

Diet of the Australian sea lion (*Neophoca cinerea*): an assessment of novel DNA-based and contemporary methods to determine prey consumption



Kristian John Peters

BSc (hons), LaTrobe University, Victoria

Submitted in fulfilment of the requirements for the degree of

Doctor of Philosophy

University of Adelaide (October, 2016)



## **DECLARATION OF ORIGINALITY**

I certify that this work contains no material which has been accepted for the award of any other degree or diploma in my name, in any university or other tertiary institution and, to the best of my knowledge and belief, contains no material previously published or written by another person, except where due reference has been made in the text. In addition, I certify that no part of this work will, in the future, be used in a submission in my name, for any other degree or diploma in any university or other tertiary institution without the prior approval of the University of Adelaide and where applicable, any partner institution responsible for the joint-award of this degree.

I give consent to this copy of my thesis when deposited in the University Library, being made available for loan and photocopying, subject to the provisions of the Copyright Act 1968.

I acknowledge that copyright of published works contained within this thesis resides with the copyright holder(s) of those works.

I also give permission for the digital version of my thesis to be made available on the web, via the University's digital research repository, the Library Search and also through web search engines, unless permission has been granted by the University to restrict access for a period of time.

Signed: Kristian John Peters

Date: 28 October 2016



# TABLE OF CONTENTS

DECLARATION OF ORIGINALITY .....	3
LIST OF FIGURES .....	10
LIST OF TABLES .....	14
THESIS ABSTRACT .....	18
ACKNOWLEDGMENTS .....	20
LIST OF PUBLICATIONS.....	23
<b>CHAPTER 1</b> .....	<b>25</b>
<b>General Introduction</b> .....	<b>25</b>
INTRODUCTION.....	26
THESIS ORGANISATION AND STRUCTURE .....	39
REFERENCES.....	43
<b>CHAPTER 2</b> .....	<b>63</b>
<b>Diet of the endangered Australian sea lion (<i>Neophoca cinerea</i>) in South Australia.</b> .....	<b>63</b>
ABSTRACT.....	64
STATEMENT OF AUTHORSHIP .....	65
INTRODUCTION.....	67
MATERIALS AND METHODS .....	70
Sample collection.....	70
Hard part analysis .....	72

Data analysis .....	74
RESULTS .....	75
Prey hard-parts .....	75
Diet diversity .....	76
Fish and crustaceans.....	77
Cephalopods .....	80
DISCUSSION .....	86
Insights into habitat use.....	89
Potential overlap with fisheries .....	91
Conclusions and future directions.....	92
Acknowledgements.....	92
REFERENCES .....	93
<b>CHAPTER 3.....</b>	<b>107</b>
<b>PCR-based techniques to determine diet of the endangered Australian sea lion</b>	
<b>(<i>Neophoca cinerea</i>): a comparison with morphological analysis .....</b>	<b>107</b>
ABSTRACT .....	108
STATEMENT OF AUTHORSHIP .....	109
INTRODUCTION .....	111
MATERIALS AND METHODS .....	114
Trial animals .....	114
Daily Feeding and experimental diet .....	114
Male and female diets .....	115
Faecal collection and preparation .....	116
DNA preparation and extraction.....	116
Morphological analysis preparation.....	116
Primer design.....	117
Conventional PCR .....	118
Sequencing .....	119
Real-time quantitative PCR (qPCR) .....	119
Data analysis.....	120
RESULTS .....	120

Sample collection.....	120
Prey hard-parts.....	121
PCR optimisation.....	121
Prey detection by PCR and comparison to hard parts.....	123
Comparison of prey detection between PCR techniques .....	123
qPCR prey comparisons .....	124
<b>DISCUSSION</b> .....	127
Hard part analysis .....	128
Limitations of DNA-based study.....	130
PCR techniques.....	130
Conclusion and future directions .....	133
<b>ACKNOWLEDGEMENTS</b> .....	134
<b>REFERENCES</b> .....	135
<b>CHAPTER 4</b> .....	143
<b>Fine-scale diet of the Australian sea lion (<i>Neophoca cinerea</i>) using DNA-based analysis of faeces</b> .....	143
<b>ABSTRACT</b> .....	144
<b>STATEMENT OF AUTHORSHIP</b> .....	145
<b>INTRODUCTION</b> .....	147
<b>MATERIALS AND METHODS</b> .....	149
Sample collection.....	149
Molecular analysis .....	150
16S Fish primer set .....	151
16S Cephalopod primer set .....	156
PCR reactions .....	156
Clone sequencing.....	157
Sequence screening.....	157
Data analysis.....	158
<b>RESULTS</b> .....	160
Prey hard-parts.....	160

