.9 ind m⁻³; Table 3). The dominant families of fish larvae collected on the east Madagascan shelf with the Neuston net were Mullidae and Sphyraenidae on the Madagascan shelf, together, comprising > 60 % of total larval fish abundance. Outside of the eddy (E-Out) Centropomidae comprised 74.2 % of total larval fish abundance, and in the eddy periphery Mullidae comprised 26.3 % of total larval fish abundance. Mean larval fish abundances collected with the Bongo net (Table 3) was highest at the west shelf station (71.5 ind m⁻³), and in the eddy abundance was greatest in the western periphery (W-Ed (17.9 ind m⁻³). Dominant fish families include the Carangidae, Bregmacerotidae, Lutjanidae and Myctophidae, on both the Madagascan shelf and in the eddy. Collectively Bregmacerotidae, Lutjanidae and Myctophidae dominated on the west shelf and comprised 82.4 % of total larval fish abundance.

Moderate to low Neuston invertebrate and larval fish abundances on the Madagascan shelf (east and west) were associated with cool near-surface water (22-23 °C) and moderate nearsurface chlorophyll a concentration (0.2-0.3 mg m⁻³). In the eddy, moderate invertebrate and larval fish abundances outside of the eddy (E-Out) and on the eddy perimeter (W-Ed), was associated with a moderate near-surface chlorophyll a concentration in the eddy perimeter (0.15 mg m⁻³), but a much lower concentration outside the eddy (0.08 mg m⁻³). The highest near-surface chlorophyll *a* concentration in the core (0.35 mg m⁻³) was associated with low neuston invertebrate and larval fish abundance (Table 4). Higher Bongo net invertebrate and larval fish abundances on the Madagascan shelf were associated with cool water (< 23°C) and high chlorophyll a concentration in the upper 100 m, with higher chlorophyll a concentration on the west shelf (0.88 mg m⁻³) compared to the east shelf (0.12 mg m⁻³). In the eddy, moderate Bongo net invertebrate and larval fish abundances in the eddy perimeters, E-Ed and W-Ed, were associated with moderate chlorophyll a concentration in the W-Ed (0.11 mg m⁻³) and higher chlorophyll *a* concentration in the E-Ed (0.28 mg m⁻³). Lower Bongo net invertebrate and larval fish abundances in the eddy core were associated with high chlorophyll *a* concentration (0.30 mg m^3) (Table 5).

Groups	East shelf no.m ⁻³	%	West shelf no.m ⁻³	%	E- Out no.m ⁻³	%	E-Ed no.m ⁻³	%	Core no.m ⁻³	%	W-Ed no.m ⁻³	%
Neuston												
Prawn larvae	0.88	33.33	-	-	3.10	50.00	0.66	60.0	2.65	92.31	5.97	43.55
Crab larvae	1.33	50.00	1.55	63.64	1.77	28.57	0.44	40.00	0.22	7.69	6.64	48.39
Shrimp larvae	0.22	8.33	-	-	1.33	21.43	-	-	-	-	1.11	8.06
Phyllosoma larvae	0.22	8.33	0.88	36.36	-	0.00	-	-	-	-	-	-
Total	2.65	100	2.43	100	6.19	100	1.11	100	2.88	100	13.71	100
Bongo												
Prawn larvae	13.85	33.33	11.26	20.24	1.07	33.33	4.98	45.45	1.60	50.00	26.79	68.18
Shrimp larvae	21.54	51.85	28.48	51.19	1.42	44.44	2.99	27.27	0.53	16.67	8.33	21.21
Crab larvae	6.15	14.81	14.57	26.19	0.36	11.11	2.99	27.27	0.53	16.67	2.98	7.58
Phyllosoma larvae	-	-	1.32	0.56	-	-	-	-	-	-	1.19	3.03
Bivalve larvae	-	-	-	-	0.36	11.11	-	-	0.53	16.67	-	-
Total	41.54	100.00	55.63	100.00	3.20	100.00	10.95	100.00	3.19	100.00	39.29	100.00

Table 2 Mean (ind m⁻³) and relative abundances (% of total) of invertebrate larvae of various taxonomic groups collected with the Neuston net (top) and Bongo net (bottom) on the Madagascan shelf and in the eddy zones.

Families	East shelf no.m ⁻³	%	West shelf no.m⁻³	%	E-Out no.m ⁻³	%	E-Ed no.m⁻³	%	Core no.m⁻³	%	W-Ed no.m⁻³	%
Neuston												
Bothidae	-	-	-	-	0.22	3.23	-	-	-	-	0.44	10.53
Bregmacerotidae	-	-	-	-	-	-	-	-	-	-	0.22	5.26
Carangidae	-	-		-							0.22	5.26
Centropomidae	-	-	-	-	5.09	74.19	-	-	-	-	0.22	5.26
Clupeidae	0.22	6.67	-	-	0.22	3.23	-	-	-	-	0.44	10.53
Exocoetidae	0.22	6.67	-	-	-	-	-	-	-	-	-	-
Mullidae	0.88	26.67	-	-	-	-	-	-	-	-	1.11	26.32
Myctophidae	-	-	-	-	1.11	16.13	-	-	-	-	-	-
Scombridae	0.22	6.67	-	-	-	-	-	-	-	-	0.22	5.26
Scorpaenidae	-	-	-	-	-	-	-	-	-	-	0.22	5.26
Serranidae	0.22	6.67	-	-	-	-	-	-	-	-	0.44	10.53
Sphyraenidae	1.33	40.0	-	-	-	-	-	-	-	-	0.22	5.26
Synodontidae	-	-	-	-	0.22	3.23	-	-	-	-	-	-
Unidentified larvae	0.22	6.67	0.22	100.0	-	-	-	-	0.22	10.0	0.44	10.53
Total	3.32	100	0.22	100	6.85	100	0.00	0.00	0.22	100	4.20	100
Bongo												
Apogonidae	-	-	1.99	2.78	-	-	-	-	-	-	1.79	10.00
Blennidae	1.54	5.56	0.66	0.93	-	-	-	-	-	-	-	-
Bothidae	-	-	-	-	-	-	-	-	-	-	-	-
Bregmacerotidae	7.69	27.78	1.32	1.85	-	-	0.50	5.26	0.53	7.69	4.17	23.33
Carangidae	-	-	58.94	82.41	-	-	-	-	-	-	2.98	16.7
Carapidae	-	-	-	-	-	-	0.50	5.26	-	-	-	-
Centropomidae	-	-	-	-	1.07	21.43	-	-	-	-	-	-
Clupeidae	1.54	5.56	3.31	4.63	-	-	-	-	-	-	-	-
Exocoetidae	-	-	-	-	-	-	-	-	0.53	7.69	-	-
Gonostomatidae	1.54	5.56	-	-	-	-	0.50	5.26	-	-	1.19	6.67
Labridae	-	-	0.66	0.93	0.36	7.14	-	-	-	-	0.60	3.33
Lutjanidae	7.69	27.78	1.32	1.85	-	-	-	-	-	-	4.17	23.33
Mullidae	-	-	-	-	-	-	-	-	-	-	2.38	13.33
Myctophidae	7.69	27.78	-	-	2.85	57.14	5.97	63.16	5.85	84.62	2.98	16.67
Nomeidae	-	-	-	-	0.36	7.14	-	-	-	-	-	-
Scombridae	1.54	5.56	1.32	1.85	-	-	1.00	10.53	-	-	-	-
Scorpaenidae	-	-	-	-	-	-	-	-	-	-	-	-
Serranidae	-	-	0.66	0.93	-	-	-	-	-	-	1.79	10.00
Sphyraenidae	-	-	1.32	1.85	-	-	0.50	5.26	-	-	-	-
Synodontidae	1.54	5.56	-	0.00	-	-	0.50	5.26	-	-	-	-
Trichuridae	1.54	5.56	-	-	0.36	7.14	-	-	-	-	-	-
Unid larvae	3.08	11.11	1.32	1.85	-	-	-	-	-	-	-	-
Total	27 69	100.00	71.52	100 00	4.98	100 00	9 45	100 00	6 91	100 00	17 86	100.00

Table 3 Mean (ind m⁻³) and relative abundances (% of total) of fish larvae of various families collected with the Neuston net (top) and Bongo net bottom) on the Madagascan shelf and in the eddy zones.

