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Spawning biomass of Jack Mackerel (*Trachurus declivis*) and Sardine (*Sardinops sagax*) between western Kangaroo Island, South Australia and south-western Tasmania

T. M. Ward, G. L. Grammer, A. R. Ivey, J. J. Smart and J. P. Keane

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Report to the Australian Fisheries Management Authority

T. M. Ward, G. L. Grammer, A. R. Ivey, J. J. Smart and J. P. Keane

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South Australian Research and Development Institute
SARDI Aquatic Sciences
2 Hamra Avenue
West Beach SA 5024
Telephone: (08) 8207 5400
Facsimile: (08) 8207 5415
http://www.pir.sa.gov.au/research

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Author(s): T. M. Ward, G. L. Grammer, A. R. Ivey, J. J. Smart and J. P. Keane

Reviewer(s): J. Tanner, O. Burnell (SARDI) and K. Bennetts (AFMA)

Approved by: S. Mayfield
Science Leader - Fisheries

Signed: SMayfield

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ABBREVIATIONS

Abbreviation	Full Name
AFMA	Australian Fisheries Management Authority
CTD	Conductivity Temperature Depth
DEPM	Daily Egg Production Method
GAB	Great Australian Bight
GLM	Generalised Linear Models
NSW	New South Wales
PIRSA	Primary Industries and Regions South Australia
RBC	Recommended Biological Catch
SA	South Australia
SARDI	South Australian Research and Development Institute
SPF	Commonwealth Small Pelagic Fishery
TAC	Total Allowable Catch
TAS	Tasmania

EXECUTIVE SUMMARY

Background and Need

The Harvest Strategy for the Small Pelagic Fishery (SPF) specifies that estimates of spawning biomass obtained using the Daily Egg Production Method (DEPM) are the primary biological performance indicator for target species. Estimates of spawning biomass are used to set Recommended Biological Catches (RBCs) and Total Allowable Catches (TACs).

Prior to this study, the DEPM had been applied to all SPF target species in the East sub-area, and to Blue Mackerel in the West sub-area. The need to apply the DEPM to Jack Mackerel and Redbait in the West sub-area increased in 2014/15, when a factory trawler entered the SPF and began operating in both sub-areas. In the West sub-area, the factory trawler operated between western Kangaroo Island, South Australia and south-western Tasmania.

The DEPM was applied to Jack Mackerel in waters between western Kangaroo Island, South Australia and south-western Tasmania in December 2016 to February 2017. Exploratory egg sampling was also undertaken in Bass Strait and off north-eastern Tasmania.

Objectives

The objectives of this study were to:

1. Determine distribution and abundance of eggs of Jack Mackerel and Sardine between western Kangaroo Island, South Australia and south-western Tasmania.
2. Estimate adult reproductive parameters of Jack Mackerel during the peak spawning period between western Kangaroo Island and south-western Tasmania.
3. Estimate the spawning biomass of Jack Mackerel and Sardine between western Kangaroo Island and south-western Tasmania.

The original proposal for this study did not include application of the DEPM to Australian Sardine. This species was added to the objectives when it became evident that significant numbers of eggs of Australian Sardine were present in the plankton samples.

Methods

The rationale for the DEPM is that spawning biomass can be calculated by dividing the mean number of eggs produced per day (i.e. total daily egg production) by the mean number of eggs produced per unit weight of adult fish (i.e. mean daily fecundity).

To estimate total daily egg production, ichthyoplankton samples were collected from the *RV Ngerin* from 306 sites in shelf waters between western Kangaroo Island, South Australia and

south-western Tasmania between 2 December 2016 and 6 February 2017. Ichthyoplankton samples were also collected opportunistically from the *FV Western Alliance* at 41 sites in Bass Strait and along the coast of north-eastern Tasmania. A total of 347 sites was sampled.

Jack Mackerel and Sardine eggs were identified using standard laboratory procedures. Egg identifications of Jack Mackerel were confirmed using molecular techniques. Spawning area was estimated using the Voronoi nearest neighbour method. Five models were used to estimate egg production (P_0). For Jack Mackerel, the value of P_0 used to estimate spawning biomass was the mean estimate from four models. For Sardine, the estimate of P_0 used to estimate spawning biomass was the value obtained from the log-linear model.

Modified demersal trawls for adult Jack Mackerel were undertaken from the *FV Western Alliance* at 12 sites in shelf and slope waters between Portland, Victoria and western Tasmania during 30 January to 3 February 2017. Few adult Jack Mackerel and no adult Sardine were collected. Adult parameters for Jack Mackerel used in this study were obtained from a trawl survey conducted off eastern Tasmania and Victoria during 2014. Adult parameters for Sardine were obtained from surveys conducted off South Australia between 1998 and 2016.

Sensitivity analyses were undertaken to determine the influence of uncertainty in individual parameters on estimates of spawning biomass.

Results, Discussion and Implications

A total of 639 live Jack Mackerel eggs were collected from 55 of the 347 sites. The highest densities of eggs were recorded in waters north-west of King Island, south-east of Kangaroo Island and in Bass Strait. Most Jack Mackerel eggs were collected from sites with bottom depths of 48–97 m and sea surface temperatures (SSTs) of 16.0–19.6°C. The estimated spawning area from the extended survey was 13,898 km^2, comprising 15.9% of the total survey area (87,374 km^2). Mean daily egg production (P_0) was 9.6 eggs·day^{-1}·m^{-2}. Adult parameters [mean (min–max)] from samples collected off eastern Tasmania and Victoria in 2014 were: sex ratio (R): 0.47 (0.38–0.56), female weight (W): 208.8 g (133.9–250.9), batch fecundity (F): 34,068 eggs (16,599–94,743), and spawning fraction (S): 0.056 (0.000–0.134). The estimate of spawning biomass from the extended survey of ~31,000 t is indicative of adult abundance between western Kangaroo Island and south-western Tasmania, but is an underestimate of the total abundance of Jack Mackerel in the West sub-area. Sensitivity analysis showed that, for this study, spawning area had a larger effect on estimates of spawning biomass than S or P_0.

A total of 4,837 live Sardine eggs were collected from 105 of the 347 sites. The highest densities of Sardine eggs were collected south-east of Kangaroo Island, north of King Island

and in Bass Strait. Most Sardine eggs came from sites with bottom depths of 22–156 m and SSTs of 15.8–20.4°C. The estimate of spawning area from the extended survey was 26,366 km^2 (30.2% of the 87,374 km^2 total survey area). Mean daily egg production (P_0) was 33.2 eggs·day^{-1}·m^{-2} (95% CI = 19.5–63.5). Adult parameters [mean (min–max)] from Sardine collected off South Australia during 1998–2016 were: sex ratio (R): 0.54 (0.36–0.68), female weight (W): 57.0 g (45.2–78.7), batch fecundity (F): 17,116 eggs (10,904–24,790), and spawning fraction (S): 0.114 (0.040–0.179). The estimate of spawning biomass from the extended survey of ~47,000 t is indicative of adult abundance between western Kangaroo Island and south-western Tasmania, but is an underestimate of the total abundance of Sardine in the West sub-area. Sensitivity analysis showed that the egg production model had a strong influence on estimates of P_0 and spawning biomass. For Sardine, the log-linear model usually provides estimates of P_0 that are more precise and lower than those from other models.

The estimates of spawning biomass of Jack Mackerel (31,069 t) and Sardine (47,283 t) for the portion of the West Sub-area between western Kangaroo Island and south western Tasmania, where a factory trawler operated in 2014/15 and 2015/16, are underestimates of the spawning biomass in the West sub-area. Exploratory ichthyoplankton sampling suggested that key spawning habitat in Bass Strait was not included in the survey. Both Jack Mackerel and Sardine also occur west of the survey area.

Our results suggest that distinct sub-populations of both Jack Mackerel and Sardine occur between the Bonney Coast and southern NSW, including waters off north-eastern Tasmania, and that Bass Strait is an important spawning area for both species. Future DEPM studies should be designed to cover this entire area.

Keywords: Jack Mackerel, *Trachurus declivis*, Australian Sardine, *Sardinops sagax*, Daily Egg Production Method, Spawning Biomass, Small Pelagic Fishery, eastern Australia, Tasmania, Bass Strait

1 INTRODUCTION

1.1 Background

A large purse-seine fishery for small pelagic fishes developed off Tasmania in the mid-1980s. The majority of the catch was Jack Mackerel (*Trachurus declivis*), with relatively small quantities of Redbait (*Emmelichthys nitidus*) and Blue Mackerel (*Scomber australasicus*) taken as by-product. Catches of Jack Mackerel peaked at ~40,000 t in 1986/87, making it Australia's largest fishery by weight at that time (Kailola et al. 1993, Pullen 1994, Ward and Grammer 2017).

The Commonwealth Small Pelagic Fishery (SPF) was established in 2000. The SPF is a purse-seine and mid-water trawl fishery. It is managed by the Australian Fisheries Management Authority (AFMA) and operates in Commonwealth waters (3–200 nm) from southern Queensland to south-western Western Australia, including Tasmania. The fishery is divided into two sub-areas (East and West) at longitude 146°30'E (AFMA 2009). The target species are Jack Mackerel, Redbait, Blue Mackerel and Australian Sardine (*Sardinops sagax*).

A detailed history of the SPF is described in Moore and Skirtun (2012). Catch and effort in the SPF have fluctuated over time, driven by a combination of social, economic and biological factors. Catch and effort increased in 2014/15 to 2015/16 when a factory trawler operated in both sub-areas (Ward and Grammer 2017).

The SPF Harvest Strategy and Management Plan were implemented in 2008/09 (AFMA 2008, 2009). The SPF Harvest Strategy was last revised in 2017. The SPF Harvest Strategy is used to set Total Allowable Catches (TACs) for each species and sub-area. Estimates of spawning biomass obtained using the Daily Egg Production Method (DEPM) are the primary biological performance indicator for target species. Estimates of spawning biomass are used to set Recommended Biological Catches (RBCs) and Total Allowable Catches (TACs) under guidelines outlined in the Harvest Strategy.

The DEPM has previously been applied to Jack Mackerel in the East sub-area (Ward et al. 2015b, Ward et al. 2016). The present study is the first application of the DEPM in the West sub-area of the SPF. It was conducted in the area between western Kangaroo Island, South Australia and south-western Tasmania to focus on the portion of the West sub-area where the factory trawler was operating in 2014/15 and 2015/16.

1.2 Daily Egg Production Method (DEPM)

The difficulties associated with using fishery-dependent methods for stock assessment of schooling fishes have been recognised widely for many years (e.g. Walters and Maguire 1996, Barange et al. 1999, Gaertner and Dreyfus-Leon 2004). For example, over-estimation of stock size is a major risk when commercial catch-per-unit-effort (CPUE) is used as an index of abundance; this approach has contributed to the collapse of several major fisheries (e.g. Walters and Maguire 1996). The use of fishery-dependent data is particularly problematic in new and developing fisheries, such as the SPF, where fishing activity is often sporadic and focused on a small and unknown portion of the total stock, and fishing methods, including vessels, change rapidly (see Ward et al. 2017). The Daily Egg Production Method (DEPM) has been widely applied to small pelagic fish because it is often the most practical method available for fishery-independent stock assessment (Parker 1980, Lasker 1985, Ward and McLeay 1998, Stratoudakis et al. 2006, Ward et al. 2009, 2017). However, acoustic methods have replaced or been used in conjunction with the DEPM in situations where the schooling behaviour of the target species is well understood (e.g. Coetzee 2000), and the resources (e.g. research vessels and sampling equipment) needed to produce reliable acoustic-based estimates of relative or absolute abundance are available (e.g. Barange et al. 1999, Zwolinski et al. 2012).

The rationale for the DEPM is that the adult biomass of a species present in the spawning area during the spawning season can be calculated by dividing the mean number of eggs produced per day (i.e. total daily egg production) by the mean number of eggs produced per unit weight of adult fish (i.e. mean daily f0ecundity). The equation underpinning the DEPM and definitions of the key parameters are shown in Table 1 (Equation 1).

The DEPM is applied to determinate or indeterminate spawning fishes that spawn multiple batches of pelagic eggs over an extended spawning season (Parker 1980, Ganias 2013). Parameters used to calculate total daily egg production, i.e. mean daily egg oroduction (P_0) and spawning area (A), are estimated from structured ichthyoplankton surveys, typically undertaken from research vessels (e.g. Stratoudakis et al. 2006). Adult samples used to calculate mean daily fecundity, i.e. female weight (W), sex ratio (R), batch fecundity (F) and spawning fraction (S), can be sampled from the vessel undertaking the ichthyoplankton survey or chartered or commercial vessels operating in the survey area during the study period (e.g. Stratoudakis et al. 2006).

Table 1. The Daily Egg Production Method (DEPM) equation to calculate spawning biomass (*SB*) for Jack Mackerel and Sardine.

Model Name	Equation	Eq. No.	Parameters	Reference
Daily Egg Production Method	$SB = \frac{P_0\, A\, W}{R\, F\, S}$	(1)	*SB:* Spawning Biomass P_0: mean daily egg production *A*: total spawning area *W*: mean female weight *R*: mean sex ratio *F*: mean batch fecundity *S*: mean spawning fraction	Parker 1985

The key assumptions of the DEPM are that: 1) surveys are conducted during the main (preferably peak) spawning season; 2) the entire spawning area is sampled; 3) eggs are sampled without loss and identified without error; 4) levels of egg production and mortality are consistent across the spawning area; and 5) representative samples of spawning adults are collected during the survey period (Parker 1980, Alheit 1993, Hunter and Lo 1997, Stratoudakis et al. 2006). Several of these assumptions are not met in many applications of the DEPM (see Bernal et al. 2012, Dickey-Collas et al. 2012).