Clone library overview .....	161
Inter-colony and individual diet comparisons .....	161
16S Fish primer set .....	161
16S Cephalopod primer set .....	164
Dietary comparison between sites .....	165
Comparisons between individual and pooled DNA data sets .....	166
Assessment of prey diversity from individual and pooled datasets.....	167
Effectiveness of sample size (number of individuals) and prey diversity .....	168
<b>DISCUSSION</b> .....	<b>172</b>
Limitations.....	173
Prey diversity .....	174
Pooled and individual clone library datasets .....	177
Ecological implications .....	178
Conclusions and future directions.....	179
<b>ACKNOWLEDGEMENTS</b> .....	<b>180</b>
<b>REFERENCES</b> .....	<b>181</b>
<b>CHAPTER 5</b> .....	<b>193</b>
<b>Insights into seasonal prey use of the Australian sea lion (<i>Neophoca cinerea</i>) using faecal DNA and high-throughput sequencing</b> .....	<b>193</b>
<b>ABSTRACT</b> .....	<b>194</b>
<b>STATEMENT OF AUTHORSHIP</b> .....	<b>195</b>
<b>INTRODUCTION</b> .....	<b>197</b>
<b>MATERIALS AND METHODS</b> .....	<b>200</b>
Sample collection.....	200
Hard part analysis .....	201
DNA extraction.....	202
Primer sets .....	202
Primer adjustments for GS-FLX sequencing .....	204
PCR reactions .....	204
Roche GS-FLX sequencing and analysis .....	205
Data analysis .....	206



Assessment of sampling effort .....	207
RESULTS .....	208
Prey hard parts .....	208
DNA analysis overview .....	208
Fish primer set and prey composition .....	209
Cephalopod primer set and prey composition .....	216
Seasonal and yearly comparisons .....	216
DISCUSSION .....	221
Study limitations .....	222
DNA analysis .....	224
Prey diversity at Seal Bay .....	224
Conclusion and future directions .....	228
ACKNOWLEDGEMENTS .....	229
REFERENCES .....	229
<b>CHAPTER 6</b> .....	<b>247</b>
<b>General Discussion and Future Directions</b> .....	<b>247</b>
GENERAL DISCUSSION .....	248
FUTURE STUDIES OF ASL DIET .....	256
REFERENCES .....	258

# LIST OF FIGURES

## CHAPTER 1

**Figure 1.** The distribution of ASL breeding colonies in Western Australia ▲ (A, B) and South Australia ○ (C-F)..... 29

## CHAPTER 2

**Figure 1.** Location of ASL breeding colonies where faecal (n = 345) and regurgitate (n = 8) samples were collected in South Australia..... 71

**Figure 2.** Box plots indicating size ranges of estimated mantle length (mm) and mass (g) of cephalopods based on regression equations from key families detected in this study (Ommastrephidae, Loliginidae, Octopodidae and Sepiidae)..... 83

**Figure 3.** Mantle length (mm) and mass (g) (mean ± SD) of cephalopods (Octopodidae, Loliginidae, Sepiidae and Ommastrephidae) based on data from the minimum number of individuals recovered from faeces (n = 345) and regurgitates (n = 8) collected at nine breeding colonies of ASL in South Australia between 2003 and 2007.. ..... 84

**Figure 4.** Mass (mean ± SD) of cephalopods consumed by ASL by taxonomic family estimated in the current study and from regurgitates and stomachs derived by McIntosh et al. (2006) from the Seal Bay colony. .... 85

**Figure 5 (supplementary).** Box plots indicating size ranges estimated from mass (g) regression equations of key cephalopod families detected in this study (Ommastrephidae, Loliginidae, Octopodidae and Sepiidae).. ..... 86

### CHAPTER 3

**Figure 1.** Striped perch, squid and shark qPCR estimates from faeces collected from the male. Quantitative estimates were compared for faeces collected during the dietary proportions fed (60%, 50%, 30% and 10%)..... 126

**Figure 2.** Comparison of striped perch qPCR estimates from faeces collected from the male and female Australian sea lion when daily dietary proportions contained 50% (3 kg) striped perch..... 127

