Commercialising translocation of Southern Rock Lobster

Caleb Gardner, Klaas Hartmann, Bridget Green, Hilary Revill and Rodney Treloggen

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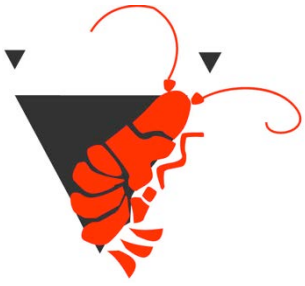
IMAS INSTITUTE FOR MARINE AND ANTARCTIC STUDIES

Tasmanian Government

Southern Rocklobster LIMITED



This project was conducted by:

Institute for Marine and Antarctic Studies (IMAS), University of Tasmania, Private Bag 49, Hobart TAS 7001
Caleb.Gardner@utas.edu.au; +61 3 62277233,

Department of Primary Industries, Parks, Water and Environment (DPIPWE), Tasmanian Government, PO Box 44, Hobart TAS 7001,

and

The Tasmanian Rock Lobster Fishermen's Association (TRLFA), PO Box 109, South Hobart, TAS 7004

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Office Mark Oliphant Building, Laffer Drive, Bedford Park SA 5042
Postal Box 26, Mark Oliphant Building, Laffer Drive, Bedford Park SA 5042
Tollfree 1300 732 213 Phone 08 8201 7650 Facsimile 08 8201 7659
Website www.seafoodcrc.com ABN 51 126 074 048

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Non-Technical Summary

2011/744 Commercialising translocation of Southern Rock Lobster

PRINCIPAL INVESTIGATOR: Caleb Gardner, IMAS, University of Tasmania

ADDRESS: Private Bag 49, Hobart, 7001

PROJECT OBJECTIVES:

- To apply and test governance systems for managing commercial scale translocation operations
- To assess feasibility of field operations at commercial scale
- To test economic and stock benefits from translocation through pilot scale operations
- To develop a decision making system for controlling the scale of future operations based on economic and stock factors (such as beach price, fuel costs and catch rates)
- To conclude the CRC with Southern Rock Lobster translocation established as an ongoing, self-sustaining, commercial operation

This project attempted to extend previous research on the biology and economics of Southern Rock Lobster translocation into a commercial operation. The project developed processes and governance for ongoing commercial scale operations. These will occur at a modest scale for the next three years, producing 50 tonnes per annum of additional harvest. A decision making process has been developed implemented so that the total allowable commercial catch can be readily increased, should the industry wish to further increase the size of the harvest at some point in the future.

OUTCOMES ACHIEVED

This project moved translocation from pilot scale research operations to full commercial operations. Previous research had examined a range of biological issues and concluded that translocating lobsters to areas of higher growth was a feasible option for increasing production in the Tasmanian fishery. Moving to commercial scale operations through this project involved collecting funds from commercial fishers through the annual quota renewal process. The project moved an average of 80,000 lobsters per annum, which resulted in an increase in the allowable commercial catch of 52 tonnes each year. This is an approximate increase in revenue of $6 million over the two years of the project, assuming an average market price of $60/kg.

Each kilogram of additional production was obtained at a cost to industry of $2, which is only 9% of the current lease price of $22.

Quota unit values reflect cash flow from lease payments to the units. These cash flows increase with translocation so that approximately $1300 of the market value of each quota unit is attributable to translocation (based on current market yield of 7.7%) or $13.6 million capitalisation across the fishery.

At the conclusion of the project the industry voted to continue commercial scale operations using the approach developed in 2012 and 2013. They will now collect funds and manage operations through an industry committee.

LIST OF OUTPUTS PRODUCED

This project developed and implemented the system for ongoing management of translocations in the Tasmanian Southern Rock Lobster fishery. These include the tender process, governance, and site selection. Translocation has now been incorporated into the annual process for setting the total allowable commercial catch. This can respond to any increase in scale of operations, which appear to be well below that which could occur.