Estimates of spawning biomass obtained using the DEPM are imprecise (e.g. Alheit 1993, Hunter and Lo 1997, Stratoudakis et al. 2006, Bernal et al. 2012, Dickey-Collas et al. 2012). Interannual variations in estimates of spawning biomass are driven mainly by three parmaters: P_0, *A* and *S*. There are considerable uncertainties associated with estimation of both P_0 and *S* (Fletcher et al. 1996, McGarvey and Kinloch 2001, Ward et al. 2001a, 2001b, Gaughan et al. 2004, McGarvey et al. 2018). In contrast, several authors have noted the advantages of presence-absence sampling used to estimate *A* and the high correlation of spawning area with spawning biomass (Mangel and Smith 1990, Gaughan et al. 2004). Confidence limits surrounding estimates of P_0 are usually high. A recent study evaluated the use of a variety of statistical approaches for estimating P_0, and identified options for reducing imprecision (Ward et al. 2018). One of the options identified was to use the most precise method, which had a likely negative bias and reduced the potential for over-estimation of stock size (see Ward et al. 2018). Uncertainties in the estimation of *S* mainly relate to difficulties obtaining representative samples of the adult population. However, uncertainty also arises from the challenge of estimating the age of post-ovulatory follicles (Ganias 2012). Uncertainties associated with estimation of *S* are most problematic for species with low spawning fraction, where small changes in *S* (e.g. from 5% to 15%) can have a major impact on estimates of biomass (Stratoudakis et al. 2006).

1.3 Jack Mackerel

Egg production methods have been applied to several trachurid species. For example, since 1995, annual egg production surveys have been applied to Horse Mackerel (*Trachurus trachurus*) off the Iberian Peninsula (Ward et al. 2015a). The DEPM was first applied to this stock in 2007. The DEPM has been successfully applied to Chilean Jack Mackerel (*Trachurus murphyi*) off the central coast of Chile (1999-2006; Ruiz et al. 2008) and also to Yellowtail Scad (*Trachurus novaezelandiae*) off eastern Australia in 2009 (Neira 2009).

Jack Mackerel (*Trachurus declivis*) is widely distributed throughout coastal waters of southern Australia and New Zealand (Gomon et al. 2008). It occurs in depths up to 500 m but is most common in shelf waters <200 m (Pullen 1994), where it feeds primary on krill and other aquatic crustaceans (Stevens et al. 1984, Bulman et al. 2008, McLeod et al. 2012). A review by Bulman et al. (2008) concluded that it was likely that there are two separate sub-populations of Jack Mackerel in Australian waters; one off eastern Australia, including eastern Tasmania, and one west of Tasmania, including the Great Australian Bight and Western Australia.

Jack Mackerel is a serial spawner (Marshall et al. 1993, Neira 2011). It spawns in spring along the New South Wales (NSW) coast (Maxwell 1979, Keane 2009) and during summer further south off Tasmania and in the Great Australian Bight (Stevens et al. 1984, Jordan et al. 1995, Ward et al. 2016, Sexton et al. 2017). The main spawning area is thought to be located off south-eastern Australia in eastern Bass Strait and off eastern Tasmania, Victoria and southern NSW (Bulman et al. 2015). Off eastern Tasmania, spawning occurs continuously from December to February (Williams and Pullen 1986, Jordan 1994, Neira 2011). Limited information is available on the spawning patterns in the West sub-area (Stevens et al. 1984).

Jack Mackerel eggs are positively buoyant and 0.97–1.03 mm in diameter (Neira 2011). They are morphologically similar to Yellowtail Scad eggs, but slightly larger (Yellowtail Scad egg diameter: 0.78–0.88 mm; Neira 2009). Previous studies have demonstrated a high level of success in identifying Jack Mackerel eggs from morphological characteristics (Neira 2011, Ward et al. 2015b).

The first dedicated application of the DEPM to Jack Mackerel off the south-east coast of Australia was done in 2014 (Ward et al. 2015b). The estimate of spawning biomass of 157,805 t (95% CI) was based on reliable estimates of key adult parameters and considered robust. A preliminary study based on samples collected off south-eastern Australia in 2002–2004 provided estimates of spawning biomass in the range of 114,000–169,000 t (Neira 2011). Ecosystem modelling estimated the spawning biomass of Jack Mackerel of south-east Australia to be 130,000–170,000 t (Fulton 2013). Similar ecosystem modelling suggested the

biomass of Jack Mackerel west of Tasmania was approximately 60,000–110,000 t (Smith et al. 2015).

1.4 Australian Sardine

Sardines (*Sardinops, Sardina, Sardinella*) form the basis of some of the world's largest fisheries (Schwartzlose et al. 1999) and have been the focus of extensive research (e.g. Stratoudakis et al. 2006). The DEPM has been widely applied to Sardines both within Australia and overseas. For example, the DEPM has been used since 1994 to estimate the spawning biomass off California and is the longest fishery-independent biomass index for Pacific Sardine (*Sardinops sagax*) (Ward et al. 2015a). The DEPM has also been applied to Sardine populations off Peru (*S. sagax*), the Iberian Peninsula (*Sardina pilchardus*), and Brazil (*Sardinella brasiliensis*) (Alheit 1993, Ward et al. 2015a).

Sardine (*Sardinops sagax*) occurs throughout temperate Australian waters from Rockhampton (Queensland) to Shark Bay (Western Australia), including northern Tasmania (Gomon et al. 2008). Australian Sardine is structured as a meta-population where extensive mixing occurs among neighbouring sub-groups (Whittington et al. 2008, Izzo et al. 2017). An integrated analysis by Izzo et al. (2017) suggested there were at least four stocks: 1) south-western Australia; 2) South Australia; 3) south-eastern Australia; and 4) eastern Australia. There is also evidence that two separate spawning groups occur off eastern Australia: a northern group off southern Queensland and northern NSW, and a southern group off southern NSW to Tasmania (Sexton et al. in press).

Commercial fishing for Sardine in Australia began in the 1800s (Kailola et al. 1993), however combined national catches did not exceed 1,000 t until the 1970s. Purse-seine fisheries developed off south-western Western Australia and South Australia in the 1980s and 1990s, respectively (Kailola et al. 1993, Ward and Staunton-Smith 2002). Mass mortality events in 1995 and 1998/9 caused by a herpesvirus reduced the adult biomass of Australian Sardine populations by ~70% (Ward et al. 2001b, Gaughan et al. 2004). The fishery off South Australia recovered quickly and is now Australia's largest fishery by weight, with a total catch of over 40,000 t in 2017 (Ward et al. 2017). In contrast, the fishery off Western Australia has remained relatively small, with a total catch of approximately 1,500 t in 2014 (Fletcher and Santoro 2015). Off eastern Australia, the annual catch of Sardine increased rapidly during the early 2000s, peaking at almost 5,000 t in 2008/09, but since then has declined due to a variety of factors that have reduced the level of fishing effort (Izzo et al. 2017, Ward and Grammer 2017).

In Australia, Sardines spawn in open waters between the coast and shelf break (Blackburn 1950, Fletcher and Tregonning 1992, Fletcher et al. 1994). They are serial spawners with asynchronous oocyte development and indeterminate fecundity. Spawning peaks in winter–early spring in the northern part of its range, off southern Queensland and northern NSW and in summer further south (Sexton et al. in press).

The DEPM has been used to estimate the spawning biomass of Australian Sardine in South Australia since 1995 (Ward et al. 2017). During 2014, DEPM surveys for Sardine were undertaken off eastern Australia during both summer and winter/spring (Ward et al. 2015b, 2015c). The summer survey in January 2014 from southern NSW to central Tasmania estimated the spawning biomass to be approximately 11,000 t (Ward et al. 2015b). The winter/spring survey in August/September 2014 between southern Queensland and NSW estimated the spawning biomass to be approximately 50,000 t (Ward et al. 2015c).

1.5 Need

The SPF Harvest Strategy specifies that estimates of spawning biomass obtained using the DEPM are used to set RBCs and TACs for each species and sub-area. Prior to this study, the DEPM had been applied to all SPF target species in the East sub-area, and to Blue Mackerel in the West Sub-area, but not to Jack Mackerel or Redbait in the West sub-area.

The need to apply the DEPM to Jack Mackerel and Redbait in the West sub-area increased when a factory trawler entered the SPF in 2014/15 and began taking both species in both sub-areas (Ward and Grammer 2017). As the factory-trawler operated in the part of the West sub-area between western Kangaroo Island, South Australia and south-western Tasmania, this area was identified as the region in which the DEPM surveys of Jack Mackerel and Redbait should be conducted.

A DEPM survey for Jack Mackerel was conducted between western Kangaroo Island, South Australia and south-western Tasmania in December 2016 to February 2017. A DEPM survey for Redbait was conducted in this area in October 2017. The present report documents the findings of the survey for Jack Mackerel.

1.6 Objectives

1. Determine distribution and abundance of eggs and larvae of Jack Mackerel and Sardine between western Kangaroo Island, South Australia and south-western Tasmania.
2. Estimate adult reproductive parameters of Jack Mackerel during the peak spawning period between western Kangaroo Island and south-western Tasmania.
3. Estimate the spawning biomass of Jack Mackerel and Sardine between western Kangaroo Island, South Australia and south-western Tasmania

The original proposal for this study did not include application of the DEPM to Sardine. This species was added to the objectives when it became evident that significant numbers of eggs of Sardine were present in the plankton samples. Information on the distribution of eggs and larvae obtained in this study provides important insights into the stock structure of both Jack Mackerel and Sardine off southern Australia.

2 METHODS

2.1 Total Daily Egg Production

2.1.1 Ichthyoplankton surveys

During the summer of 2016/17, ichthyoplankton samples were collected from the *RV Ngerin* in shelf waters between western Kangaroo Island, South Australia and south-western Tasmania (Figure 1). The first leg of the survey was conducted during 2–12 December 2016 between western Kangaroo Island and Portland, Victoria. The second leg was conducted from 25 January to 6 February 2017 and covered the area between Portland and south-western Tasmania (Figure 1). These two legs are collectively called the 'main survey' and included 44 transects and 306 sites (Figure 1).

During 30 January to 3 February 2017, ichthyoplankton samples were also collected opportunistically from the *FV Western Alliance* in Bass Strait and along the coast of north-eastern Tasmania (Figure 1). These 41 exploratory sites were sampled to determine if Jack Mackerel and/or Sardine spawn in Bass Strait during summer. This opportunistic sampling was done because eggs and larvae of both species were collected from eastern Bass Strait and off eastern Tasmania during an ichthyoplankton survey in the summer of 2014 (Ward et al. 2015b). The main survey combined with the opportunistic sampling sites is referred to as the 'extended survey' and includes 347 sites (Figure 1). Estimates of spawning biomass presented in this report are based on the results of the extended survey.

2.1.2 Plankton sampling

Paired bongo nets (0.6 m internal diameter, 500 µm mesh, plastic cod-ends) were deployed to 10 m above the sea floor or to a maximum depth of 200 m and retrieved vertically at ~1 $m \cdot s^{-1}$. Water temperature profiles were recorded with a Sea-Bird™ Conductivity-Temperature-Depth (CTD) attached to the nets (main survey only). General Oceanics™ 2030 flow-meters and factory calibration coefficients were used to estimate the distance travelled by the nets during each tow. If there was >5% difference between the paired flow-meters, then the relationship between wire length released and flow-meter units was used to determine which meter was more accurate, and that value was used for both nets. At each sampling site, plankton collected in the paired net cod-ends were combined into one sample and fixed in a 5% buffered formalin and seawater solution. At every second site on every second transect, a duplicate sample was collected for genetic validation; the paired cod-ends were combined and preserved in 95% ethanol. Exploratory samples collected in Bass Strait were fixed in formalin only. Location, sampling date/time, and depth were also recorded for each plankton sample.