### CHAPTER 4

**Figure 1.** Study sites of two Australian sea lion colonies Lilliput Island and Kangaroo Island..... 152

**Figure 2.** Outline of experimental procedure used to generate prey sequence data from Australian sea lion faeces collected from Kangaroo and Lilliput Island, South Australia. .. 153

**Figure 3.** Hierarchical similarity cluster analysis of fish and cephalopod prey sequences obtained from Australian sea lions at Kangaroo Island (KI ▼) and Lilliput Island (LI ○). . 166

**Figure 4.** Asymptotic curves of prey sequence diversity obtained for fish (○) and cephalopods (●) from individual clone libraries..... 169

**Figure 5.** Asymptotic curves of prey sequence diversity obtained for fish (○) and cephalopods (●) from individual clone libraries for Lilliput Island (LI). ..... 170

**Figure 6.** Asymptotic curves of fish prey sequence diversity obtained for combined (pooled) DNA from 6 individuals at KI (o) and LI (▲).. ..... 171

**Figure 7.** The relationship between the number of prey taxa identified from cloning PCR products and the number of individuals sampled. .... 172

## CHAPTER 5

**Figure 1.** Location of study site, Seal Bay on Kangaroo Island. Local benthic habitat is indicated low profile reef (dark grey) and sea grass meadow with unvegetated soft bottom (light grey) (Edyvane *et al.* 1999; Bryars, 2003).. ..... 202

**Figure 2.** Asymptotic curves of prey sequence diversity obtained using next-generation sequencing for fishes (top left) and cephalopods (bottom right) from ASL faecal DNA. Asymptotes were calculated as a function of (A) total number of sequences and (B) the number of seasons sampled... ..... 212

**Figure 3.** Number of taxa (upper) and Shannon diversity index (lower) of fish and cephalopod prey identified from DNA sequences and hard parts recovered from ASL faeces collected across seasons at Seal Bay, Kangaroo Island between 2005 and 2007. Error bars are 95% confidence intervals. .... 219

**Figure 4.** Cumulative percent (%) of bony fish and cartilaginous fish prey sequences by taxonomic order for each season, and for the total number of sequences recovered (combined seasons). Data were standardised within seasons and across seasons and years..... 220

**Figure 5.** Cumulative percent (%) of cephalopod prey sequences by taxonomic order for each season, and for the total number of sequences recovered (combined seasons)..... 221

# LIST OF TABLES

## CHAPTER 1

**Table 1.** ASL prey from colonies in South Australia (SA) and Western Australia (WA). Colony names and areas are: Seal Bay (SB) (Kangaroo Island), Yorke Peninsula (YP), Lewis Island (LE) (Eyre Peninsula), Dangerous Reef (DR) (Spencer Gulf), Lilliput Island (LI) (Nuyts Archipelago) (see Fig. 1). Sample types are regurgitate (R), stomachs from dead ASL (S), faeces (F) and videos attached to ASL (V)..... 32

## CHAPTER 2

**Table 1.** The distribution of sampling effort, frequency of occurrence (FO) and numerical abundance (NA) of diagnostic prey structures (cephalopod beaks, fish otoliths, vertebral processes and crustacean carapaces) recovered from faeces (n = 345) and regurgitates (n = 8) from nine breeding colonies of ASL in South Australia between 2003 and 2007.. ..... 72

**Table 2.** Regression formulae used to estimate prey mass (g) and length (mm) from fish otoliths and cephalopod beaks recovered from faeces and regurgitates of ASL..... 74

**Table 3.** Frequency of occurrence (FO) and numerical abundance (NA) of diagnostic prey items recovered from Australian sea lion faecal (n = 345) and regurgitate (n = 8) samples.. 78

**Table 4.** Biomass (g) (mean  $\pm$  SD), median, range, total mass) and length (mm) (mean  $\pm$  SD), median, range) estimates of fish consumed by ASL based on prey items in faeces and regurgitates.. ..... 79

**Table 5.** Biomass (g) (mean  $\pm$  SD), median, range, total mass) and mantle length (mm) (mean  $\pm$  SD), median, range) estimates of all cephalopods consumed by ASL based on prey items in faeces and regurgitates..... 81

**Table 6.** Estimated mass (g) and percent biomass contribution (BM) (%) of cephalopods by taxonomic family consumed by ASL based on prey items in faeces and regurgitates..... 82