Acknowledgements

The project team acknowledges and thanks the following people for their contributions:

- TRLFA translocation committee and tender approval committee members: Mal Maloney, John Sansom, Rob Rattray, David Wyatt, Damien Hursey, David Llewellyn, Willy Beadle, Kevin Hursey, Matthew Oakley, Brendan Taylor, Kent Way, Robert Rex, Chris Parker, Stephen Glover, and Mark Natoli;
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1. Introduction and Background

1.1. Background

Previous projects have shown that Southern Rock Lobster translocation could be used to address several problems that affect the Tasmanian Southern Rock Lobster fishery. Some areas of the fishery are "growth overfished", meaning that larger harvests would be sustainable if lobsters were able to grow to a larger size before being caught. At the other extreme, large areas in deep water off the remote west coast are under-fished because the animals are pale and fetch a lower price. These areas are however good areas for juvenile lobsters to settle from the plankton and grow as juveniles. Density of lobsters in these areas is extraordinarily high, with an average catch of over 30 per pot. Although lobsters are numerous, they don't contribute to the harvest because their growth is stunted by competition for food. Translocation simply involves moving lobsters from places where they are slow growing and abundant to places where they are fast growing and depleted. Although conceptually simple, there were naturally a lot of issues and concerns that required research.

In 2005, the first translocation involved moving 1000 tagged animals onto reefs that should have been productive but had been depleted by fishing. Within months fishers started catching tagged lobsters that had grown remarkably fast. Fishers were also excited because these lobsters had changed colour to become premium grade quality for markets. Larger scale translocations were conducted over the following years with 30,000 lobsters shifted to different locations around Tasmania. In each case lobsters increased their growth rate, usually by five-fold compared those at their original location. Growth of females was especially rapid and was often double that of local lobsters (we don't understand the physiology involved here).

Survival was high after release, egg production was enhanced, and lobsters remained close to the release site establishing new home dens and foraging ranges. The enhanced populations made the ecosystem more natural because density was closer to the natural state. The effect of removing lobsters from the deep water reef was also examined with growth picking up a little as density was reduced. Population and economic analyses of the fishery have shown that movement of 500,000 lobsters per year is sustainable, economically feasible and will result in continued recovery of lobster populations and the fishery.

This project was a pilot scale step towards commercialisation and involved the movement of 160,000 lobsters over two years in a test of the governance and operational systems required to operate on a larger scale. Individual fishing businesses contributed funds to pay for vessel charter, which is required for ongoing commercial operations.

The benefit of translocation was through increase in price and increase in productivity of the stock. Operations were highly attractive on a return on investment basis, but the scale of costs and benefit was modest for any one individual operator at this pilot scale.

The translocations conducted increased quota allocations by 5 kg per unit relative to the base allocation of 100 kg per unit – there was thus a 5% increase in catch. Sites used for removal and release were based off western Tasmania because of the presence of sites with high density of stunted lobsters and shorter travel distances to high growth areas.

This project took Southern Rock Lobster translocation into commercial scale operations and extended two previous projects, the first a small desktop study on feasibility, the second a larger scale experimental project that has recently concluded (CRC2006/220). This innovation addresses the focus of the CRC's theme to manage Australia's fisheries for profitability not just production. It creates a more profitable fishing industry while also a step towards restoring the coastal ecosystem to a more natural state.

1.2. Need

AS-CRC 2006/220 demonstrated that translocation was successful in changing the colour, growth rate and nutritional value of Southern Rock Lobster. Based on these results, the Tasmanian Southern Rock Lobster industry was overwhelmingly supportive of a commercial scale trial as indicated by an industry vote in support of this project. This project was ranked number 1 in the Crustacean Research Advisory Group process by both industry and management as a tool to conserve stocks, maximise productivity of the fishery and increase the gross value of production, profit margins, productivity and opportunities, as per the current FRDC priorities under Theme 7. This project was developed following the recommendations and guidelines developed by Sustainability and Profitability Options Committee (SPOC) of the TRFLA.