Table 4 Mean (\pm standard deviation) of Neuston net invertebrate and fish larval abundance (ind m⁻³), near-surface (7 m) chlorophyll a concentration (mg m⁻³), near-surface (7 m) temperature on the shelf on the west and east shelf and across the eddy zones.

Zones	Inverts (ind m ⁻³)	Fish larvae (ind m ⁻³)	Chlorophyll <i>a</i> (mg m ⁻ ³)	Temperature (°C)
East shelf	5.3 ± 1.95	0.26 ± 0.38	0.2 ± 0.04	22.86 ± 0.001
West shelf	0.97 ± 0.93	0.02 ± 0.06	0.28 ± 0.03	21.86 ± 0.001
E-Out	2.47 ± 2.10	0.53 ± 1.31	0.08 ± 0.02	22.87 ± 0.001
E-Ed	0.44 ± 0.42	0	0	22.49 ± 0.06
Core	1.15 ± 1.32	0.02 ± 0.06	0.35 ± 0.06	22.06 ± 0.001
W-Ed	5.48 ± 4.87	0.32 ± 0.27	0.15 ± 0.03	22.53 ± 0.003

Table 5 Mean (\pm standard deviation) of Bongo net invertebrate and fish larval abundance (ind m⁻³), chlorophyll *a* concentration (mg m⁻³) and temperature in the upper 100 m on the west and east shelf and across the eddy zones

Zones	Inverts (ind m ⁻³)	Fish larvae (ind m ⁻³)	Chlorophyll a (mg m	Temperature (°C)
			3)	
East shelf	8.31 ± 9.33	1.32 ± 2.30	0.12 ± 0.10	21.98 ± 0.53
West shelf	11.31 ± 11.54	3.41 ± 12.76	0.88 ± 0.39	21.72 ± 0.06
E-Out	0.64 ± 0.58	0.24 ± 0.65	0.08 ± 0.07	22.33 ± 0.81
E-Ed	2.19 ± 2.16	0.45 ± 1.30	0.28 ± 0.15	22.33 ± 0.36
Core	0.64 ± 0.58	0.33 ± 1.28	0.30 ± 0.19	21.80 ± 0.52
W-Ed	7.86 ± 11.85	0.85 ± 1.30	0.11 ± 0.12	21.95 ± 0.49

4.4 DNA analysis

4.4.1 COI analysis

Traditional microscope identifications were difficult due to a lack of available reference material, and most of the decapod larvae were only identified to a high taxonomic level. However, with DNA barcoding analysis, more detailed identifications were possible. Due to budget constraints, randomly selected specimens both invertebrate and vertebrate larvae from each sampling station were used for DNA barcoding and the results include only the presence of taxa and not their abundance. A total of 51 barcodes were obtained for both invertebrate and fish larvae. Most sequences were identified to the generic level only, given the lack of online reference data. For the purpose of this thesis, divergence thresholds, which were first proposed by Hebert et al. (2004b), were used to identify unknown sequences. Past barcoding studies of marine fish (Ward et al. 2005) and decapods (da Silva et al. 2011) established ranges of sequences divergences that characterise individuals belonging to the same species. Hebert et al. (2003b) further demonstrated that a wide gap exists between the divergence values obtained in intraspecific and interspecific comparisons among congeners. These divergences increase with increasing taxonomic level (i.e., at generic, familial or ordinal level). For this study, sequence divergences were used for species identification, and to assess generic placement and family membership based on these divergence thresholds.

For decapod larvae, two sequences were identified to species level: the shrimp *Rhynchocinetes durbanensis* and squat lobster *Allogalathea elegans* (Table 10). A further 18 sequences were identified to genus level. These included decapod larvae of crabs of the genera *Ashtoret, Calappa, Ebalia, Pilumnus, Portunus, Pseudoliomera* and *Xaiva,* prawns (*Bentheogennema, Marsupenaeus, Metapenaeopsis* and *Solenocera*), and shrimp (*Acanthephyra, Eualus, Periclimenes,* and *Plesionika*) (Table 6). These invertebrate larvae were found on both the Madagascan shelf and along the eddy transect. Fish larvae identified to species level included *Decapterus macrosoma, Parupeneus fraserorum, Pseudanthias squamipinnis* and *Sarda orientalis* (Table 7). There were two possible candidate species identification of these species in the BOLD reference database. In this case, identification was made to genus level (Table 11). Those larvae that were identified to genus level include the genera *Bregmaceros, Callionymus, Chromis, Epinephelus, Gonostoma, Halichoeres, Lotella, Nealotus, Ostorhinchus, Oplegnathus, Polysteganus, Priacanthus, Pseudanthias, Pyramodon, Scomber, Symbolophorus, Taaningichthys and Vinciguerria. Fish larvae*

identified to family level included Ammodytidae, Bothidae, Gonostomatidae, Myctophidae and Notosudidae.

4.4.2 16S analysis

In cases of failed amplification with COI, amplification of 16S rDNA was used instead. Two unknown phyllosoma larvae and one fish larva were identified using 16S rDNA. These included phyllosoma larvae of the genus *Scyllarus* and *Panulirus* (Table 6), and a fish larva of the genus *Paralabrax* (Table 7).

Unknown	Family	Genus	Species	Gene	BOLD %	GenBank %
specimen number	-		-		similarity	similarity
C1	Portunidae	Xaiva		COI	98.2	
C2	Portunidae	Portunus		COI	86.29	
C3	Leucosiidae	Ebalia		COI	86.29	
C7	Matutidae	Ashtoret		COI	87.71	
C8	Xanthidae	Pseudoliomera		COI	99.81	
C9	Pilumnidae	Pilumnus		COI	84.67	
C13	Calappidae	Calappa		COI	100	
P1.2	Penaeidae	Metapenaeopsis		COI	89.05	
P1.4	Benthesicymidae	Bentheogennema		COI	86.18	
P3	Solenoceridae	Solenocera		COI	89.38	
P5	Penaeidae	Marsupenaeus		COI	89.27	
S1	Acanthephyridae	Acanthephyra		COI	98.89	
S2	Palaemonidae	Periclimenes		COI	100	
S3	Hippolytidae	Eualus		COI	86.62	
S4	Rhynchocinetidae	Rhynchocinetes	durbanensis	COI	100	
S5	Pandalidae	Plesionika		COI	84.26	
C11	Galatheidae	Allogalathea	elegans	COI	100	
Ph1	Scyllaridae	Chelarctus	-	COI	82.36	
Ph2	Scyllaridae	Scyllarus		16S		81
Ph3	Palinuridae	Panulirus		16S		99

 Table 6
 Unknown invertebrate larvae identified through DNA barcoding. Taxa in bold indicate sequences identified to species level.