### **CHAPTER 3**

**Table 1.** Contribution of diet, prey species, number of days fed, and number of scats collected for hard-part and DNA-based diet analyses for the adult male and female experimental trial.. ..... 115

**Table 2.** Primer sequences used to amplify prey DNA from ASL faeces in this study. .... 118

**Table 3.** Total number of fish otoliths ingested and number recovered from scats for experimental diets fed to the male Australian sea lion..... 122

**Table 4.** Frequency of occurrence (FOO) and numerical abundance (NA) of prey items recovered from faeces produced by the male Australian sea lion. .... 122

**Table 5.** Diet assessment methods used to detect prey (presence / absence) in faeces collected from the adult male Australian sea lion. Samples (1 - 28) correspond to faeces collected during the experimental diet periods (see text)..... 125

## CHAPTER 4

<b>Table 1.</b> DNA extracted from fish, crustacean and cephalopod species used as positive controls to test the suitability of the mitochondrial 16S fish and cephalopod and primer sets. .....	154
<b>Table 2.</b> Primer sequences (5' - 3') used to amplify fish and cephalopod prey DNA from Australian sea lion faecal samples..	155
<b>Table 3.</b> Taxonomic assignment and numerical abundance of prey sequences obtained from Australian sea lion faeces collected from KI and LI, South Australia. ....	162
<b>Table 4.</b> Estimated number of clone sequences required to achieve 95 % coverage of the asymptotic prey diversity for each clone library..	168
<b>Table 5.</b> Total number of prey identified per site and estimate of the number individuals required to be sampled per site and combined sites to achieve 95 % coverage of the asymptotic number of prey taxa.....	171

## CHAPTER 5

<b>Table 1.</b> Primer sequences (5' - 3') used to amplify fish and cephalopod prey DNA from ASL faecal samples collected from Seal Bay, Kangaroo Island.....	203
<b>Table 2.</b> Numerical abundance and frequency of occurrence (in parentheses) of diagnostic prey items identified from hard-parts recovered from ASL faecal samples (n = 176)..	211



**Table 3.** The number of sequences and seasons analysed, and estimate of the asymptotic number of sequences or seasons required to achieve 95% prey diversity. All data excluding the winter analysis† indicated the mean asymptotic number of sequences or seasons sampled was similar to, or fewer than the number sampled for both fish and cephalopod datasets. .. 213

**Table 4.** Taxonomic assignment and numerical abundance of prey DNA sequences obtained from ASL faecal samples collected seasonally from Seal Bay Kangaroo Island, South Australia.. ..... 214

**Table 5.** Number of taxa, total sequences and overall percent of DNA sequences obtained for each family of fish prey taxa.. ..... 217

**Table 6.** Number of taxa, total sequences, and overall percent of DNA sequences obtained for each family of cephalopod prey taxa. Prey DNA sequences were generated from ASL faecal samples obtained at Seal Bay on Kangaroo Island between 2005 and 2007. .... 218

## **CHAPTER 6**

**Table 1.** Advantages and disadvantages of different DNA-based analyses and hard part analyses to determine diet in ASL. .... 251

## THESIS ABSTRACT

A fundamental prerequisite in the conservation and management of endangered species is knowledge of diet, because diet provides information on habitat use and resource requirements. However, understanding diet in marine mammals is difficult because direct feeding events are rarely observed. To overcome these limitations, many studies use the identification of skeletal remains (hard parts) recovered from faeces, or regurgitates. Yet, for the endangered Australian sea lion (*Neophoca cinerea*) (ASL), one of the rarest pinniped species in the world, diet remains a key knowledge gap that impedes our understanding of the species ecology and connectedness to other taxa in the marine ecosystem.

When this thesis commenced, knowledge of ASL diet was based on few hard part studies comprising small sample sizes, which were limited in temporal and spatial extent. Knowledge of prey utilised by ASL was poor because prey hard parts are completely digested, or, if recovered in faeces, heavily eroded. Therefore, traditional methods of dietary analysis are ‘unreliable’ and biased toward robust prey. However, limitations notwithstanding, the analysis of Australian sea lion diet via traditional methods still provides useful information on prey species consumed that cannot be readily obtained using other methods. For example, alternative biochemical methods, such as fatty acid and stable isotope analyses, have provided important insights into habitat use the broader trophic levels of prey consumed by ASL; however, they are yet to provide reliable taxonomic information on the diversity of prey species consumed, at least not without first having a thorough understanding of Australian sea lion prey.