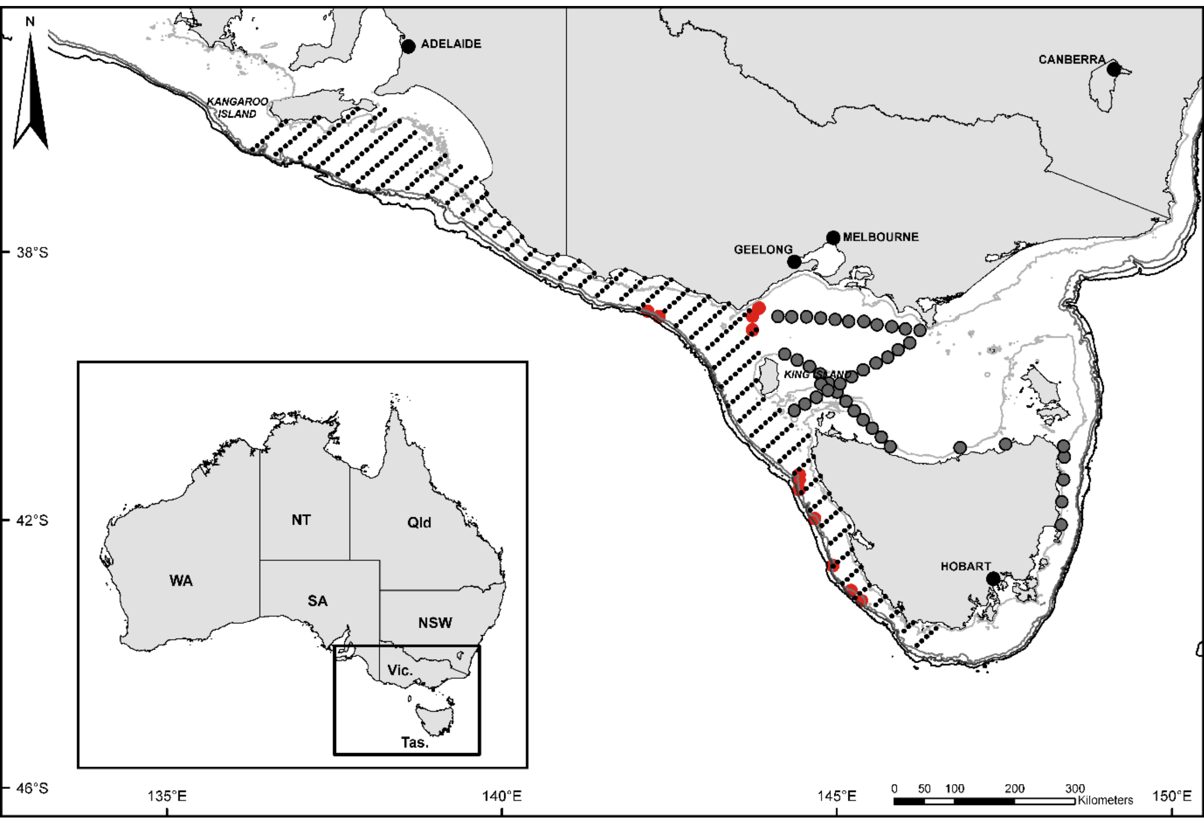

Figure 1: DEPM survey area along the continental shelf of south-eastern Australia. Locations are shown of the main survey sites (black dots), opportunistic sites in Bass Strait (grey dots), and adult trawl sites (red dots).

2.1.3 Egg identification and validation

Eggs of Jack Mackerel and Sardine were identified using the morphological features in published descriptions for the same or closely related species (Table 2). Identifications of Jack Mackerel eggs preserved in ethanol were validated using the molecular techniques developed by Perry (2011) and refined by Neira et al. (2015). These results were used to evaluate the morphological identification of the formalin preserved samples. This validation was done because Jack Mackerel eggs have similar characteristics to other common species, especially Yellowtail Scad (*Trachurus novaezelandiae*) (See Appendix 1).

All eggs were staged using the 'universal' egg staging method described by Ward et al. (2018) (Figure 2). The distinctive developmental characteristics of the 'universal' stages help to reduce staging errors in the laboratory. Stages also have a similar duration (Ward et al. 2018). Total counts of eggs per stage per sample were recorded.

Table 2. References used to identify the eggs of Jack Mackerel and Sardine and for species-specific egg temperature-development rates.

Species	Egg identification Reference: Species	Egg temperature-development rates Reference: Species
Jack Mackerel	Ahlstrom and Ball (1954): *Trachurus symmetricus* Crossland (1981): *T. declivis* Cunha et al. (2008): *Trachurus trachurus* Ward et al. (2015): T. declivis	Cunha et al. (2008): *T. trachurus*
Sardine	Lo et al. (1996): *Sardinops sagax* White and Fletcher (1998): *S. sagax* Neira et al. (1998): *S. sagax*	Lo et al. (1996): *S. sagax*

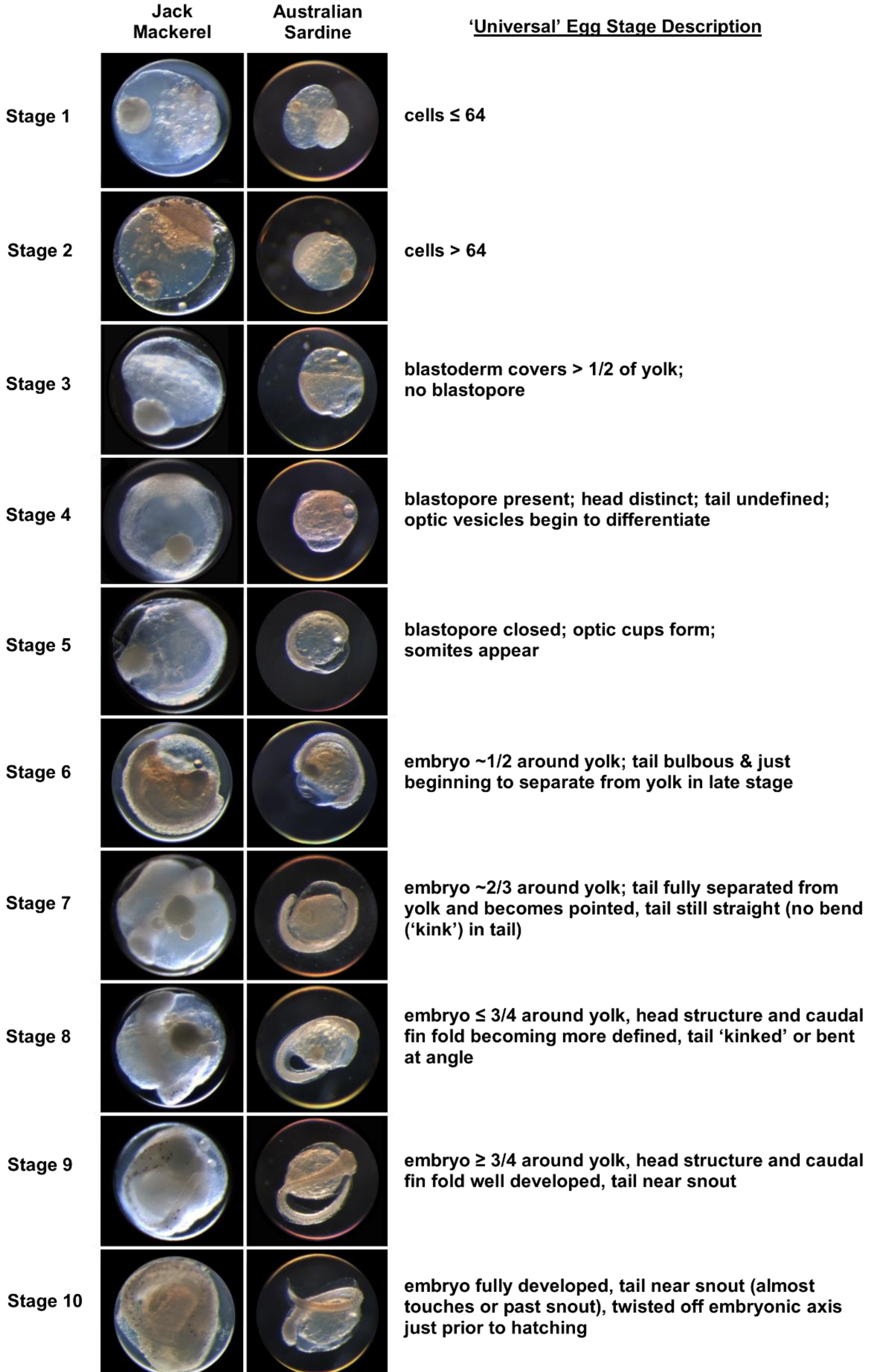

Figure 2. Representative egg stages of Jack Mackerel and Sardine using the 'universal' egg stages of Ward et al. 2018.

2.1.4 Egg ageing and treatment of zero count egg samples

Egg samples were binned into three temperature bands, based on the CTD temperature data (main survey) and a hull-mounted temperature sensor (opportunistic sites), that covered the range of temperatures typically sampled in DEPM surveys off eastern and southern Australia (14–18°C, 18–22°C, and 22–26°C). The temperature bins made the staged survey eggs comparable to published temperature egg development rates from the same or a closely related species (Table 2). These rates were used to assign a mean age to each egg (Ward et al. 2018). Generally, pelagic marine fish eggs of about 1 mm diameter hatch in about 48 hours at temperatures of 18-22°C, >48 hours in waters <18°C and <36 hours in waters >22°C (Pauly and Pullin 1988).

After the eggs were given a mean age, eggs in each sample were aggregated into daily cohorts by stage. This is done because more than one night's spawning could be represented in a sample. Total egg count and average age for each daily cohort was calculated by assigning each egg stage to a day of spawning (e.g. day 0, day 1, day 2), summing the number of eggs, and averaging their ages across stages within the daily cohort. Average cohort ages were weighted by the number of eggs observed in each stage.

Samples were also identified where a zero count should (and should not) be allocated to one or more daily egg cohorts (Ward et al 2018). Samples with no eggs were excluded from the analyses and were not considered part of the spawning area. Samples with eggs could contain several possible combinations of daily cohorts depending on the ambient water temperature, the spawning time and sampling time: (i) eggs of age <1 day (most recent cohort) and no eggs from older cohorts; (ii) no eggs of age <1 day and some eggs from older cohorts; or (iii) eggs of age <1 day and eggs from older cohorts. Since spawning occurs each night, zero counts were allocated for daily cohorts where the cohort was expected, but not found, in the sample.

2.1.5 Egg density (P_s)

The density of eggs under one square metre of water (P_s) was estimated for each sample (Equation 2, Table 3).

Table 3. Equations used to estimate mean daily egg production (P_0) and instantaneous egg mortality rate (z) for Jack Mackerel and Sardine.

Model Name	Equation	Eq. No.	Parameters	Reference
Egg Density (sample)	$P_s = \frac{C\,D}{V}$	(2)	P_s: density of eggs in a sample C: number of eggs of each age in each sample V: volume of water filtered (m^3) D: depth (m) of net cast	Smith and Richardson (1977)
Exponential egg mortality model (P_0)	$P_t = P_0 e^{-z\,t}$	(3a)	P_t: egg density at age t z: the instantaneous rate of daily egg mortality	Lasker (1985)
Non-linear Least Squares regression	$nls(P_t \sim P_0 e^{-z\,t})$	(3b)	P_t: egg density at age t z: the instantaneous rate of daily egg mortality	
Log-Linear				
Negatively biased estimate (P_b)	$\ln P_{i,t} = \ln P_b - z\,t$	(4a)	P_b: negatively biased P_0 $P_{i,t}$: density of eggs of age t at site i z: instantaneous rate of daily egg mortality	Picquelle and Stauffer (1985)
Bias corrected (P_0)	$P_0 = e^{\ln P_b + \sigma^2/2}$	(4b)	P_b: negatively biased estimate of daily egg production σ^2: variance of P_b estimate	
Generalised Linear Models (GLMs) with error structures of: negative binomial, quasi, and quasi-Poisson	$E[P_0] = g^{-1}(-zt + \varepsilon)$	(5)	E[P_0]: expected value of P_0 g^{-1}: inverse-link function zt: the instantaneous rate of daily egg mortality at age t ε: error term	Wood (2006), Ward et al. (2011, 2018)

2.1.6 Spawning area (*A*)

The Voronoi natural neighbour (VNN) method (Watson 1981) was applied using the 'deldir' function in the R package deldir (Turner 2015; R 3.4.1) and used to generate a polygon around each sampling site with the boundary as the midpoint equidistant between each sampling site (Figure 3). The area represented by each site (km^2) was determined using the 'areaPolygon' function in the geosphere R package (Hijmans 2015). The VNN tessellations could not be applied to the exploratory sampling sites due to their spacing. The mean area of individual main survey sites was used to calculate the additional spawning area of these exploratory sites. This was considered appropriate as the main sampling sites were spaced about 9 km × 28 km apart and therefore provided a consistent spawning area per site. The spawning area (*A*) was defined as the total area of grids where live Jack Mackerel or Sardine eggs were collected.

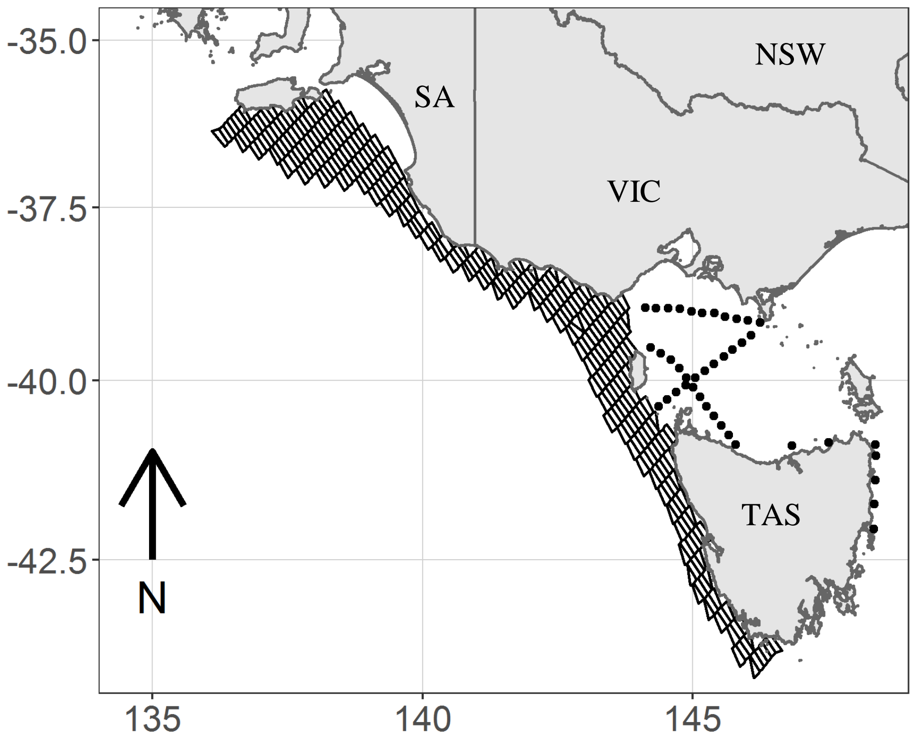

Figure 3. Voronoi natural neighbour polygons used to estimate spawning area within the main survey + exploratory sites. Dots: area estimated for exploratory sampling sites outside main survey area.