Unknown	Family	Genus	Species	Gene	BOLD % similarity	Genbank % similarity
specimen number	0					
F2	Oplegnathidae	Oplegnathus	peaolopesi/robinsoni	COI	100	
F4	Bothidae	_		COI		89
F5	Mullidae	Parupeneus	fraserorum	COI	100	
F8	Notosudidae	_		COI	96.45	
F11	Carangidae	Decapterus	macrosoma	COI	100	
F12	Priacanthidae	Priacanthus	aff. arenatus/ arenatus/ hamrur	COI	99.11	
F13	Serranidae	Epinephelus		COI	99.65	
F14	Bregmacerotidae	Bregmaceros		COI	98.2	
F16	Scombridae	Scomber	colias/japonicus	COI	100	
F17	Myctophidae	Symbolophorus		COI	99.03	
F18	Myctophidae	· ·		COI	90.41	
F19	Gempylidae	Nealotus		COI		91
F20	Labridae	Halichoeres		COI	99.41	
F21	Carapidae	Pyramodon		COI	98.92	
F22	Apogonidae	Östorhinchus		COI		82
F24	Pomacentridae	Chromis		COI	92.88	94
F25	Serranidae	Pseudanthias		COI	99.52	
F26	Callionymidae	Callionymus		COI	99.36	
F27	Moridae	Lotella		COI	91.59 cf. tosaensis	94 rhacina
F28	Carangidae	Decapterus	macrosoma	COI	100	
F29	Mullidae	Parupeneus	fraserorum	COI	100	
F30	Scombridae	Sarda	orientalis	COI	100	
F32	Serranidae	Pseudanthias	squamipinnis	COI	100	
F33	Serranidae	Paralabrax		16S		98
F34	Myctophidae	Taaningichthys		COI	98.28	
F35	Phosichthyidae	Vinciquerria		COI	98.21	
F36	Gonostomatidae	0		COI	99.38	
F37	Ammodytidae			COI	93.24	
F38	Sparidae	Polysteganus		COI	93.43	91 coeruleopunctatus
F39	Gonostomatidae	Gonostoma	elongatum/ denudatum	COI	100	,
F40	Mullidae	Parupeneus	fraserorum	COI	100	

Table 7 Unknown fish larvae identified through DNA barcoding. Taxa in bold indicate sequences identified to species level.

4.5 Phylogenetic Analysis

Sequences obtained in this study were combined with sequences downloaded from BOLD and GenBank (Table 12) to produce a Neighbour-joining (NJ) tree (Figure 13). The NJ tree was used to display a graphic representation of the divergence patterns and distance relationships between sequences. Due to a lack of online reference data and available sequences for the invertebrate larvae, the NJ tree was produced using only larval fish sequences. Tight clusters and short branch lengths among unknown larvae and downloaded data for representative species indicate very small genetic distances and, together with high bootstrap support, confirm highly accurate species identifications for these larvae. Sequence divergences were calculated using the K2P model (Kimura 1980) are presented in Appendices A and B. K2P distances among specimens in each of these clusters varied from 0% to 0.2%. These clusters represent Decapterus macrosoma, Parupeneus fraserorum, Pseudanthias squamipinnis and Sarda orientalis. Those unknown fish larvae which had two possible candidate species identifications (Gonostoma elongatum, Oplegnathus robinsoni, Priacanthus aff. arenatus and Scomber colias also showed tight clusters with downloaded fish species data and fell within the 2% threshold characterising conspecifics species. Certain unknown fish larvae also showed tight clusters with Callionymus marleyi, Epinephelus rivulatus, Halichoeres zeylonicus and Pseudanthias connelli respectively, but had higher genetic distances (from 3 to 8%), falling beyond the 2% threshold characterising congeneric species.

Some of the unknown larvae are clearly associated with representatives of some species and a particular genus in neat clusters, but with slightly longer branch lengths and, hence, larger genetic distances. This might suggest that the unknown larvae are congeneric, but belonging to a different species. These genetic distances between unknown larvae are congeneric, but belonging to a different species. These genetic distances between unknown larvae and downloaded data for species (*Callionymus marleyi, Chromis chrysura, Lotella* sp., *Nealotus tripes, Polysteganus baissaci, Pyramodon* sp. *Scopelosaurus lepidus, Symbolophorus rufinus, Taaningichthys minimus* and *Vinciguerria nimbaria* were between 1 and 10%.

Sequences separated by rather longer branches and K2P distances varying from 10 and 20% indicated that unknown larvae belong to a different genus, but to the same families as *Ammodytoides* sp., *Arnoglossus polyspilus, Cyclothone microdon* and *Diogenichthys laternatus*, for which data were downloaded.

Using both the K2P distances and NJ tree, DNA barcoding proved to be 100% successful at identifying unknown sequences to family level, 55% at genus level and 23% at species level.

 Table 8
 Fish COI sequences downloaded from BOLD or GenBank and used in conjunction with the present sequences to obtain a neighbour-joining tree.

 Sequences highlighted in blue are unpublished.

Species name	Location collected	BOLD Specimen number	Genbank Accession number
Oplegnathus robinsoni	South Africa, KwaZulu-Natal	TZMSC416-05	JF494026
Oplegnathus robinsoni	South Africa, KwaZulu-Natal	TZMSC575-06	JF494028
Arnoglossus polyspilus	China, Guangdong	FSCS116-06	EF607331
Arnoglossus polyspilus	China, Guangdong	FSCS117-06	EF607330
Parupeneus fraserorum	South Africa	DSFSF391-09	GU805064
Parupeneus fraserorum	South Africa	DSFSG628-11	KF489698
Scopelosaurus lepidus		MAECO527-09	
Scopelosaurus lepidus		MAECO528-09	
Decapterus macrosoma	Malaysia, Terengganu, South China Sea	DBMF279-10	JX261515
Decapterus macrosoma	Malaysia, Sabah, Sulawesi Sea	DBMF675-10	JX261514
Decapterus macrosoma	Malaysia, Sabah, South China Sea	DBMF754-10	JX261170
Decapterus macrosoma	South Africa, KwaZulu-Natal	TZMSB169-04	JF493342
Priacanthus aff. arenatus	South Africa, KwaZulu-Natal, Richards Bay	TZMSA195-04	DQ885041
Priacanthus aff. arenatus	South Africa, KwaZulu-Natal, Richards Bay	TZMSA209-04	DQ885042
Epinephelus rivulatus	South Africa, KwaZulu-Natal, Park Rynie	TZMSB198-04	DQ885003
Epinephelus rivulatus	South Africa, KwaZulu-Natal, Park Rynie	TZMSC151-05	DQ885006
Scomber colias	Portugal, Faro, Algarve	FCFPS118-06	JQ774713
Scomber colias	Portugal	FCFPW043-06	JQ775114
Symbolophorus rufinus	-		
Diogenichthys laternatus		ANGBF1270-12	HQ127668
Diogenichthys laternatus	Pacific Ocean	LIDMA1138-12	
Nealotus tripes	Taiwan, Northwestern, Taiwan	LFTW070-12	
Halichoeres zeylonicus	Mozambique	DSFSE680-08	JF493603
Pyramodon sp. W1	Australia	FOAF724-07	
Hemieleotris latifasciatus			AY722173.1
Chromis chrysura	Reunion, Hermitage	IPCOM365-10	JF458036
Chromis chrysura	Reunion, St Leu	IPCOM439-10	JF434873
Pseudanthias connelli	South Africa	DSFSF628-09	JF494282
Pseudanthias connelli	South Africa, KwaZulu-Natal, Durban	TZMSC542-06	JF494284
Callionymus marleyi	South Africa, KwaZulu-Natal	TZMSC053-05	JF493006
Lotella sp.	Australia	FOAF746-07	
Lotella sp.	Australia	FOAF747-07	
Sarda orientalis	China, Zhejiang, Zhejiang	GBGCA7703-15	KM055424
Sarda orientalis	South Africa, KwaZulu-Natal	TZMSC144-05	JF494396
Pseudanthias squamipinnis	South Africa	DSFSG568-11	KF489711
Pseudanthias squamipinnis	Sri Lanka, Western, Kochchikade	TZAIB904-07	FJ583946
Taaningichthys minimus		GBGCA11187-15	KJ555472
Taaningichthys minimus		GBGCA5879-13	AP012244
Vinciguerria nimbaria		GBGCA356-10	FJ918934
Cyclothone microdon	Atlantic Ocean	MAECO094-06	EU148135
Polysteganus baissaci	Mauritius		
Gonostoma elongatum		MAECO302-06	EU148180
Gonostoma elongatum		MAECO351-06	EU148179