Given the paucity of information on ASL diet, I initially aimed, as presented in Chapter 2, to investigate the diet of the ASL at different breeding colonies in South Australia. This initial study provided insights into some of the prey taxa consumed by ASL, which were

subsequently used to develop a range of DNA-based dietary analyses to determine consumption of different prey.

In order to apply DNA-based dietary analysis methods to wild populations, it was important to assess the application of different methods in a controlled environment to understand methodological constraints and refine the methods. In Chapter 3, I present feeding trials on captive ASL, with the aim to: i) assess end-point PCR and quantitative real-time PCR (qPCR) DNA-based techniques to determine their suitability to amplify and detect prey in ASL faeces and, ii) compare the DNA diet results with prey detected and identified using traditional hard-part methodology.

Having successfully applied faecal DNA-based methods in a controlled feeding experiment to identify different prey, I applied DNA-based methods to faecal samples collected from two ASL breeding colonies in South Australia and identified a range of prey. The aims of Chapter 4 were to: (i) determine the diversity of prey taxa by sequencing a large number of clones from a few individuals, (ii) compare the prey taxa recovered at two study sites, and (iii) determine whether pooling faecal DNA from multiple individuals provides a useful means to characterise diet at the colony/population level.

Finally, Chapter 5 utilised and extended the information gained from using the DNA-based faecal analyses presented in previous chapters, by integrating next-generation sequencing (NGS). Next-generation sequencing has the capacity to provide a greater depth of DNA sequencing than the cloning-sequencing approach, with the method potentially improving prey diversity information for the ASL. The aim of this study was to use DNA-based faecal analysis and NGS technology at one breeding colony to investigate seasonal and annual variation in prey consumed by ASL.

## ACKNOWLEDGMENTS

*“The very basic core of a man’s living spirit is his passion for adventure. The joy of life comes from our encounters with new experiences, and there is no greater joy than having an endlessly changing horizon”.* McCandless

There are few opportunities as an ecologist that you get to spend time exploring the unknown. This has been particularly true for this project on the Australian sea lion (*Neophoca cinerea*); few have visited the island colonies and even fewer have had the opportunity to co-exist with the inhabitants. My PhD presented an opportune moment akin to historical exploration; though modern equipment has engaged a more comfortable existence in times of adversity, there is a certain allure that draws one back to these rugged, windswept, and captivating islands. Working on a project to assist the future conservation management of an endemic and endangered species has also been a humbling experience. The behavioural characteristics among individuals at different colonies presented many challenging moments. Some could be regarded as “lover’s sunsets”, others not so passionate endeavours to a point of “you take my DNA and I’ll take some of yours”. Battle scars aside, Australian sea lions exhibited an unusual tenacious resilient spirit, which deserves full respect and support through future conservation programs.

Many people need to be thanked for the folds of this PhD. First, I would like to thank my PhD supervisors Prof Simon Goldsworthy and Dr Kathy Ophelkeller. Simon, we have spent many years together, catching and tracking sea lions and had some of the most memorable adventures and encounters. Thank you for your ongoing support and guidance as program leader of Threatened, Protected, and Endangered Species (TEPS) at South Australian Research and Development Institute (SARDI). Ultimately, your passion of Australian sea lions and their conservation is the key reason I have been able to experience

this today. Kathy, your support through SARDI Molecular Diagnostics has been instrumental. From inception, Dr Alan McKay and the team (Dr. Dina, Dr. Nathan Bott, Teresa Mammone and Ina Dumitrescu) provided an unfathomable level of guidance.

To my lab mates at SARDI and now long-term, yet controversial friends: Dr A. Baylis, Dr B. Page, Dr J. McKenzie, Dr L. Einoder, Dr R. McIntosh, Dr D. Hamer, Dr A. Wiebkin, Dr P. Rogers, Dr L. McLeay, Dr C Huveneers, Dr A. Lowther, and Dr H. Ahonen. You are an intangible force. Your tenacity and knowledge is the life-blood of marine science. Thank you for reviewing drafts and being supportive shoulders. In particular, Bayleaf and BP. Your countless fisherman's tales, assassin bears, red jock moments, shark tears, McAffers and ginger cats provided the essence of laughter. Beck. Dangerous Reef sea lion colony is where it all began. You provided some wonderful memory-etched moments. You have been incredible over the years and I thank you endlessly.