2.1.7 Daily egg production (P_0) and egg mortality (z)

P_0 is the mean daily density of eggs produced per unit area within the spawning area (eggs·m^{-2}·day^{-1}). Prior to estimating P_0, total egg density for each daily cohort was weighted by the relative size of each sampling area (i.e. area of a site in the VNN tessellation). Daily cohort egg densities and their average ages were used to estimate P_0.

Based on the findings of Ward et al. (2018), five different models were fitted to estimate mean daily egg production (P_0) and instantaneous egg mortality rate (z, day^{-1}). P_0 and z are difficult to estimate precisely (e.g. Stratoudakis et al. 2006, Bernal et al. 2012, Dickey-Collas et al. 2012, Ward et al. 2018). The distributions of daily cohort egg densities may vary among species and surveys; different models may be suitable for different datasets (Ward et al. 2011, Ward et al. 2018).

The underlying model used to calculate mean daily egg production (P_0) was the exponential egg mortality model (Equation 3a, Table 3). The model was applied in several ways. Non-linear least squares regression was used to fit Equation 3a (Equation 3b, Table 3). A linear version of the exponential egg mortality model (Equation 4a) with a bias correction factor (Equation 4b, Table 3) was also used, which we refer to as the 'log-linear model'. The linear version of the exponential model requires bias correction as the uncorrected model has a strong negative bias (Picquelle and Stauffer 1985). For more complex error distributions, data were fitted using three general linear models (GLMs, Equation 5, Table 3). Models were fitted using three different error structures: negative binomial, quasi and quasi-Poisson. The different GLMs are referred to using the error structures as descriptors. Negative binomial and quasi error structures are considered suitable for over-dispersed data, such as egg density by age (e.g. Ward et al. 2011, 2018). Instantaneous egg mortality rate (z) was estimated as a free parameter in each of the models (Table 3).

All five of the models ('Log-Linear', 'Non-linear Least Squares', 'Negative Binomial GLM', 'Quasi GLM', 'Quasi-Poisson GLM') were fitted to the egg samples for both Jack Mackerel and Sardine. Model choice for each survey followed recommendations by Ward et al. (2018). The mean value of egg production calculated from four models that provided plausible estimates of z was used to estimate spawning biomass for Jack Mackerel, while the value of egg production from the log-linear model was used to estimate spawning biomass for Sardine.

2.2 Adult Reproductive Parameters

2.2.1 Sampling methods

Adult Jack Mackerel were sampled using a modified demersal trawl net deployed from the *FV Western Alliance* in shelf and slope waters between Portland, Victoria and western Tasmania from 30 January to 3 February 2017 (Figure 1). Four of the 12 trawls caught substantial amounts of Jack Mackerel, but most specimens were small and immature. Adult Sardine were not collected during the survey.

2.2.2 Parameter estimation methods

Too few mature Jack Mackerel were collected during the trawl survey to estimate adult reproductive parameters. Instead, adult reproductive parameters used to calculate spawning biomass were obtained from the survey of Jack Mackerel conducted off south-eastern Australian during the summer of 2014 (Ward et al. 2015b).

Values of adult reproductive parameters of Australian Sardine used to calculate spawning biomass were obtained from surveys conducted off South Australia between 1998 and 2016.

The following sections describe the methods used to estimate adult parameters in the 2014 Jack Mackerel survey and 1998-2016 South Australian Sardine surveys. When adult Jack Mackerel were collected, the ovaries of mature females were removed, labelled and fixed in a 10% formalin-seawater solution. Females (sans ovaries) and mature males were labelled and frozen for laboratory processing. A similar process has been used for Australian Sardine, however, mature females were preserved whole in the formalin solution rather than only the ovaries.

Female weight (*W*)

In the laboratory, mature females from each sample were removed from formalin or thawed and weighed (± 0.01 g). Fixation in formalin has a negligible effect on fish weight (Lasker 1985). The mean weight of mature females in the population was calculated from the average of sample means weighted by proportional sample size (Equation 6, Table 4). Mature males in each sample were thawed and weighed (± 0.01 g).

Batch fecundity (F)

Batch fecundity was estimated from ovaries containing hydrated oocytes using the methods of Hunter and Macewicz (1985). Both ovaries were weighed and the number of hydrated oocytes in three weighed ovarian sub-sections counted. The total batch fecundity for each female was calculated by multiplying the mean number of oocytes per gram of ovary segment

by the total weight of the ovaries. The relationship between female weight (ovaries removed) and batch fecundity was determined by linear regression and used to estimate the mean batch fecundities of mature females in all samples.

Sex ratio (*R*)

The mean sex ratio of mature individuals in the population was calculated from the average of sample means weighted by sample size (Equation 7a and 7b, Table 4).

Spawning fraction (*F*)

Ovaries of mature females were processed using standard histological procedures and stained with haematoxylin and eosin. Several sections from each ovary were examined to determine the presence/absence of post-ovulatory follicles (POFs). POFs were aged according to the criteria developed by Hunter and Goldberg (1980) and Hunter and Macewicz (1985), and refined by Ganias (2012). The spawning fraction of each sample was calculated as the mean proportion of females with hydrated oocytes plus day-0 POFs (*d*0) (assumed to be spawning or have spawned on the night of capture), day-1 POFs (*d*1) (assumed to have spawned the previous night) and day-2 POFs (*d*2) (assumed to have spawned two nights prior) (Equation 8a, Table 4). The mean spawning fraction of the population was calculated from the average of sample means weighted by proportional sample size (Equation 8b, Table 4).

Table 4. Details of the equations used for the adult parameters of Jack Mackerel and Australian Sardine to estimate spawning biomass.

Adult Parameter	Equation	Eq. No.	Parameters	Reference
Female Weight	$W = \overline{\left[\frac{\overline{W_i}\, n_i}{N}\right]}$	(6)	$\overline{W_i}$: mean female weight of each sample *i*; *n*: number of fish in each sample *N*: total number of fish collected in all samples	Lasker (1985)
Sex Ratio: sample	$\overline{R_i} = \frac{F_i}{F_i + M_i}$	(7a)	F_i: total weight of mature females in each sample *i* M_i: total weight of mature males in each sample *i*	Lasker (1985)
Sex Ratio: population	$R = \overline{\left[\frac{\overline{R_i}\, n_i}{N}\right]}$	(7b)	$\overline{R_i}$: mean sex ratio of each sample *n*: number of fish in each sample *N*: total number of fish collected in all samples and	Lasker (1985)
Spawning Fraction: sample	$\overline{S_i} = \frac{d0 + d1 + d2}{3\, n_i}$	(8a)	*d*0, *d*1 and *d*2: the number of mature females with POFs aged day 0, 1 or 2 in each sample n_i: is the total number of females within a sample.	Lasker (1985)
Spawning Fraction: population	$S = \overline{\left[\frac{\overline{S_i}\, n_i}{N}\right]}$	(8b)	$\overline{S_i}$: mean spawning fraction of each sample *n*: number of fish in each sample *i* *N*: total number of fish collected in all samples	Lasker (1985)

2.3 Spawning Biomass (*SB*)

Jack Mackerel

Spawning biomass for Jack Mackerel was calculated according to Equation 1 (Table 1) using the mean value of P_0 obtained from the four models, spawning area (*A*) of the extended survey and adult parameters for *R, F, S,* and *W* estimated from the 2014 Jack Mackerel survey in south-eastern Australia.

Sardine

Spawning biomass for Sardine was similarly calculated using the mean value of P_0 obtained from the log-linear model fit, spawning area (*A*) of the extended survey, and adult parameters for *R, F, S,* and *W* estimated from Australian Sardine DEPM surveys in South Australia form 1998–2016.

2.4 Sensitivity Analysis

Sensitivity analyses were conducted to assess the effects of varying the parameter values used to calculate spawning biomass on the estimate of spawning biomass. The sensitively analysis focuses on the parameters of the extended survey. Each parameter in Equation 1 was varied in turn, while keeping all other variables constant. Estimates of adult parameters for the sensitivity analyses were minimum and maximum values taken from the 2014 Jack Mackerel survey off south-eastern Australia and from Sardine surveys in South Australia between 1998 and 2016. The minimum value used for spawning area (*A*) was the *A* of the main survey in our current study. The maximum *A* value an estimate of the total spawning area of the SPF West sub-area from 146°30'E to Kangaroo Island. This was calculated by estimating the unsampled area of Bass Strait west of 146°30'E (~35,400 km^2) and multiplying that by the percentage of opportunistic sites containing live eggs for each species (54% for Jack Mackerel and 78% for Sardine). Values of egg production (P_0) resulted from egg production models for each species in the current extended survey. The P_0 value from the 2014 DEPM off south-east Australian was added as an additional comparison for Jack Mackerel.

3 RESULTS

3.1 Jack Mackerel

A total of 639 live Jack Mackerel eggs were collected at 55 of 347 sites in the extended survey. Within the main survey, 508 live eggs were collected at 33 sites. At the exploratory sites, 131 live eggs were collected at 22 sites. Bottom depths where live eggs were collected ranged from 38–179 m (mean: 75.1 m), and SSTs were 16.0–20.4°C (mean 17.6°C). Molecular identification of Jack Mackerel eggs from ethanol preserved samples in the main survey confirmed these findings (Appendix 1).

3.1.1 Egg density (P_t)

Egg densities were highest north-west of King Island (TAS), south-east of Kangaroo Island and in Bass Strait (Figure 4). The majority of eggs (P_t >10 eggs·m^{-2}) were collected at sites where the bottom depth was 48–97 m (mean: 73.6 m). The highest density of eggs was north-west of King Island (154 eggs·m^{-2}). Most Jack Mackerel eggs were collected at sites with SST ranging from 16.0–19.6°C (mean 17.5 °C). The mean SST for sites with eggs north-west of King Island was 17.9 °C; the mean SST where eggs occurred off Kangaroo Island was 16.6 °C. In Bass Strait, the mean temperature where eggs were collected was 17.4 °C.

3.1.2 Spawning area (A)

The estimated spawning area for Jack Mackerel in the extended survey was 13,898 km^2, comprising 15.9% of the total area sampled (87,374 km^2, Table 5). The main survey covered 77,051 km^2 with a spawning area of 8,358 km^2 (10.8%, Table 5). The spawning area around Kangaroo Island was 2,789 km^2 of the extended survey spawning area (20%; A excluding Kangaroo Island: 11,109 km^2).

Table 5. Spawning Area (A) and total area surveyed for Jack Mackerel in the main survey and with the addition of the Bass Strait exploratory sites (extended survey).

Region	Survey Area (km^2)	Spawning Area (A)	Area with Eggs (%)
Extended Survey	87,374	13,898	15.9
Main Survey	77,051	8,358	10.8

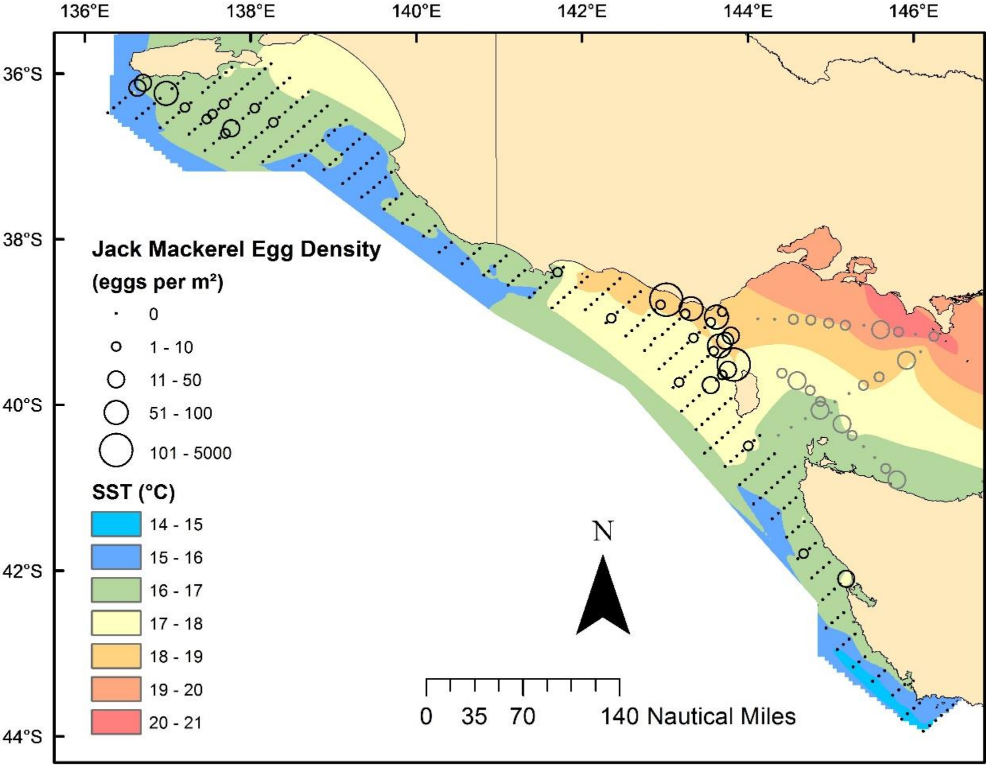

Figure 4. Spatial patterns of Jack Mackerel egg distribution and abundance between December 2016 and February 2017. Black circles are egg density (eggs·m^{-2}) in main survey area. Grey circles are egg density from exploratory sites in Bass Strait. Sea surface temperature (SST) data in Bass Strait for the exploratory sites a hull-mounted temperature sensor.