Figure 11 Neighbour-joining tree of COI sequences to display a graphic representation of the divergence patterns and distance relationships between sequences. The scale represents 2% K2P distance. Sequences in blue are unknown sequences, red represents unpublished data and black data are extracted from BOLD or GenBank. Numbers at nodes represent bootstrap values.

CHAPTER 5: DISCUSSION

5.1 Zooplankton biovolume on the Madagascan shelf

In this study, a higher mean zooplankton biovolume was recorded with the Bongo net (500 μ m) on the Madagascan shelf (0.63 mL m⁻³) compared to the eddy (0.19 mL m⁻³), whereas mean zooplankton biovolume collected with the Neuston net did not differ much between the Madagascan shelf (0.08 mL m⁻³) and the eddy (0.06 mL m⁻³). Knowledge of zooplankton biomass in the SWIO is scarce. Broad scale sampling was conducted during the International Indian Ocean Expedition (IIOE) between 1959-1965 and zooplankton biovolumes in the SWIO were lower compared to higher biovolumes found in the northern monsoon-driven part of the Indian ocean (Rao 1973). In the SWIO highest zooplankton biomass has been recorded mainly in coastal waters, for example, Huggett (2014) recorded a high mean mesozooplankton (>200 μ m) biovolume (1.9 mL m⁻³) near the coast, ~ 15°S south of Nacala, Mozambique, during a cruise in April/May 2010. Sampling of macrozooplankton during fisheries surveys between August 1977 to June 1978 off the Mozambique Coast vielded mean displacement volumes <0.5 mL m⁻³, with higher values on the Sofala Bank, Mozambique (Saetre and de Paula e Silva 1979). Displacement volumes are more accurate compared to settled volume, due to the different shapes of organisms which may become evident while settling; with displacement volume this effect is minimised (Harris et al. 2000). Nehring et al. 1987 found higher zooplankton biomass on the Sofala Bank, between 20 and 40 mg m⁻³ over the outer shelf, whereas values up to 160 mg m⁻³ were found on the inner shelf. However, at Angoche which is farther north along the Mozambican shelf (~ 18°S), values reached 320 mg m⁻³. A more detailed study by Leal et al. (2009) on the Sofala Bank (~ 18-20°S) of the Mozambican coast between 5-8 December 2007 revealed higher zooplankton biovolumes (settled biovolumes) nearshore (0.77-7.11 mL.I⁻¹) compared to a lower biovolume offshore (0.28 mL.I⁻¹). The Sofala Bank is a productive shelf region influenced by tidal currents and great hydrological variability determined by the Zambezi Delta discharges, as well as by mesoscale oceanographic features of the MC (Lutjeharms 2006b, Ternon et al. 2014). Malauene et al. (2014) found that elevated chlorophyll a concentrations north of Mozambique near Angoche (~ 16°S) are largely driven by north-easterly monsoon winds, but also through cyclonic/anticyclonic eddies interacting with the shelf. In the present study, elevated sea surface chlorophyll a concentration and low sea surface temperature on the southern Madagascan shelf were associated with elevated zooplankton biovolume. These oceanographic conditions have been observed previously on the southern coast of Madagascar, where hydrographic data, and satellite and sea surface temperature imagery showed elevated chlorophyll *a* and cooler water, indicating upwelling, on the south-east coast of Madagascar (Di Marco *et al.* 2000, Machu *et al.* 2002). Similar conditions were also noted in a more recent study on the southern coast of Madagascar (26°S). Pripp *et al.* (2014) found elevated chlorophyll *a* and primary production on the south coast in response to upwelling as revealed by high sea surface salinity and low sea surface temperature.

5.2 Zooplankton biovolume in the eddy

In this study, highest mean zooplankton biovolumes were recorded in the eddy periphery, with lower zooplankton biovolumes in the eddy core. This is in contrast to chlorophyll a concentrations, which were highest in the eddy core (0.5-0.7 mg m⁻³) and intermediate in the eddy periphery (0.3-0.5 mg m⁻³). This pattern could be due to top-down control by zooplankton grazers as the main controlling primary producers on the eddy peripheries. Zooplankton biomass in the open ocean has previously been found to be relatively high in cyclonic eddies. In the MC, Huggett (2014) found higher mesozooplankton biovolume (0.3 mL m⁻³) in cyclonic eddies compared to anti-cyclonic eddies, although the coarser sampling resolution, compared to this study, was not adequate to detect differences in biovolume between the core and periphery of the eddies. Landry et al. (2008) recorded mesozooplankton biomass in a cyclonic eddy to be 80% greater than the surrounding waters of the Hawaiian Islands. In the Western Bay of Bengal, mesozooplankton biomass was five times and density 18 times greater in cold-core eddies (Fernandes and Ramaiah 2009). In the Gulf of Mexico, acoustic backscatter intensity reflected from epipelagic zooplankton communities revealed elevated zooplankton and micronekton in cold-core eddies compared to warm-core eddies.