While the completed pilot scale experiment demonstrated that at low levels of translocation, the Southern Rock Lobster stock can be successful enhanced and productivity improved, the next critical stage was to assess the feasibility and economics of achieving this on a large scale, with greater densities. There was also a need to apply/refine the business and policy structures required for this operation to proceed.

The project helped address a need for stock rebuilding in the Tasmanian fishery due to an unusually prolonged period of below average recruitment. Translocation increases the productivity of individual recruits, which creates stock rebuilding when combined with a constraining TAC. In the current situation, we need to make the most of the reduced number of recruits that are entering the fishery. To illustrate, an average of only 22% 60-65 mm lobsters from the SW (area 8) grow to legal size and contribute to the catch. Of those that do reach legal size, their average weight is only 757 g. At the other extreme, an average of 70% of 60-65 mm lobsters from the NE grow contribute to the fishery with an average weight of 1227 g. The translocation conducted promoted stock rebuilding without a cut in the TAC.

1.3. Objectives

1. To apply and test governance systems for managing commercial scale translocation operations
2. To assess feasibility of field operations at commercial scale
3. To test economic and stock benefits from translocation through pilot scale operations
4. To develop a decision making system for controlling the scale of future operations based on economic and stock factors (such as beach price, fuel costs and catch rates)
5. To conclude the CRC with Southern Rock Lobster translocation established as an ongoing, self-sustaining, commercial operation

2. Methods

2.1. Governance

The main elements of the governance structure was determined by group discussion at TRLFA meetings with details developed by a sub-committee, and sent back to the wider industry in a discussion paper for comment and revision.

Operations were overseen by a translocation steering committee that consulted with other stakeholders, defined source and release areas, conducted tenders and made operational decisions as required. Membership included fisheries managers, scientists and industry representatives. Commercial fishing industry members were nominated at a TRLFA meeting.

2.2. Commercial scale translocation

The project planned to translocate 100,000 lobsters (~ thirty tonnes) across four stock assessment areas off western Tasmania (areas 5, 6, 7, and 8) in each of two years. The number moved from each area is to be approximately 30,000 lobsters from area 6; 10,000 lobsters from area 7; and 60,000 lobsters from area 8.

Movement was to industry-selected sites inshore and also to the north where growth tends to be higher. For example, lobsters from deep water block 8 (far south west) were moved to the inshore of block 7 (around 70 km to the north). Movements were discussed with and approved by the Chief Veterinary Officer based on negligible disease transfer risk.

Table 1. Summary of the number of lobsters planned and actual moved from deep water capture areas to shallow water release areas in 2011/12 and 2012/13.

	Planned			Actual		
	Capture area	**Release area**	**planned Number**	**capture area**	**release area**	**Actual Number**
2011/12	8	8	20,000	8	8	21,219
	8	7	40,000	8	7	39,567
	7	6	10,000	7	6	0
	6	5	30,000	6	5	0
2012/13	8	8	20,000	8	8	20,000
	8	7	40,000	8	7	40,000
	7	6	10,000	8	6	10,000
	6	5	30,000	8	5	30,000
Total			**200,000**			**160,000**

Detail on the release and removal sites are provided in Appendix 3.

Discrete sites were used for operations to assist monitoring the effects of translocation into the future. Sites were selected by industry members of the steering committee. All operations were on the west coast of Tasmania and are in areas with negligible harvesting other than by commercial fishers, which removes any direct sectoral interactions. This was important

because the economic rationale for the project would disappear if the commercial sector funded operations that only resulted in an increase in recreational catch.

Translocations were carried out using boats and skippers selected by tender (Appendix 4 and 5). Eligible skippers had Southern Rock Lobster licences, and experience of operating on the west coast in deep water. They needed to have the respect of industry and DPIPWE as model operators. To be eligible, each boat was required to have seawater tanks with a minimum holding capacity of two tonnes of fish, highly efficient pumps, quality crates and capacity to carry an observer.