3.1.3 Daily egg production (P_0) and egg mortality (z)

The estimate of mean daily egg production (P_0) for the extended survey was 9.6 eggs·day^{-1}·m^{-2} (95% CI: 3.7–21.2) and instantaneous daily egg mortality (z, day^{-1}) was 0.18 (Table 6, Figure 5). These values were calculated by averaging the results from the non-linear least squares and the three GLM model fits, since the log-linear model produced a biologically unrealistic mortality estimate (-0.01; Table 6, Figures 5 and 6).

Table 6. Point estimates of mean daily egg production (P_0, eggs·day^{-1}·m^{-2}) and instantaneous daily mortality (*z,* day^{-1}) for Jack Mackerel in the extended survey generated by the five egg production models fits.

Egg Production Model	Extended Survey		Main Survey	
	P_0 eggs·day^{-1}·m^{-2} (95% CI)	**z day^{-1}**	**P_0 eggs·day^{-1}·m^{-2}**	**z day^{-1}**
Log-Linear	4.7 (3.1–10.3)	-0.005	6.6	0.029
Non-linear Least Squares	8.8 (4.0–16.0)	0.124	12.2	0.182
Quasi GLM	10.4 (3.5–25.7)	0.228	15.5	0.336
Quasi-Poisson GLM	8.9 (3.6–18.1)	0.156	12.5	0.228
Negative Binomial GLM	10.3 (3.5–25.1)	0.221	15.3	0.329
Mean of all model fits excluding Log-Linear	**9.6 (3.7–21.2)**	**0.182**	13.9	0.269

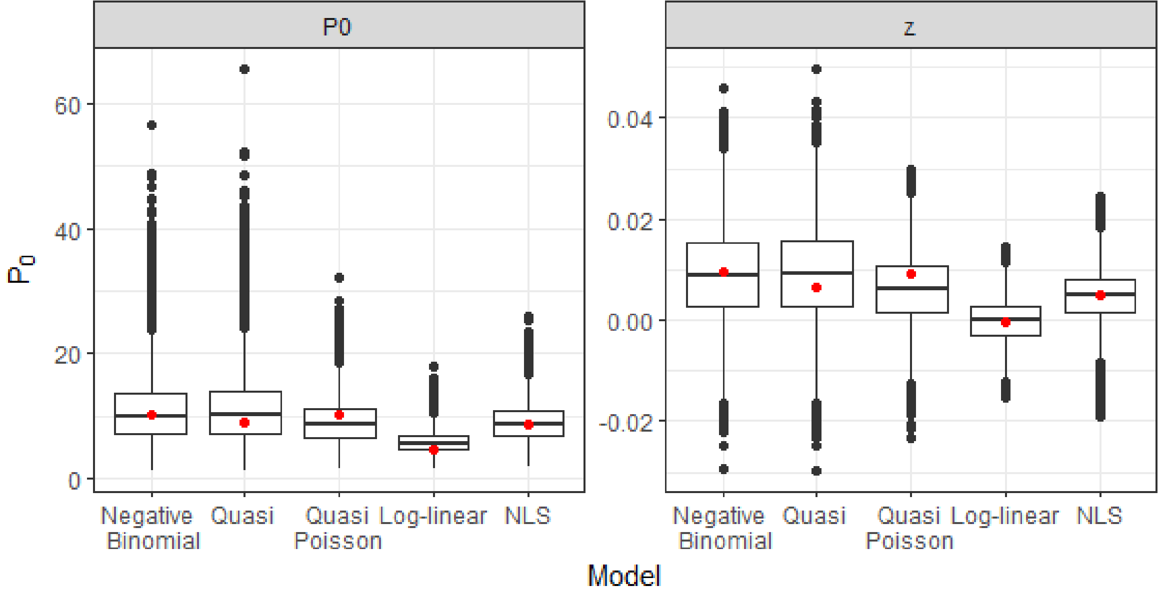

Figure 5. Estimates of mean daily egg production (P_0, eggs·day^{-1}·m^{-2}) and instantaneous daily mortality (*z,* day^{-1}) for Jack Mackerel in the extended survey from the five egg production models fits. NLS: Non-linear Least Squares.

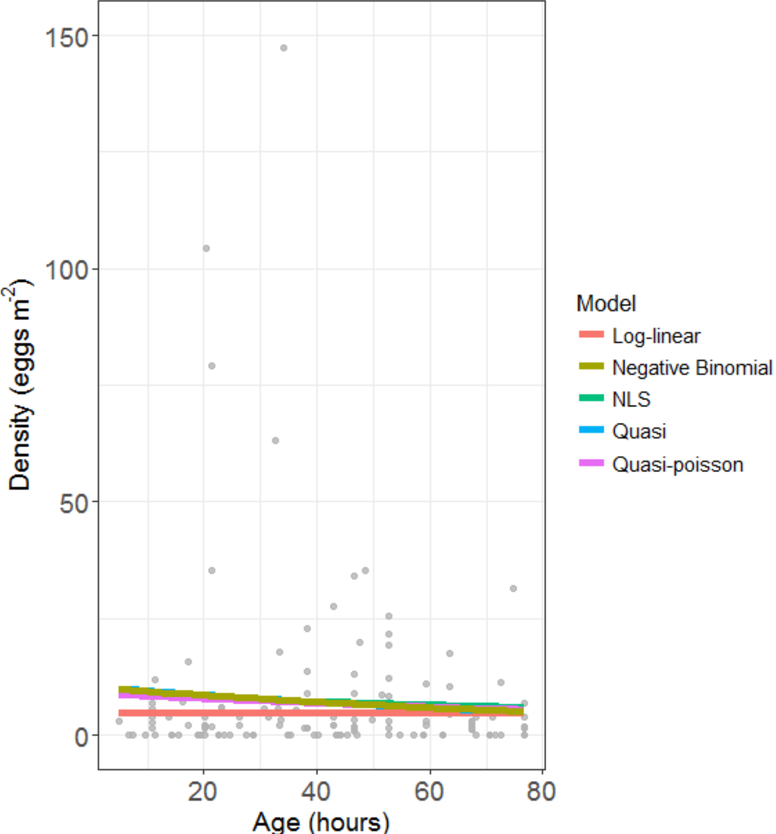

Figure 6. Egg production model fits to cohort egg densities (eggs·m^{-2}) plotted by egg age (hours) for Jack Mackerel. NLS: Non-linear Least Squares.

3.1.4 Female weight (*W*)

Four of the 12 trawls undertaken from the *FV Western Alliance* caught significant numbers of Jack Mackerel. Most Jack Mackerel caught were small and juvenile; the catch during the only shot with large adults was small. Data from the south-eastern Jack Mackerel DEPM survey in 2014 (Ward et al. 2015b) were used to estimate the reproductive parameters of adult Jack Mackerel (Table 7). The mean weight of mature females collected during the Jack Mackerel survey off south-eastern Australia in 2014 was 208.8 g (Table 7).

Table 7. Mean, minimum and maximum adult parameters calculated for Jack Mackerel during the 2014 DEPM survey off eastern Tasmania and southern NSW.

Reproductive Parameter	2014 Mean (min–max)
Female Weight (*W*, g)	208.8 (133.9–250.9)
Batch Fecundity (*F*, eggs·female^{-1})	34,068 (16,599–94,743)
Sex Ratio (*R*)	0.47 (0.38–0.56)
Spawning Fraction (*S*)	0.056 (0.000–0.134)

3.1.5 Batch fecundity (*F*)

The mean batch fecundity for Jack Mackerel from south-eastern Australia in 2014 was 34,068 eggs·female^{-1} (Table 7).

3.1.6 Sex ratio (*R*)

The mean sex ratio for Jack Mackerel from south-eastern Australia in 2014 was 0.47 (Table 7).

3.1.7 Spawning fraction (S)

The mean spawning fraction for Jack Mackerel from south-eastern Australia in 2014 was 0.056 (Table 7).

3.1.8 Spawning Biomass (*SB*)

The estimate of spawning biomass for Jack Mackerel from the extended survey was 31,069 t. This value was calculated using the mean of all model fits, excluding the log-linear model, to estimate P_0 (Table 6) and the mean values of adult parameters from south-eastern Australia in 2014 (Table 7).

3.1.9 Sensitivity Analysis

The three parameters with the strongest influence on spawning biomass are spawning area, *A*, mean daily egg production P_0, and spawning fraction *S* (Figure 7). The presence of Jack Mackerel eggs in 54% of the exploratory samples in Bass Strait suggested that the survey did not cover the entire spawning area and that spawning biomass was under-estimated. If spawning occurred in 54% of the area that was not surveyed, the estimate of spawning biomass for Jack Mackerel in the West sub-area (146°30'E to Kangaroo Island) would have been ~74,000 t (Figure 7). The effects of *S* and P_0 on estimates of spawning biomass of Jack Mackerel in the current survey are small compared to the effect of spawning area.

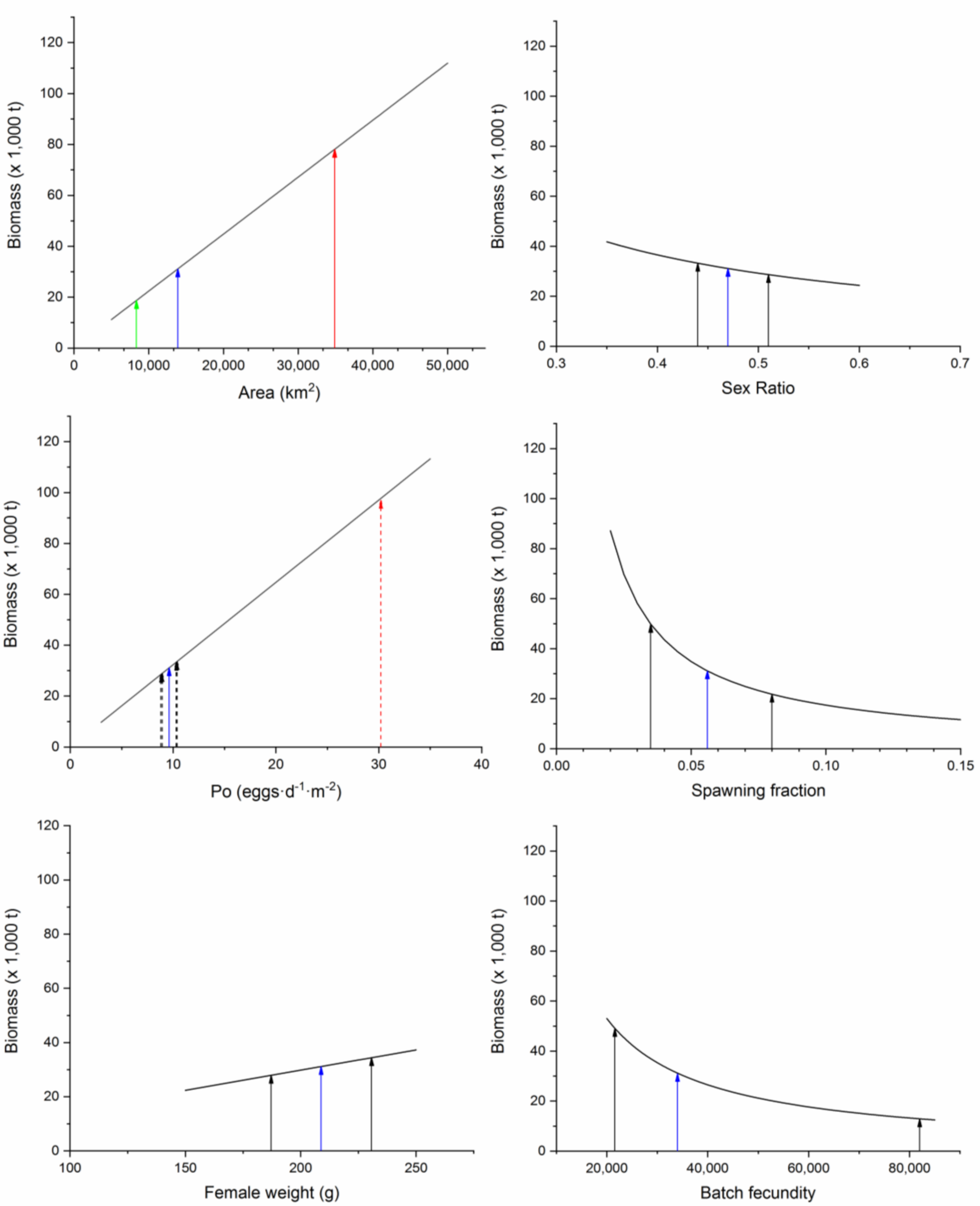

Figure 7. Sensitivity analysis of the effects of each parameter on estimates of spawning biomass of Jack Mackerel. Blue: parameters used in the current DEPM calculations to estimate spawning biomass; Green: spawning area of main survey; Red solid: estimated spawning area of SPF West sub-area from 146°30'E to Kangaroo Island; Black dashed: P_0 values from all egg production models, excluding the log-linear model. Red dashed: P_0 value from the 2014 Jack Mackerel survey; Black arrows: minimum and maximum values from the 2014 Jack Mackerel survey.

3.2 Sardine

A total of 4,837 live Sardine eggs were collected at 105 of 347 sites in the entire extended survey (Figure 8). This included 4,180 live Sardine eggs collected at 73 of the 306 sites in the main survey and 657 live eggs at 32 of the 41 opportunistic sites. Bottom depths where live eggs were collected ranged from 22–156 m (mean: 68.9 m), and SST was 15.8–20.4°C (mean 17.4°C).