It is unclear in this study as to why zooplankton would accumulate in the eddy peripheries and not the core where more food is available. Interestingly studies conducted in the Sargasso Sea documented similar observations to this study with higher zooplankton biomass recorded in a cyclonic eddy's periphery compared to the core (Goldthwait and Steinberg 2008). Hernandez-LeonTorres *et al.* (2001) also found elevated biomass in the eddy periphery compared to the core of the eddy in the vicinity of the Canary Islands. In both

the above studies, the eddies were mature and it was suggested that higher zooplankton biovolume or biomass found at eddy peripheries could be due to an outward drift of zooplankton toward the eddy periphery during the eddy winding down, i.e. decaying or in the "spinning down" phase (Bakun 2006). In this study, however, the cyclonic eddy was sampled when it was about a month old, which was evident from the thermal structure of the eddy with a lack of doming in the temperature profile, indicating that the eddy was not fully "spun up". Furthermore, studies on micronekton and top predators in the MC also found higher abundance at the eddy peripheries (Weimerskirch *et al.* 2004, Sabarros *et al.* 2009, Tew-Kai and Marsac 2009, Sanchez-Velasco *et al.* 2013); these studies suggested that eddies tend to advect coastal waters at their periphery when they propagate along the coast and thereby distribute nutrient-rich waters in the open ocean. It is thus suggested that productive coastal waters on the southern Madagascan shelf become entrained into the eddy periphery as the eddy passes along the shelf and advects coastal rich waters into the open ocean.

5.3 Meroplankton distribution and species composition

5.3.1 Invertebrate larvae

No clear spatial patterns of abundance and species composition were observed for the invertebrate larvae collected with the Neuston and Bongo nets. Invertebrate larvae were evenly distributed on the Madagascan shelf and in the eddy (Table 9). Larvae of prawns, shrimps and crabs were the dominant decapods, with phyllosoma larvae also present but in lower numbers and mainly on the Madagascan shelf, with one only found in the eddy. Dominant prawn larvae represented two families, Penaeidae and Benthesicymidae. Penaeidae are normally found in shallow waters along the continental shelf and occur in large quantities (Chan 1998), while Benthesicymidae are either deep benthic dwellers or members of the meso- and bathypelagic fauna (Vazquez-Bader *et al.* 2004).

Shrimp larvae were dominated by the family Palaemonidae, genus *Periclimenes*. This genus is known to associate with anemones and is found throughout the world in warmer waters, with greatest diversity on tropical reefs (Bruce 2004). One larval shrimp identified to species level was the rhynchocinetid shrimp *Rhynchocinetes durbanensis*. This species, initially known only from South Africa (Gordon 1936) is widely distributed in the Indo-West Pacific and is associated with coral or rocky reefs in shallow waters (Gordon 1936).

Dominant crab larvae included portunids from the family Portunidae and were found on both the Madagascan shelf and in the eddy. Portunid crabs are commonly found in tropical and subtropical estuarine and nearshore habitats (Shields 1992).

Phyllosoma larvae represented two families, Palinuridae (spiny lobsters) and Scyllaridae (slipper lobsters). Spiny lobsters are inhabitants of reef and rocky shores in tropical and temperate seas (Diaz *et al.* 2002). The genus *Panulirus* is characteristic of shallow tropical waters and has a wide geographic distribution (Ptacek *et al.* 2001). Scyllaridae are widespread in shallow temperate and tropical waters, but are more abundant in tropical waters and have also been recorded in waters deeper than 300 m (Baisre 1994). Phyllosoma larvae identified from this study fall under the subfamily Scyllarinae. This subfamily consists of small lobsters which are found in tropical lagoons, on continental shelf and slopes, and on deep sea ridges and seamounts (Booth *et al.* 2005).

Lastly, a squat lobster larva was also identified to species level. *Allogalathea elegans*, widely distributed in the Indo-West Pacific region and sighted off northern Mozambique and Madagascar (Baba *et al.* 2008), is a shallow water species, but is sometimes found down to 146 m, and is associated with crinoids (Cabezas *et al.* 2011).

	W-Ed	E-Ed	Core	E-Out	West shelf	East shelf
	Penaeidae	Penaeidae	Penaeidae	Penaeidae	Penaeidae	Penaeidae
Prawn Iar∨ae	Benthesicymidae	Benthesicymidae	Benthesicymidae	Benthesicymidae	Benthesicymidae	Benthesicymidae
	Rhynchocinetidae	Rhynchocinetidae	Rhynchocinetidae	Rhynchocinetidae	Rhynchocinetidae	Rhynchocinetidae
Shrimp lar∨ae	Palaemonidae	Palaemonidae	Palaemonidae	Palaemonidae	Palaemonidae	Palaemonidae
Crab larvae	Portunidae	Portunidae	Portunidae	Portunidae	Portunidae	Portunidae
Phyllosoma Iar∨ae	Palinuridae				Scyllaridae	Scyllaridae

Table 9 Table of decapod larval groups recorded on the Madagascan shelf and in the eddy zones.

5.3.2 Fish larvae

In contrast to the invertebrate larvae, clear spatial patterns of species composition were observed for the fish larvae, with more larvae recorded on the Madagascan shelf and in the western eddy periphery, and fewer larvae recorded in the eddy core (Table 10). Dominant fish larvae collected from the Neuston and Bongo nets belonged to coastal/reef, benthic, epipelagic and mesopelagic families. The coastal/reef fish families included the Centropomidae, Mullidae and Serranidae, epipelagic fish families included the Sphyraenidae and Carangidae, benthic fish families included the Bothidae and Bregmacerotidae, and mesopelagic fish families included the Myctophidae and Gonostomatidae. Carangids have been described as coastal or shelf families off eastern Australia (Keane and Neira 2008). The presence of Myctophidae is easily explained, being a diverse family of oceanic fishes which have been collected in many regions of the world and which represent a high proportion of the total larvae collected in oceanic plankton samples (Olivar and Beckley 1994). This also explains their high abundance in both nets. Myctophids also dominated eddy peripheries in the MC, with few caught in the eddy core, during a study on the influence of mesoscale features on micronekton and large pelagic fish communities in the MC (Potier et al. 2014). The genus Symbolophorus was one of the myctophids which prevailed in fish assemblages (Potier et al. 2014) and was also present in this study.

Fish larvae identified to species level include the scad mackerel *Decapterus macrosoma*, the serranid *Pseudanthias squamipinnis* (sea goldie), the goat fish *Parupeneus fraserorum* and the striped bonito *Sarda orientalis*. *D. macrosoma* is reef-associated, found in depth ranges between 20 to 214 m and widely distributed in the tropical Indo-West Pacific (Paxton et al. 1989). *P. squamipinnis* is widely distributed in the Indo-West Pacific and is a reef-associated fish, occurring in shallow waters down to 55 m (Randall *et al.* 1997). The goat fish *Parupeneus fraserorum* is a newly described mullid species from the coast of KwaZulu-Natal, South Africa, in a depth range of 39-57 m but has also been recorded off the southeastern coast of Madagascar from a depth range of 27-87 m (Randall and King 2009). According to Randall and King (2009), *P. fraserorum* is known only from KZN and the southeastern coast of Madagascar. *S. orientalis* is a coastal species occurring at a depth range of 1-167 m and has a wide distribution in the Indo-Pacific region, from the east coast of Africa to the west coast of America in the Eastern Pacific region (Collete and Nauen 1983).