I owe tremendous gratitude to Dr Peter Shaughnessy for the countless reviews of manuscript drafts. Pete, you are my Jacques Cousteau of pinnipeds. I have no words to describe what it has meant to have your support over the years.

Numerous volunteers tested their courage and assisted with fieldwork. Chris Fulton, Clarry Kennedy, Alastair Baylis, Rebecca McIntosh, Eve Ayliffe, Mary-Anne Lea, Robert Sleep, David Peters, Amandine Emeric, Jonathon and Kylie Bire, Pat and Heidi and Gomez. You all have incredible enthusiasm and enabled this project to be accomplished.

Thanks also to Dr Simon Jarman and Dr Bruce Deagle of the Australian Antarctic Division, who both supported this project from day one and provided countless hours of molecular guidance that has been instrumental to the completion of this project.

There are a host of organisations that I want to thank for the support of this project. The University of Adelaide was instrumental in securing research scholarship funding and SARDI with Marine Innovation South Australia provided funding, infrastructure and

logistics. I would like to thank the Department of Environment, Water and Natural Resources (DEWNR) particularly B. Haddrill, B. Dalzel and their staff for permission to conduct Australian sea lion research in South Australia. The staff at Seal Bay, Kangaroo Island have always provided support for this project. I wish to thank Zoos South Australia and staff for use of their facility and sea lions. Particular thanks to Dr. C. West, C. Fulton and J. Hakof for their in-kind contribution to this project. This project was supported by external funds from Australian Government National Heritage Trust, Nature Foundation South Australia, the Wildlife Conservation Fund, and the Australian Marine Mammal Centre. Thank you to SeaLink and Mountain Designs for their in-kind support.

To my family. I am indebted for all your gracious support during my PhD. You have always told me anything is possible and that nothing is impossible. Mum, I have been away for some time now in pursuit of this dream- now I might need some dinner. Dad, thank you for taking time out of to assist with fieldwork. Your dream of oceanography, world mariners and marine ecology has finally come together.

Most importantly, to my wonderful partner, Jamie Hicks. Words cannot describe the level of encouragement and support you have provided over the years. I am blessed you see the world through the same aqua marine, and that Australian sea lions have captured your imagination. I am truly fortunate to have such a special person. This is a part of you as much as it is a part of me.

# LIST OF PUBLICATIONS

## Chapter 2

Peters, K. J., McIntosh, R. R., Shaughnessy, P. D., Baylis, A. M. M. and Goldsworthy S. D.  
Diet diversity and estimates of prey size of the endangered Australian sea lion  
(*Neophoca cinerea*) in South Australia. *In review*.

## Chapter 3

Peters, K. J., Ophelkeller, K., Bott, N. J., Herdina, H., and S. D. Goldsworthy. (2014). PCR-based techniques to determine diet of the endangered Australian sea lion (*Neophoca cinerea*): a comparison with morphological analysis. *Marine Ecology*, **36** (4), 1428 – 1439. doi: 10.1111/maec.12242

## Chapter 4

Peters, K. J., Ophelkeller, K., Bott, N. J., Deagle, B. E., Jarman, S. J., and S. D. Goldsworthy (2014). Fine-scale diet of the Australian sea lion (*Neophoca cinerea*) using DNA-based analysis of faeces. *Marine Ecology*, **36** (3), 1–21. doi: 10.1111/maec.12145.

## Chapter 5

Peters, K. J., Ophelkeller, K., Bott, N. J., Deagle, B. E., Jarman, S. J., and S. D. Goldsworthy.  
Insights into seasonal prey use by the Australian sea lion (*Neophoca cinerea*) using faecal DNA and high-throughput sequencing. *In review*.

### **Additional publication containing results from thesis**

Goldsworthy, S. D., Page, B., Rogers, P. J., Bulmand, C., Wiebkin, A., McLeay, L. J., Einoder, L., Baylis, A. M. M., Braley, M., Caines, R., Dalye, K., Huveneers, C., Peters, K., Lowther, A. D., Ward, T. M. (2013). Trophodynamics of the eastern Great Australian Bight ecosystem: Ecological change associated with the growth of Australia's largest fishery. *Ecological Modelling*, **255**, 38–57.