3.2.1 Egg density (P_s)

Most Sardine eggs were collected from Bass Strait waters west to Portland, Victoria and in shelf waters to the south and south-east of Kangaroo Island (Figure 8). The majority (P_t >10 eggs·m^{-2}) f eggs were collected at sites where the bottom depth was 22–156 m (mean: 67.4 m). The highest density of eggs was 2,614 eggs·m^{-2} south-east of Kangaroo Island. The second highest density was 1,315 eggs·m^{-2} south-west of Cape Otway (VIC). Most Sardine eggs were collected at sites with SSTs ranging from 15.8–20.4 °C (mean 17.4°C). The mean SST of the sites with eggs between Cape Otway and King Island was 17.7°C. The mean SST of sites with eggs south and south-west of Kangaroo Island was 16.7°C.

3.2.2 Spawning area (*A*)

The estimated spawning area for Sardine in the extended survey was 26,366 km^2, comprising 30.2% of the total area sampled (87,374 km^2, Table 8). The main survey covered 77,051 km^2 with a spawning area of 18,309 km^2 (23.8%, Table 8). The spawning area around Kangaroo Island was 9,441 km^2 of the extended survey spawning area (36%; *A* excluding Kangaroo Island: 16,925 km^2).

Table 8. Spawning Area (*A*) and total area surveyed for Australian Sardine in the main survey, and with the addition of the Bass Strait exploratory sites (extended survey).

Region	Survey Area (km^2)	Spawning Area (A)	Area with Eggs (%)
Extended Survey	87,374	26,366	30.2
Main Survey	77,051	18,309	23.8

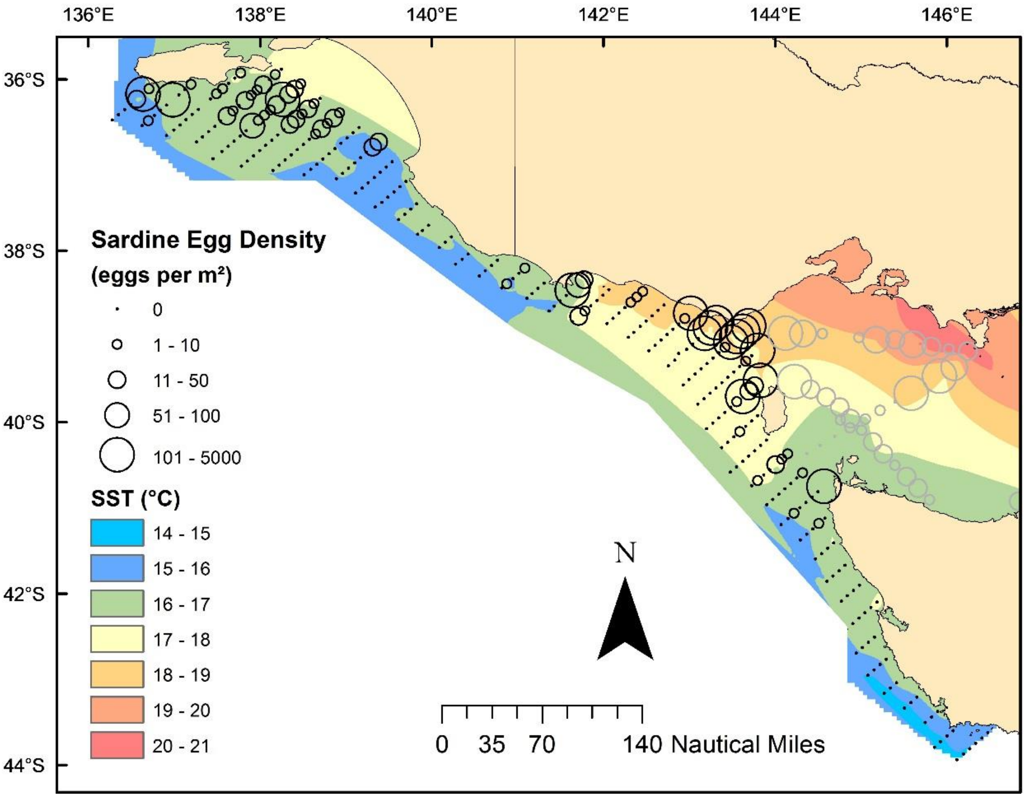

Figure 8: Spatial patterns of Sardine egg distribution and abundance between December 2016 and February 2017. Black circles are egg density (eggs·m^{-2}) in main survey area. Grey circles are egg density from opportunistic sampling in Bass Strait. Sea surface temperature (SST) data in Bass Strait are approximations from vessel surface thermometers.

3.2.3 Daily egg production (P_0) and egg mortality (z)

The estimate of mean daily egg production (P_0) for the extended survey obtained using the log-linear model was 33.2 eggs·day^{-1}·m^{-2} and instantaneous daily egg mortality was 0.33 (z, day^{-1}) (Table 9, Figures 9 and 10). Ward et al. (2018) recommended the use of the log-linear model for estimating egg production in Australian Sardine because this model is more precise and not influenced as strongly as other models by a few samples with very high densities of eggs (e.g. > 1,000 eggs·m^{-2} in some of the current survey samples; Figures 9 and 10).

Table 9. Point estimates of mean daily egg production (P_0, eggs·day^{-1}·m^{-2}) and instantaneous daily mortality (*z,* day^{-1}) for Australian Sardine in the main and extended survey generated by the five egg production models fits.

Egg Production Model	Extended Survey		Main Survey	
	P_0 eggs·day^{-1}·m^{-2}	z day^{-1}	P_0 eggs·day^{-1}·m^{-2}	z day^{-1}
Log-Linear	**33.2**	**0.33**	19.7	0.13
Non-linear Least Squares	100.0	0.45	46.4	0.21
Quasi GLM	415,942.1	4.90	264.0	1.46
Quasi-Poisson GLM	45.2	0.40	47.0	0.33
Negative Binomial GLM	263.6	1.46	88.4	0.77

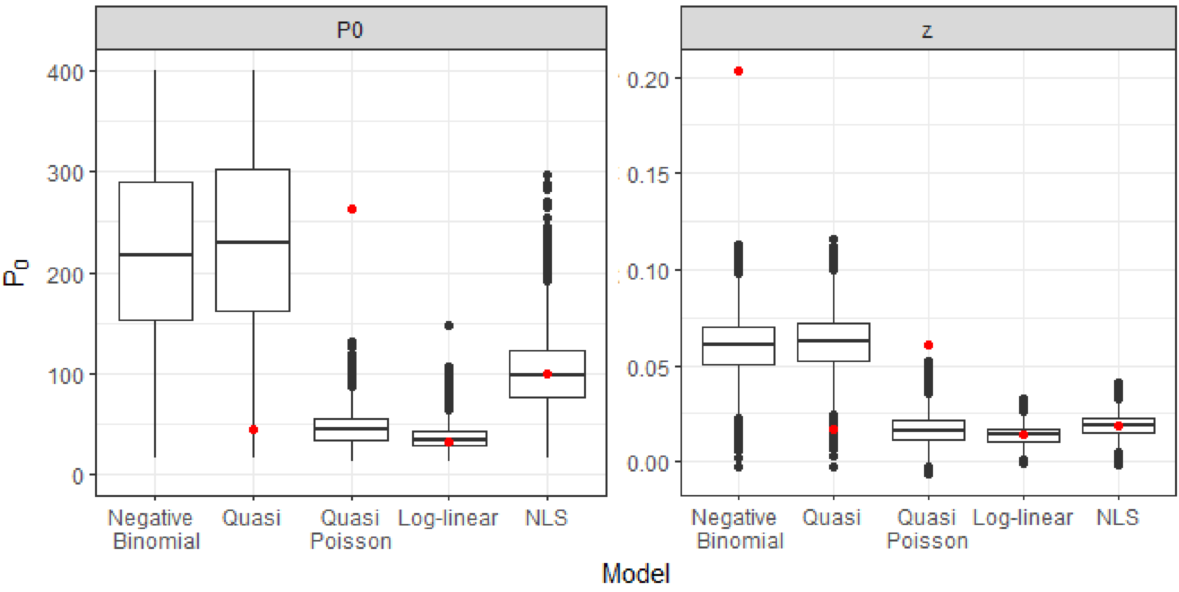

Figure 9. Estimates of mean daily egg production (P_0, eggs·day^{-1}·m^{-2}) and instantaneous daily mortality (*z,* day^{-1}) for Australian Sardine in the extended survey from the five egg production model fits. NLS: Non-linear Least Squares. Note: Extreme P_0 values (negative binomial and Quasi fits) beyond 400 eggs·day^{-1}·m^{-2} are not shown on plot.

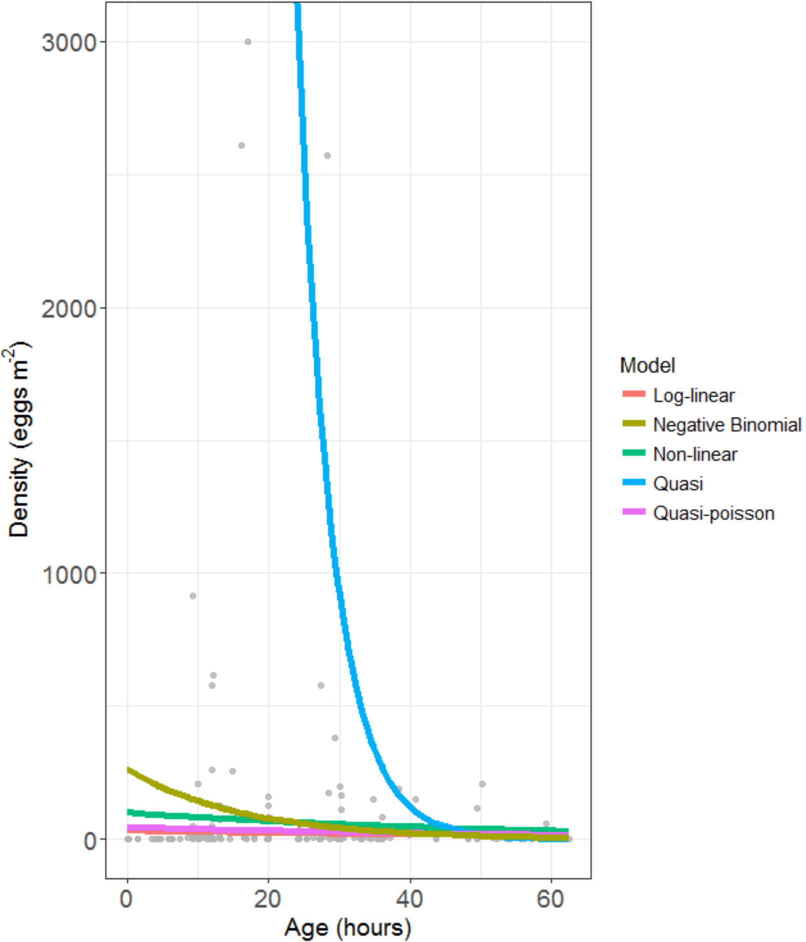

Figure 10. Egg production model fits to cohort egg densities (eggs·m^{-2}) plotted by egg age (hours) for Sardine

3.2.4 Female weight (*W*)

Adult Sardine were not collected during the survey. Data from South Australia between 1998 and 2016 were used to estimate the reproductive parameters of adult Australian Sardine (Table 10). The mean weight of mature females collected during these surveys was 57.0 g. The minimum and maximum weights were 45.2 g (1998) and 78.7 g (2004) (Table 10).

3.2.5 Batch fecundity (*F*)

The mean batch fecundity for Sardine from South Australia during 1998–2016 was 17,116 eggs·female^{-1}. The minimum and maximum values were 10,904 eggs·female^{-1} (2003) and 24,790 eggs·female^{-1} (2004) (Table 10).

Table 10. Mean, minimum and maximum adult parameters calculated for Australian Sardine from South Australian DEPM surveys between 1998 and 2016.

Reproductive Parameter	Mean (min–max)
Female Weight (*W*, g)	57.0 (45.2–78.7)
Batch Fecundity (*F*, eggs·female^{-1})	17,116 (10,904–24,790)
Sex Ratio (*R*)	0.54 (0.36–0.68)
Spawning Fraction (*S*)	0.114 (0.040–0.179)

3.2.6 Sex ratio (*R*)

The mean sex ratio for Australian Sardine collected during South Australian surveys from 1998 to 2016 was 0.54. The minimum and maximum values were 0.36 (2009) and 0.68 (2013) (Table 10).

3.2.7 Spawning fraction (S)

The mean spawning fraction for Australian Sardine collected during South Australian surveys from 1998 to 2016 was 0.114. The minimum and maximum values were 0.040 (2014) and 0.179 (2001) (Table 10).

3.2.8 Spawning Biomass (*SB*)

The estimate of spawning biomass for Sardine from the extended survey was 47,283 t. These estimates were calculated using the log-linear model to estimate P_0 (Table 9) and the mean values of adult parameters from South Australia from 1998 to 2016 (Table 10).

3.2.9 Sensitivity Analysis

The sensitivity analysis for Sardine shows the strong influence that the model used to estimate P_0 had on estimates of spawning biomass (Figure 11). Using the log-linear model for Sardine usually provides estimates that are more precise and lower (probably negatively biased) than the other models (Ward et al. 2018). In some situations, all other models produce estimates of P_0 that are implausible. The presence of Sardine eggs in 78% of the opportunistic sites in Bass Strait, suggests that the survey did not cover the entire spawning area and that spawning biomass was under-estimated. If spawning occurred in 78% of the area that was not surveyed, the estimate of spawning biomass for Sardine in the West sub-area (146°30'E to Kangaroo Island) would have been ~97,000 t (Figure 11).