Other fish larvae identified in this study but not found in high abundance include families of reef-associated fishes. The Priacanthidae are distributed in tropical and subtropical waters of

the Atlantic, Indian and Pacific Oceans, and are generally associated with rock formations or coral reefs (Starnes 1988). The genus *Pseudanthias* (subfamily Anthiinae, family Serranidae), are small colourful, coral-reef fishes mainly from the Indo-Pacific (Randall 2011). The Labridae inhabit tropical marine and temperate waters around the world, and are mainly found in shallow-water habitats, such as coral reefs, rocky reefs, sand, grass and algae (Westneat and Alfaro 2005). The Apogonidae, also known as cardinal fishes, are nocturnal, active inhabitants of tropical, subtropical and warm temperate reefs (Fraser and Allen 2010). The Pomacentridae (damsel fishes) occur in all tropical oceans, mainly the Indo-Pacific (Allen 1991). Lastly, the Sparidae are widely distributed in tropical and temperate waters and occur in rocky and sandy areas nearshore or on offshore reefs to 450 m (Heemstra and Heemstra 2004). It was evident that reef associated fish dominated the dominated the Madagascan shelf as well as the eddy zone (W-Ed).

5.3.3 Larval entrainment in eddies

Several studies portrayed the entrainment and advection of planktonic larvae by mesoscale eddies in other oligotrophic waters. Graber and Limouzy-Paris (1997) found that fish larval assemblages within spin-off eddies in the Straits of Florida consisted predominantly of reef fishes, indicating that fish larvae were entrained from the shelf. In the Gulf of California, the highest plankton larval abundance was concentrated at the edge of an eddy, offshore, consisting mainly of coastal pelagic and demersal species. This suggests that the edge of the eddy "captured" larvae close to the coast and transported them around the eddy (Sanchez-Velasco *et al.* 2013). In the Leeuwin Current, larval fish assemblages collected within the eddy were different from the surrounding oceanic waters (Holliday *et al.* 2011). The eddy larval assemblages consisted mainly of oceanic meso-pelagic fishes, but neritic taxa were also present. Holliday *et al.* (2011) therefore confirmed that the occurrence of neritic taxa in the eddy was due to larvae being incorporated within the eddy as it developed in proximity to the shelf.

The majority of the fish larvae found in this study were reef associated and were present on the Madagascan shelf, but also in the eddy periphery (W-Ed) in the Mozambique Basin. The occurrence of coastal/reef fish larvae on the Madagascan shelf is to be expected, with the majority being coastal/reef associated. However, the presence of coastal/reef fish families in the open ocean is less easily explained. Coastal/reef- associated fish present in the eddy periphery (W-Ed) in the Mozambique Basin suggests that fish larvae were wrapped around the edges of the cyclonic eddy, which originated on the southern Madagascan shelf, and

were transported into the MC. Higher zooplankton biovolumes, larval abundances and reefassociated larval assemblages found in the periphery of the cyclonic eddy, compared to the core in this study provide support for the suitcase hypothesis that planktonic organisms are entrained within eddies as they propagate south-westwards of the Madagascan shelf.

Table 10Table of fish larval species composition recorded on the Madagascan shelf and in the eddy zones.Colour codes indicate habitats of larval fish.

	W-Ed	Core	E-Ed	E-Out	West shelf	East Shelf
	Priacanthus (Bigeyes)	Diogenichthys (lanternfish)	Bregmaceros (Codlets)	Arnoglossus (Flounders)	Ostorhinchus (Cardinal fish)	Bregmaceros (Codlets)
	Halichoeres (Wrasses)	Symbolophorus (lanternfish)	<i>Lotella</i> (Morid cods)	<i>Nealotus</i> (Snake mackerel)	Chromis (Damselfish)	<i>Nealotus</i> (Snake mackerel)
	<i>Ostorhinchus</i> (Cardinal fish)	Lotella (Morid cods)	Pyramodon (Pearlfishes)	Symbolophorus (Lanternfish)	Polysteganus (Seabream) Halisboares	Cyclothone (Bristlemouths)
	Chromis (Damselfish)		Diogenichthys (Lanternfish)	Halichoeres (Wrasses)	(Wrasses)	Symbolophorus (Lanternfish)
	Pseudanthias squamipinnis (Sea goldie)		Gonostoma (Bristlemouth)		Bregmaceros (Codlets)	Pseudanthias (Sea goldie)
	Polysteganus (Seabream)		Symbolophorus (Lanternfish)		Callionymus (Dragonets)	
	Parupeneus fraserorum (goatfish)		Polysteganus (Seabream)		<i>Bleekeria</i> (Sand lances)	
	Reef				Epinephelus (Groupers)	
	Epipelagic				Scomber (Mackerels)	
I	Mesopelagic				Sarda orientalis (Striped bonito)	
ł	Benthic				Decapterus (Kingfish)	

5.4 Connectivity between the Madagascar and South Africa?

The overall aim of this thesis was to determine whether eddies off southern Madagascar create a potential pathway for gene flow across the MC to southern Africa. The goatfish *P. fraserorum*, a newly described mullid which is found off the coasts of both Madagascar and KZN, was identified and its larvae were present on the Madagascan shelf and in the eddy. Invertebrate and fish larvae identified in this study were either coastal or reef-associated and found on the Madagascan shelf and in the eddy. Based on these findings, it is suggested that cyclonic eddies do entrain planktonic larvae from the Madagascan shelf and transport them into the open ocean. It has also been observed through numerical models and altimetry data (Quartly and Srokosz 2004, Halo *et al.* 2014b) that cyclonic eddies off the southwest region of Madagascar have strong vorticity, and are most energetic, living longer and travelling longer distances compared to eddies from the southeast region, suggesting that they are most likely to trap material in their cores and to transport them over long distances.

Assuming that eddies can entrain larvae from the Madagascan shelf, can they transport larvae across the MC in time before metamorphosis? The core of a cyclonic eddy is clearly a favourable niche for larvae; however, the propagation speed of cyclonic eddies recorded crossing the Mozambique Channel from south-west Madagascar is 6-9 km.day⁻¹, which would take 5-7 months (Marsac *et al.* 2014). This would not be feasible for the survival of most marine organisms, especially benthic species. For example, some benthic organisms have a pelagic larval phase of 80 days (Shulman and Bermingham 1995). Another possible route for biota to cross the MC in a suitable time-frame for larval survival is via the regions between contra-rotating eddies (Marsac *et al.* 2014). Hancke *et al.* (2014) recorded a (westward) horizontal velocity of 52-170 km day-1 in contra-rotating eddies. In this case, it would take less than 50 days to cross the MC, favouring larval survival for most benthic and pelagic species.

5.5 Efficacy of DNA barcoding of plankton

DNA barcoding of meroplankton has been revealed to be an effective tool for identification in this study, although taxonomic identification could mostly be done only to genus level. This indicates the limited reference information available for invertebrate and fish species in this region. On a global scale, DNA barcoding has been successful as an identification tool, identifying basic groups of zooplankton (Webb *et al.* 2006, Machida *et al.* 2009, Bucklin *et al.* 2010, Heimeier *et al.* 2010, Cheng *et al.* 2014) and fish larvae (Pegg *et al.* 2006, Valdez-Moreno *et al.* 2010, Baldwin *et al.* 2011). DNA barcoding has also confirmed the accurate identification and discrimination within various groups of holozooplankton, for example, copepods (Bucklin *et al.* 2003, Bucklin and Frost 2009, Blanco-Bercial *et al.* 2014), cnidarians (Ortman 2008, Ortman *et al.* 2010), euphausiids (Bucklin *et al.* 2007), ostracods (Angel *et al.* 2008), pteropods (Jennings *et al.* 2010a) and chaetognaths (Jennings *et al.* 2010b).