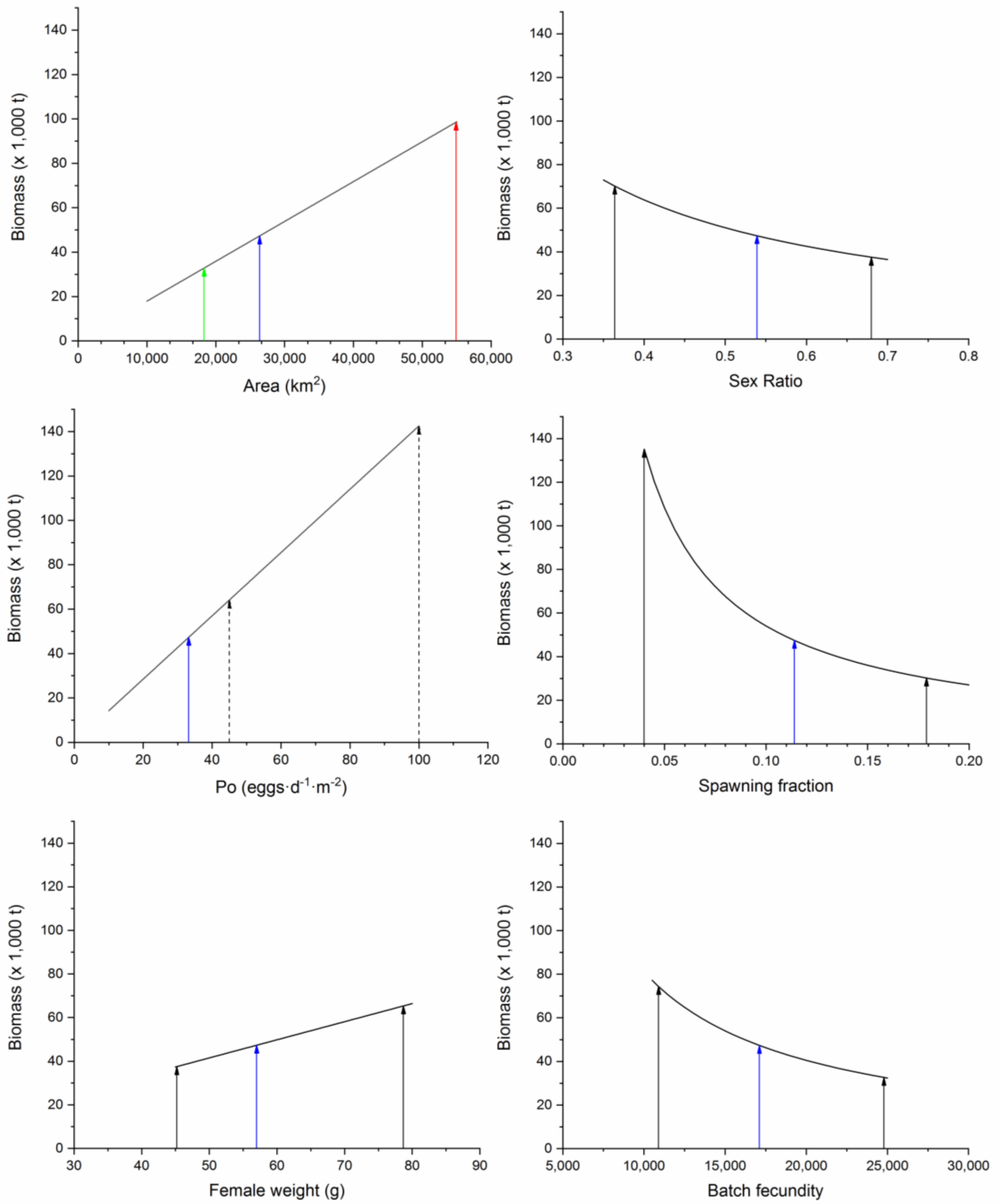

Figure 11. Sensitivity analysis of the effects of each parameter on estimates of spawning biomass of Sardine. Blue: parameters used in the current DEPM calculations to estimate spawning biomass; Green: spawning area of main survey; Red: estimated spawning area of SPF West sub-area from 146°30'E to Kangaroo Island; Dashed: P_0 values from the non-linear least squares and Quasi-Poisson GLM egg production models. Black arrows: minimum and maximum values for South Australian Sardine DEPM surveys between 1998 and 2016.

4 DISCUSSION

4.1 Distribution and stock structure

This study provides important new insights into the distribution and stock structure of Jack Mackerel off southern Australia. The presence of Jack Mackerel eggs in waters north-west of King Island (TAS) and in Bass Strait during summer has significant implications. In combination with the results of a previous survey that showed Jack Mackerel spawns off eastern Tasmania, in eastern Bass Strait and off eastern Victoria during summer (Ward et al. 2015b), these findings suggest that previous understanding of the stock structure of Jack Mackerel in Australian waters (e.g. Bulman et al. 2008) may need to be re-evaluated. Specifically, our results suggest that Bass Strait may not act as a barrier to mixing of Jack Mackerel from the East and West sub-areas of the SPF (e.g. AFMA 2009). Rather, our results suggest that a Jack Mackerel sub-population may occur vv2w off northern Tasmania and Victoria, including Bass Strait. This stock structure is similar to that identified by Izzo et al. (2017) for Sardine, a finding which was supported by the presence of Sardine eggs in Bass Strait during the present study. Both Izzo et al. (2017) and the results of the present study suggest that a Sardine sub-population occurs from western Victoria, through Bass Strait to eastern Victoria and southern NSW. Our results also suggest that a sub-population of Jack Mackerel occupies a similar area.

The discontinuity in the egg distributions of Jack Mackerel and Sardine observed in the upwelling region of the Bonney Coast suggests that for both species, this area may separate sub-populations in the GAB from those off south-eastern Australia. Izzo et al. (2017) provided clear evidence that two populations of Sardine occur off eastern Australia. Sexton et al. (in press) demonstrated the existence of two spawning groups separated by a discontinuity (egg barren) where Sardines do not spawn, even when environmental conditions (i.e. SST and depth) are suitable for spawning. In contrast, there appears to be considerable overlap in the areas where Jack Mackerel spawn during summer and winter/spring (Neira 2011), suggesting that there are not spatially distinct spawning grounds for Jack Mackerel off the east coast. It would be useful to evaluate this interpretation more thoroughly by undertaking a detailed analysis of Jack Mackerel data from historical ichthyoplankton surveys, similar to that which Sexton et al. (in press) undertook for Sardine.

4.2 Jack Mackerel

The results of both the ichthyoplankton and trawl surveys conducted in this study suggest that the spawning biomass of Jack Mackerel in waters between western Kangaroo Island and

south-western Tasmania during summer is relatively small compared to the spawning biomass off the east coast (Ward et al. 2016). Fewer eggs were collected in the current survey compared to 2014 (639 versus 3,530 eggs) from fewer sites (55 versus 117 sites). The mean estimate of P_0 obtained in the current survey (9.6 eggs·m^{-2}·day^{-1}) was low in comparison to that obtained in the 2014 survey (28.9 eggs·m^{-2}·day^{-1}). Relatively few adults were collected in the trawl survey reported in this study, whereas adult Jack Mackerel were highly abundant in every daylight trawl conducted off eastern Australia in 2014. These results are also consistent with the sporadic and localised catches of the factory trawler that operated between western Kangaroo Island, South Australia and south-western Tasmania in 2014/15 and 2015/16 (Ward and Grammer 2017).

Opportunistic sampling showed that substantial spawning occurred in western Bass Strait. The estimate of spawning biomass of ~31,000 t from the extended survey area is likely to be an under-estimate of the spawning biomass of Jack Mackerel in the West sub-area. It is likely that spawning occurred in the large area of western Bass Strait that was not surveyed. Previous studies have provided strong evidence that sizeable quantities of Jack Mackerel occur west of the study area in the Great Australia Bight (Shuntov 1969, Stevens et al. 1984, Bulman et al. 2008). For these reasons, the estimate of spawning biomass of ~31,000 t is considered to be a conservative figure for setting RBC for the West sub-area.

Approximately 20% of the Jack Mackerel spawning area identified in this study occurred off the south-western coast of Kangaroo Island, suggesting that the spawning biomass in this area may have been in the order of ~6,000 t. Recent SPF fishing activity in the West sub-area was concentrated in this location. Limiting the proportion of future catches from the West sub-area that can be taken off the south-western coast of Kangaroo Island may warrant consideration.

4.3 Australian Sardine

The estimate of spawning biomass of Sardine from the current extended survey was ~47,000 t, comprised of ~17,000 t off Kangaroo Island and ~30,000 t east of the Bonney Coast. Similar to Jack Mackerel, the presence of Sardine eggs at the opportunistic sites in Bass Strait suggests that a substantial part of the spawning area was not covered by the survey.

5 CONCLUSIONS

This is the first dedicated application of the DEPM to Jack Mackerel in the West sub-area. It provided important new insights into the stock structure of Jack Mackerel off southern Australia and confirmed a key element of the findings of a recent study of the stock structure of Sardine. Our results suggest that a distinct sub-population of each species occurs in the area between the Bonney Coast and southern NSW, including north-eastern Tasmania, and that Bass Strait is an important spawning area for both species. These findings have implications for the management of the SPF, especially the separation of the fishery into East and West sub-areas.

The estimates of spawning biomass of Jack Mackerel (31,069 t) and Sardine (47,283 t) for the portion of the West Sub-area between western Kangaroo Island and south-western Tasmania, where a factory trawler operated in 2014/15 and 2015/16 are underestimates of the spawning biomass in the West sub-area. However, exploratory ichthyoplankton sampling in Bass Strait suggested that the survey did not include key spawning habitat and under-estimated the spawning biomass of both species. Habitat modelling could be undertaken to predict the occurrence of eggs in these areas.

Future DEPM studies of the south-eastern population of each of these two species should be designed to cover the entire spawning area. Given the large size of the West Sub-area, ongoing spatial management may be needed to prevent concentration of fishing effort in small areas of the fishery. The distribution and abundance of SPF species in parts of the West sub-area located west of Kangaroo Island are poorly understood.

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APPENDICES

APPENDIX 1: Genetic identification of Jack Mackerel eggs

J P. Keane

Introduction

Identification of planktonic fish eggs to species is complex given the similarity of morphological characters that a vast number of species spawning at any one time may possess. There are over 5000 fish species in Australian waters and it is estimated that 70% of eggs are less than 1.5mm, 60% have a single oil globule and most have a smooth chorion (Ahlstrom and Moser, 1980). Identification is further complicated by the complex developmental changes from fertilisation through to hatching.

Ichthyoplankton samples are typically fixed in formalin as it results in good preservation of morphological characters (Steedman 1976). However, formaldehyde interacts with DNA making genetic identification problematic (Karaiskou et al. 2007, Goodsir et al. 2008). In contrast, ethanol is a reliable preservative for DNA but causes fish eggs to shrink and become opaque, leading to difficulties in visually identifying or assigning developmental stages to eggs (Goodsir et al. 2008). As such there is no preservation method that produces good samples for both molecular and morphological identification.

Eggs of *Trachurus declivis* (Jack Mackerel) are known to occur in shelf waters of south eastern Australia simultaneously with morphologically similar eggs of other carangids such as *T. novaezelandiae* (yellowtail scad) and *Pseudocaranx dentex* (silver trevally). The eggs of these species possess almost identical morphological characteristics apart from slightly differing but overlapping egg diameters (Neira et al. 2014). Furthermore, it is not known if eggs of other species present in the area possess similar morphological characters to *T. declivis* as the eggs of just a few fish species have been described in Australia. As a consequence morphological identification of Carangid eggs to species level remains challenging.

In this study we employ a molecular approach to identify and validate ethanol preserved eggs of *T. declivis*, as well as of eggs that possess similar morphological characteristics, to validate morphologically identified formalin preserved *T. declivis* eggs.

Methods

Samples

Ichthyoplankton samples were collected by vertical bongo hauls over two surveys in southern Australia: Survey 1, western region, (Kangaroo Island, SA, to Portland, Vic) and Survey 2 eastern region (Portland, Vic to SE Tasmania). A total of 305 sites were sampled and preserved in formalin. Replicate hauls were completed at 70 sites and captured plankton was immediately drained of excess seawater and preserved in 96% ethanol. Replicate hauls were conducted at even sites on every second transect. Ichthyoplankton samples were collected using a bongo sampler equipped with 500 µm mesh, and two 3 m long plankton nets enclosed in a purpose built, weighted stainless steel frame to facilitate vertical drops. The mouth of each net (0.6 m diameter) was fitted with a General Oceanics flowmeter to estimate total volume of water filtered during each vertical haul. The net was lowered to within 10 m of the seabed or to a maximum of 200 m. Haul speed was ca. 1.0 ms^{-1}.

Samples were sorted at the South Australian Research and Development Institute (SARDI) with eggs possessing similar morphological characters as *T. declivis* sent to the Institute for Marine and Antarctic Studies (IMAS) for validation. This included 2025 eggs from 134 sites preserved in formalin and 213 eggs from 11 sites preserved in ethanol (Table 1).