This was the first study in the SWIO, using DNA barcoding as an identification tool, to identify meroplankton. Plankton taxonomic analysis using morphological identification is time-consuming and difficult, especially for meroplanktonic organisms, but becomes even worse when dealing with fragile and damaged organisms (Bucklin *et al.* 2011). This study has shown the efficacy of DNA barcoding to identify meroplankton where only broad identifications were possible using microscope analysis. This study has also brought new knowledge on meroplankton composition and abundance in the SWIO.

CHAPTER 6: CONCLUSIONS

This study was conducted to investigate whether mesoscale eddies formed off southern Madagascar can create a pathway for gene flow between KZN and Madagascar, helping to explain the similarity of marine fauna found along both of these coasts. The highest plankton biovolumes were recorded on the Madagascan shelf and in the outer region of an eddy in the Mozambigue Channel, with lower plankton biovolumes found in the core and inner region of the eddy. It thus seems evident that biological material gets wrapped in the outer region of eddies along the southern Madagascan shelf as they move away from the shelf in a southwesterly direction. Shelf-originating decapod larvae (Allogalathea elegans and Rhynchocinetes durbanensis) and fish larvae (Pseudanthias squamipinnis and Parupeneus fraserorum) were found in the Mozambique Basin, and this clearly indicates that they were transported via the cyclonic eddy into the Mozambique Basin. The goatfish P. fraserorum, which is known from both the KZN and southern Madagascan coasts, was also recorded in the eddy, suggesting that more species that are known to occur on both these coasts could be revealed with further survey work and more comprehensive analysis. However, more detailed studies would be required to determine whether eddy-entrained larvae reach the KZN coast in time to settle. Mesoscale eddies that form off southern Madagascar take up to several (5 to 7) months to cross the MC (Marsac et al. 2014), thus only organisms with a long larval phase (e.g. > 7 months) would be able to survive such a journey. This is highly unlikely since most pelagic larval stages for benthic organisms can last for only 80 days before settlement (Shulman and Bermingham 1995). Frontal zones (between contra-rotating eddies) could provide a faster, effective route for planktonic larvae to cross the Mozambique Channel, due to fast-flowing currents that exist in these zones. Studies have shown that the journey across the Mozambique Channel in the frontal zone would take less than 50 days (Hancke et al. 2014). Further studies are therefore required, focusing mainly on these frontal zones to confirm whether planktonic larvae do indeed use this route to cross the Mozambique Channel and settle along the KZN coast.

This was the first study in the SWIO to use DNA barcoding as an identification tool to identify meroplanktonic larvae. Most taxa were successfully identified to genus level, and a few individuals were identified to species level. DNA barcoding has thus proved to be an accurate tool, even when dealing with fragile, damaged and minute planktonic larvae. This method is therefore recommended to be used in conjunction with the morphological identification of plankton for accurate results, especially when dealing with species that are morphologically similar.

This study confirms that cyclonic eddies that form off southern Madagascar can entrain planktonic larvae as they move offshore, but further studies are required to determine whether planktonic larvae are able to cross the Mozambique Channel and reach the KZN coast in time to settle.

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1) Scomber collas	
2) Scomber collas	000
3) F16 (Scomber)	
4) F34 (Taaningichthys)	0246 0246
5) Taaningichthys minimus	0.246 0.026 0.000
6) Taaningichthys minimus	0.260 0.260 0.060 0.058
7) Taaningichthys minimus	0.274 0.274 0.274 0.212 0.218
8) F17 (Symbolophorus)	0.244 0.244 0.244 0.235 0.256
9) Symbolophorus rufinus	0.222 0.222 0.220 0.211 0.227 0.247 0.032
10) Oplegnathus robinson/	0.233 0.233 0.256 0.260 0.256 0.292 0.260 0.241
11) Oplegnathus robinson/	0.233 0.233 0.236 0.266 0.292 0.260 0.241 0.000
12) F2 (Oplegnathus)	0.230 0.230 0.253 0.255 0.259 0.296 0.253 0.244 0.002 0.002
13) Epinephelus rivulatus	0.293 0.293 0.293 0.251 0.251 0.303 0.252 0.252 0.217 0.217 0.220
14) Epinephelus rivulatus	0.293 0.293 0.293 0.251 0.251 0.251 0.303 0.252 0.252 0.217 0.210 0.200
15) F13 (Epinephelus)	0.293 0.293 0.293 0.257 0.261 0.251 0.303 0.252 0.252 0.217 0.217 0.220 0.002 0.002
16) Pseudanthias connelli	0.251 0.251 0.251 0.251 0.254 0.254 0.254 0.254 0.256 0.255 0.257 0.227 0.227
17) Pseudanthlas connelli	0.251 0.251 0.251 0.251 0.255 0.254 0.253 0.256 0.255 0.259 0.227 0.227 0.227 0.000
18) F25 (Pseudanthlas)	0.255 0.255 0.255 0.268 0.261 0.251 0.270 0.267 0.264 0.259 0.263 0.233 0.233 0.233 0.004 0.004
19) F21 (Pyramodion)	0.250 0.250 0.250 0.240 0.225 0.255 0.241 0.238 0.247 0.250 0.239 0.242 0.198 0.201
20) Pyramodon sp.	0.266 0.266 0.237 0.224 0.253 0.262 0.247 0.244 0.246 0.250 0.245 0.245 0.246 0.201 0.201 0.198 0.016
21) Calllonymus marley/	0.293 0.293 0.293 0.249 0.249 0.249 0.307 0.335 0.313 0.266 0.266 0.266 0.246 0.246 0.268 0.268 0.271 0.246 0.243
22) F26 (Calllonymus)	0.300 0.300 0.300 0.252 0.246 0.246 0.310 0.335 0.320 0.269 0.272 0.243 0.243 0.243 0.264 0.268 0.253 0.249 0.009
23) Lotella sp.	0.290 0.290 0.284 0.281 0.291 0.308 0.300 0.300 0.265 0.266 0.224 0.224 0.224 0.224 0.282 0.286 0.248 0.251 0.261 0.268
24) Lotella sp.	0.290 0.290 0.284 0.281 0.291 0.308 0.300 0.300 0.265 0.266 0.224 0.224 0.224 0.224 0.282 0.286 0.248 0.251 0.261 0.268 0.000
25) F27 (Lotella)	0.295 0.295 0.295 0.287 0.281 0.301 0.305 0.288 0.256 0.256 0.252 0.250 0.250 0.250 0.283 0.286 0.281 0.278 0.271 0.098 0.098
26) Chromis chrysura	0277 0277 0277 0277 0247 0247 0247 0287 0247 0235 0219 0219 0222 0239 0239 0239 0240 0240 0247 0222 0231 0269 0276 0263 0250
27) Chromis chrysura	0277 0277 0277 0277 0247 0247 0247 0287 0247 0235 0219 0219 0222 0239 0239 0239 0240 0240 0247 0222 0231 0269 0276 0263 0263 0263 0260
28) F24 (ChromIs)	0264 0264 0263 0263 0263 0298 0267 0260 0213 0216 0249 0249 0249 0249 0235 0235 0235 027 0273 0260 0254 0.082 082
29) Gonostoma elongatum	0264 0264 0261 0281 0282 0289 0315 0261 0248 0260 0257 0287 0287 0287 0287 0289 0259 0259 0278 0299 0299 0299 0292 0272 0273 0243 0243 0245
30) Gonostoma elongatum	0264 0264 0261 0281 0282 0289 0315 0261 0248 0260 0257 0287 0287 0287 0287 0289 0259 0259 0278 0278 0299 0299 0272 0273 0243 0243 0243 0243 0243 0245 0.000
31) F39 (Gonostoma)	0264 0264 0261 0281 0282 0289 0315 0261 0248 0260 0257 0267 0267 0267 0267 0269 0259 0259 0278 0299 0299 0272 0273 0243 0243 0243 0243 0260 0000
32) Polysteganus coeruleopunctatus	0235 0235 0235 0242 0239 0249 0245 0235 0232 0245 0249 0256 0256 0253 0237 0237 0237 0234 0231 0228 0292 0303 0269 0269 0269 0265 0210 0220 0257 0257 0257
33) Polysteganus coeruleopunctatus	0241 0241 0241 0236 0233 0243 0243 0243 0232 0235 0232 0245 0246 0259 0256 0237 0237 0234 0237 0234 0288 0299 0276 0284 0207 0207 0224 0256 0256 0256 0256 0204
34) Polysteganus coeruleopunctatus	0244 0244 0249 0236 0246 0242 0235 0232 0245 0245 0248 0259 0256 0237 0237 0234 0237 0234 0292 0302 0276 0284 0210 0210 0228 0256 0256 0256 0256 0200
35) Polysteganus coeruleopunctatus	0241 0241 0241 0236 0233 0243 0243 0243 0232 0232 0245 0246 0259 0256 0237 0237 0234 0237 0234 0288 0299 0276 0284 0207 0207 0224 0256 0256 0256 0256 0004 0000 0002
36) Polysleganus coeruleopunctatus	0241 0241 0241 0.233 0.230 0.240 0.239 0.235 0.232 0.245 0.245 0.246 0.256 0.253 0.237 0.237 0.234 0.235 0.295 0.279 0.279 0.279 0.280 0.277 0.224 0.259 0.259 0.259 0.259 0.007 0.002
37) Polysleganus balssacl	0228 0228 0228 0227 0224 0228 0227 0245 0235 0235 0235 0235 0235 0235 0252 0249 0215 0215 0216 0222 0218 0272 0282 0275 0288 0.195 0.195 0215 0233 0233 0233 0273 0.075 0.075 0.075
38) F38 (Polysteganus)	0250 0250 0250 0253 0250 0244 0252 0249 0242 0239 0239 0235 0259 0256 0234 0234 0230 0241 0231 0295 0299 0266 0278 0210 0212 0227 0227 0227 0227 0286 0.088 0.086 0.085 0.086
39) F19 (Nealotus)	0259 0259 0273 0270 0286 0305 0273 0260 0235 0232 0232 0244 0244 0244 0247 0247 0247 0242 0262 0265 0276 0262 0265 0278 0253 0236 0236 0236 0238 0238 0238 0238 0238 0238 0238
40) Nealotus	0.239 0.239 0.250 0.251 0.260 0.267 0.259 0.247 0.220 0.220 0.223 0.254 0.254 0.254 0.254 0.252 0.219 0.213 0.204 0.270 0.270 0.270 0.272 0.222 0.226 0.261 0.261 0.268 0.248 0.248 0.242 0.222 0.222 0.222 0.219 0.195 0.200 0.043
 F20 (Hallchoeres) 	0.287 0.287 0.287 0.237 0.240 0.253 0.276 0.261 0.254 0.254 0.239 0.236 0.262 0.266 0.244 0.244 0.244 0.244 0.243 0.281 0.281 0.282 0.292 0.286 0.254 0.254 0.254 0.250 0.270 0.270 0.207 0.207 0.207 0.200 0.207 0.201 0.202 0.225 0.228 0.213
 Hallchoeres zeylonicus 	0.287 0.287 0.287 0.231 0.234 0.246 0.273 0.251 0.239 0.239 0.236 0.256 0.256 0.259 0.247 0.247 0.247 0.247 0.240 0.275 0.289 0.289 0.289 0.288 0.248 0.248 0.248 0.266 0.266 0.266 0.264 0.207 0.204 0.207 0.204 0.201 0.219 0.222 0.225 0.210 0.004
43) F35 (Vinciguerria)	0.317 0.317 0.317 0.279 0.279 0.279 0.276 0.276 0.276 0.276 0.269 0.269 0.269 0.269 0.269 0.269 0.269 0.269 0.269 0.246 0.271 0.278 0.253 0.253 0.253 0.253 0.255 0.235 0.235 0.230 0.320 0.320 0.320 0.246 0.252 0.252 0.253 0.268 0.269 0.259 0.233 0.233
44) Vinciguerria nimbaria	0.310 0.310 0.370 0.272 0.273 0.270 0.276 0.278 0.278 0.278 0.278 0.279 0.279 0.279 0.279 0.279 0.249 0.252 0.258 0.263 0.263 0.263 0.270 0.270 0.271 0.264 0.264 0.262 0.306 0.306 0.306 0.306 0.368 0.269 0.269 0.269 0.269 0.269 0.269 0.269 0.269 0.269 0.269 0.269 0.269 0.269 0.261 0
45) Priacanthus aff. arenatus	0.256 0.256 0.258 0.288 0.288 0.288 0.288 0.263 0.275 0.251 0.248 0.260 0.260 0.263 0.283 0.283 0.283 0.283 0.293 0.279 0.283 0.286 0.286 0.272 0.272 0.272 0.272 0.249 0.249 0.249 0.247 0.243 0.247 0.244 0.266 0.260 0.264 0.291 0.260 0.257 0.271
46) Priacanthus aff. arenatus	0.256 0.256 0.256 0.258 0.258 0.258 0.258 0.257 0.257 0.258 0.251 0.248 0.260 0.265 0.265 0.263 0.263 0.263 0.263 0.265 0.266 0.266 0.276 0.249 0.249 0.249 0.247 0.247 0.243 0.247 0.244 0.266 0.260 0.264 0.291 0.260 0.257 0.257 0.271 0.000
47) F12 (Priacanthus)	U226 U226 U226 U226 U226 U226 U226 U226

Appendix A 1 Kimura 2-parameter distances among unknown and downloaded sequences, where identifications to genus level were determined.

	1	2	3	4	5	6	7	8	9	10
1) Arnoglossus polyspilus										
2) Arnoglossus polyspilus	0.004									
3) F4 (Bothidae)	0.172	0.172								
4) Ammodytoides sp.	0.266	0.260	0.244							
5) F37 (Ammodytidae)	0.262	0.262	0.271	0.140						
6) Diogenichthys laternatus	0.276	0.276	0.300	0.277	0.225					
7) Diogenichthys laternatus	0.276	0.276	0.304	0.277	0.225	0.002				
8) F18 (Myctophidae)	0.263	0.269	0.267	0.253	0.206	0.107	0.104			
9) Cyclothone microdon	0.285	0.285	0.260	0.299	0.299	0.288	0.288	0.284		
10) F36 (Gonostomatidae)	0.281	0.288	0.264	0.319	0.337	0.304	0.304	0.275	0.114	

Appendix A 2 Kimura 2-parameter distances among unknown and downloaded sequences, where identification to family level were determined.