Table 1. Samples provided for *T. declivis* identification

	Formalin		Ethanol	
	Sites	Eggs	Sites	Eggs
Western region	76	993	5	57
Eastern region	58	1032	6	156
Total	134	2025	11	213

Morphometric identification

Eggs were identified using a combination of morphological characters described for *Trachurus* eggs by Ahlstrom and Ball (1954), Crossland (1981) and Cunha et al. (2008). The main diagnostic features are: a) spherical with a diameter ranging from approximately 0.70 to 1.03 mm, b) smooth chorion, c) narrow perivitelline space d) prominent segmented yolk sac (irregular and indistinct in early stages), e) single pigmented oil globule oriented posteriorly on yolk sac in later stages of development, f) stout bodied embryo with prominent melanophores along the dorsal surface. Formalin preserved eggs off south-eastern Australia were found to have a mean diameter of 0.954 mm (range 0.853–1.046 mm; Keane and Lyle 2015).

Preserved eggs were rehydrated in distilled water to better reflect diameters of fresh eggs, and measured digitally to 0.02 mm under a stereomicroscope.

Molecular identification

A molecular approach of Mitochondrial DNA (mtDNA) extraction, amplification, and sequencing for *Trachurus* spp. developed by Perry (2011) and refined by Neira et al. (2014) was employed to identify eggs of *T. declivis.* DNA extractions from eggs identified based on morphological characters were carried out using the QIAamp DNA Micro Kit (QIAGEN, USA) following the manufacturer's protocol for tissue extraction. Amplification by polymerase chain reactions (PCRs) were performed using MyTaq HSTM DNA Polymerase (Bioline) with PCR product purification and bi-directional sequencing performed by Macrogen Inc. (Seoul, Republic of Korea) (see Neira et al. 2014 for full methods). Sequences were aligned to reference data in the Fish Barcode of Life Database (BOLD) using BioEdit biological sequence alignment editor.

The number of eggs subjected to mtDNA testing varied between sites according to raw abundances of eggs morphologically identified as *Trachurus*. All such eggs were tested from sites with 10 or fewer eggs, while for sites with >10 eggs a minimum of 10 eggs were randomly selected for testing, with a minimum of 5 from each stage present. In addition, some eggs possessing similar characteristics to *Trachurus* (e.g. diameter, pigmentation) were selected if present for mtDNA testing.

Results of molecular identifications were used to aid identifications of formalin preserved eggs.

Results

A total of 72 eggs were selected for mtDNA analysis; 40 identified morphologically as *T. declivis*, 18 indeterminable, and 14 similar but morphologically different to *T. declivis* (Tables 2 and 3). Indeterminable eggs consisted of early stage eggs whose morphological characteristics were masked by ethanol preservation, making morphological identification problematic.

Of the 72 eggs subjected to molecular analyses, 61 yielded quality mtDNA. Seven of the 11 eggs that failed to yield quality mtDNA were from one site (JA2), which was reported to have preserved poorly (A. Ivey, SARDI, pers. comm.; Table 2). All eggs morphologically identified as *T. declivis* across five sites were successfully confirmed via mtDNA when quality mtDNA was present. Four eggs from an additional two sites, which were indeterminable by morphological identification, were also genetically identified as *T. declivis* (Table 2).

The mtDNA analysis also facilitated the identification of some non *T. declivis* eggs within the sample, including Barracouta (*Thyrsites atun*) and redbait (*Emmelichthys nitidus*) (Tables 2 and 3).

Using morphological characters and molecular validation results, 587 formalin preserved *T. declivis* eggs from the primary survey were identified from the 2025 eggs preliminarily sorted by SARDI (Table 4.)

Table 2. Eggs from 5 sites subjected to mtDNA genetic analysis from Survey 1, western region, (Kangaroo Island, SA, to Portland, Vic). Indeterminable refers to eggs whose morphological characteristics were masked by ethanol preservation, making morphological identification problematic. Eggs where quality mtDNA was unable to be extracted are listed as 'Fail'.

Site	Morphological ID	Stage	Diameter (mm)	Comments	Genetic ID
JA2	T. declivis	5	0.98		Fail
JA2	T. declivis	5	0.96		Fail
JA2	T. declivis	5	0.98		Fail
JA2	T. declivis	5	1		Fail
JA2	T. declivis	5	0.98		Fail
JA2	T. declivis	5	1.04		Fail
JA2	T. declivis	5	1.02		T. declivis
JA2	T. declivis	5	1.06		Fail
JA2	T. declivis	5	1.02		T. declivis
JA2	T. declivis	5	1.04		T. declivis
JC6	Unknown - Sp. A	6	0.96	Two distinct pig lines t	Thyrsites atun
JC6	Unknown	6	1	Unpigmented embryo, pigmented oil globule.	Centroberyx sp.
JC6	T. declivis	6	0.94		T. declivis
JC6	T. declivis	2	1		T. declivis
JC6	T. declivis	2	1		T. declivis
JG8	Indeterminable	2	0.9	No distinguishing characters visible	No match
JG8	Indeterminable	2	0.9	No distinguishing characters visible	T. declivis
JG8	Indeterminable	3	0.9	No distinguishing characters visible	Fail
JG8	Indeterminable	3	0.9	No distinguishing characters visible	Fail
JG8	Indeterminable	3	0.92	No distinguishing characters visible	Thyrsites atun
JG8	Indeterminable	3	0.94	No distinguishing characters visible	Fail
JG8	Indeterminable	3	0.94	No distinguishing characters visible	Centroberyx sp.
JG8	Indeterminable	3	1	No distinguishing characters visible	Thyrsites atun
JS2	Indeterminable	3	1.06	No distinguishing characters visible	T. declivis
JS2	Indeterminable	3	1.06	No distinguishing characters visible	T. declivis
JS2	Indeterminable	3	1.06	No distinguishing characters visible	T. declivis
JS2	Unknown	7	1.16	Too large for *T. declivis*	No match
JS6	Unknown - Sp. A	7	0.96	2 pig lines to snout, 2/3, pig yolk, like 21-24	Thyrsites atun
JS6	Unknown - Sp. A	7	0.96	2 pig lines to snout, 2/3, pig yolk, like 21-24	Thyrsites atun
JS6	Indeterminable	3	1	No distinguishing characters visible	Emmelichthys nitidus

Table 3. Eggs from 5 sites subjected to mtDNA genetic analysis from Survey 2, eastern region (Portland, Vic to SE Tasmania). Indeterminable refers to eggs whose morphological characteristics were masked by ethanol preservation, making morphological identification problematic. Eggs where quality mtDNA was unable to be extracted are listed as 'Fail'.

Site	Morphological ID	Stage	Diameter (mm)	Comments	Genetic ID
KD02	T. declivis	7	0.98		T. declivis
KD02	T. declivis	7	0.96		T. declivis
KD02	T. declivis	7	1		T. declivis
KD02	T. declivis	7	0.98		T. declivis
KD02	T. declivis	7	0.98		T. declivis
KD02	Unknown - Sp. A	8	0.98	Two distinct pig lines to snout	Thyrsites atun
KD02	Unknown - Sp. A	8	1.02	Two distinct pig lines to snout	Thyrsites atun
KD02	Unknown - Sp. A	8	1	Two distinct pig lines to snout	Thyrsites atun
KD02	Unknown - Sp. A	8	1	Two distinct pig lines to snout	Thyrsites atun
KD02	T. declivis	5	0.96		T. declivis
KD02	T. declivis	5	1		T. declivis
KD02	T. declivis	5	1		T. declivis
KD02	T. declivis	5	0.98		T. declivis
KD02	T. declivis	5	0.98		T. declivis
KD02	T. declivis	5	1		T. declivis
KF2	T. declivis	8	1		T. declivis
KF2	T. declivis	8	1		T. declivis
KF2	T. declivis	8	1.02		T. declivis
KF2	T. declivis	8	1.04		T. declivis
KF2	T. declivis	8	1		T. declivis
KF2	T. declivis	4	0.98		T. declivis
KF2	T. declivis	4	1.02		T. declivis
KF2	T. declivis	4	1		T. declivis
KF2	T. declivis	4	1		T. declivis
KF2	T. declivis	4	0.98		T. declivis
KF2	Lepidotrigla	6	1.26	*Lepidotrigla* characteristics. Pigmented chorion opposite embryo	Lepidotrigla sp.
KF2	T. declivis	7	0.94		T. declivis
KF6	Unknown	8	0.88	Too small for *T. declivis*	Neoplatycephalus sp.
KF6	Unknown	8	0.8	Too small for *T. declivis*	No match
KF6	Unknown	7	0.82	Too small for *T. declivis*	No match
KH2	T. declivis	8	0.96		T. declivis
KH2	T. declivis	8	0.98		T. declivis
KH2	T. declivis	8	0.96		Fail
KH2	T. declivis	8	0.96		T. declivis
KH2	T. declivis	8	0.98		T. declivis
KH2	Indeterminable	2	0.98	No distinguishing characters visible	T. declivis
KH2	Indeterminable	3	0.94	No distinguishing characters visible	Centroberyx sp.
KJ6	Unknown	6	1.04	Pigment just forming. No sign of segmentation.	Thyrsites atun
KP4	Indeterminable	3	1	No distinguishing characters visible	Emmelichthys nitidus
KP4	Indeterminable	3	1	No distinguishing characters visible	Fail
KP4	Indeterminable	3	0.9	No distinguishing characters visible	Thyrsites atun
KP4	Indeterminable	3	0.9	No distinguishing characters visible	Thyrsites atun

Table 4. Counts of morphologically identified *T. declivis* eggs at each developmental stage. Only positive sites listed.

Site	Stage 1	Stage 2	Stage 3	Stage 4	Stage 5	Stage 6	Stage 7	Stage 8	Stage 9	Stage 10	Total
JA1					2		17				19
JA2				1	2		3				6
JB3					11	2	2	4	16		35
JC9		5									5
JD11			1				2			1	4
JD12			2			1			2		5
JD8			8								8
JD9			1				6		1		8
JE10		1									1
JE11				1	3		10				14
JE12				1							1
JE7		3			1						4
JF7										2	2
JG5								1			1
JG8		1									1
JS2					4						4
JS7	10				1						11
KA8	1	1									2
KC7	4										4
KD2	2				63			1			66
KD3	4					2					6
KE1	2					39					41
KE2						1					1
KF1					1			2	1		4
KF2				4	22		2	10			38
KF3				4	1						5
KF4					1						1
KF6									2		2
KG1							1	4	5		10
KG2					4	4	5	5	1		19
KG3					2		2	1	25	5	35
KG4						1				1	2
KG10		3	3	3	1						10
KH1	1	1		2			17	68			89
KH2		1				1	13	6			21
KH3								1	1		2
KH4				33	2						35
KH5				3			20		3	3	29
KJ7	1										1
KK3			1								1
KP3					2		1				3
KR1		3		1		27					31
Total	25	19	16	53	123	78	101	103	57	12	587

Discussion

Molecular analyses successfully validated eggs identified as *T. declivis* using species-specific morphological characters. The analysis further confirmed the presence of *T. declivis* eggs where morphological identification was problematic in ethanol preserved samples.

The molecular analyses confirmed the presence of *T. declivis* eggs within the vicinity of Kangaroo Island and Portland in Survey 1, as well as in the vicinity of Portland, King Island and north-western Tasmania in Survey 2. Highest raw abundances were collected near Kangaroo Island and King Island.

Egg diameters of *T. declivis* eggs within this study off southern Australia (mean 0.99 mm) were similar to those reported off eastern Australia (0.95 mm; Ward et al. 2015).

The molecular analyses also facilitated the identification of some eggs possessing similar morphological characters to *T. declivis*, including barracouta, *T. atun*. Although eggs of this species were not quantified in this study, their presence was observed over a broad range and in substantial numbers, indicating the region may be a key spawning area for this species.

Molecular analyses should continue to be employed to validate fish eggs when used in stock assessments, such as the Dailey Egg Production Method (DEPM), given the complexity of fish egg identification and poor taxonomic knowledge of fish eggs in Australian waters.

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APPENDIX 2: Adult sampling locations for Jack Mackerel West DEPM

Table 1: Date, time and locations of trawls off the *FV Western Alliance* for Jack Mackerel during the 2016/17 DEPM survey.

Shot no.	Date	Start Time End Time	Start Latitude Longitude End Latitude Longitude		Temp. °C Surface: Bottom	Depth (m)
1	30/01/17	09:49 11:40	39°10.04 143°44.25	39°03.51 143°45.19	18.5:15.3	85-88
2	30/01/17	13:04 15:05	38°57.21 143°43.98	38°51.52 143°49.69	18.8:15.6	75-80
3	30/01/17	15:53 17:54	38°49.87 143°49.78	38°54.86 143°42.43	18.7:N/A	75
4	31/01/17	07:35 09:37	38°57.58 142°20.53	38°52.48 142°13.84	18.2:N/A	170-180
5	31/01/17	10:33 12:31	38°52.79 142°10.37	38°49.79 142°02.35	18.2:12.4	173-190
6	01/02/17	12:49 14:26	41°18.98 144°26.17	41°25.00 144°25.65	16.3:N/A	150-180
7	01/02/17	15:36 17:19	41°33.13 144°26.08	41°39.10 144°28.88	16.5:N/A	180-220
8	01/02/17	19:56 21:39	41°58.61 144°39.88	42°03.87 144°43.43	16.9:N/A	170-180
9	02/02/17	07:65 09:57	42°41.04 144°56.25	42°48.44 144°57.00	15.8:N/A	160-190
10	02/02/17	12:44 14:42	43°02.85 145°11.98	43°08.01 145°18.63	14.9:N/A	155-165
11	02/02/17	15:35 17:35	43°12.49 145°22.09	43°18.00 145°28.62	14.4:N/A	170-175
12	03/02/17	14:37 16:05	41°24.15 144°25.73	41°18.76 144°26.20	16.1:N/A	150-170