Observers were present on all translocation charters because of the need to confirm the numbers of lobsters moved for TAC setting purposes. This requirement remained in the final model for future management of translocation by industry.

Aside from verifying the total number of lobsters translocated, the observers collected data on a subset of animals. They tagged, measured and record colour of 200 lobsters per day.

2.3. Monitoring and data collection

Data on the performance of commercial scale translocation operations came through observer sampling aboard vessels, commercial catch and effort logs, and tag returns. This was required to determine the effect of translocation on the source area (to avoid over-depletion) and to quantify benefits at the release sites and consequent fishery wide effects.

Monitoring was required during the translocation operations to provide feedback to the steering committee on progress. This included reporting daily numbers but also information on the condition of lobsters and general progress / issues in operations.

Effects on the fishery was determined with bio-economic modelling which required input data from commercial catch rates, size structure sampling and tag returns. The collection of tagging data was encouraged by increasing rewards for the return of tags to $5 per tag.

2.4. Population genetics

Full details of the genetic methods and results are detailed in the attached manuscript (Appendix 6: Morgan et al. 2013. Investigation of Genetic Structure between Deep and Shallow Populations of the Southern Rock Lobster, *Jasus edwardsii* in Tasmania, Australia)

Lobsters were sampled from six sites across the southern coast of Tasmania in February 2012 (Figure 1). Three shallow water sites sampled (Taroona Reserve [TAR], Mutton Bird Island [MBI, South of Port Davey] and Hobbs Island [HI, North of Port Davey]), were between 0 and 30 metres water depth, and comprised of lobsters with red coloured phenotypes. Three deep water sites sampled (Maatsyuker Island [MAT, tagged and translocated into Taroona Reserve between 2004 and 2008], Cape Queen Elizabeth [CQE] and East Pyramids [EP, Port Davey]) were greater than 60 metres in depth, and were largely populated by pale coloured lobsters. Distances between sample sites (by sea) range from 10 km (between EP and MBI) to 220 km apart (between HI and TAR). In addition, tissue samples were taken from lobsters collected from Taieri Mouth, Otago Harbour and Moeraki on the south island of New

Zealand during August 2011. A clip of tissue from the pleopod was taken and stored individually in 95% ethanol at -20°C.

We considered the effects of geographic and oceanic distance, between shallow and deep populations and any potentially resulting genetic patterns on subsequent translocations within the stock.

Figure 1. Map of sample sites of Southern Rock Lobsters across the southern coast of Tasmania, Australia. Red squares indicate shallow water sites of HI, Hobbs Island; MBI, Mutton Bird Island; TAR, Taroona Reserve; white squares indicates deep water sites of EP, East Pyramids; MAT, Maatsyuker Island; CQE, Cape Queen Elizabeth. Inset (top left) depicts sampling location in NZ, New Zealand; ~2,000 km from Tasmanian sites.

2.5. Health screening

2.5.1. Sampling and External examination

Fifty five lobsters from Port Hibbs offshore site and 30 lobsters from Southern Pt Davey site were sampled from the translocation sites one month after the commercial scale translocation, on the 9th March and 12th March 2012 respectively. Lobsters were transported live to Taroona in the wells of the boat, unloaded on the 14th March and stored in tanks, until processing one week later. Size, sex, length, weight and external damage were recorded, including lesions and number of goose barnacles fouling the shell. Lobsters were then dissected and the internal organs were preserved in Davidsons fixative, followed by storage in ethanol and taken to the Animal Health Laboratory at Kings Meadow, TAS for histopathological examination.

2.5.2. Histopathological examination

Skeletal muscle, gill, carapace, ventral nerve, intestines, hepatopancreas, heart and antennal gland were paraffin embedded and sectioned for histopathological examination. The microscopic findings were graded 0−3 (0−unremarkable, 1−mild, 2−moderate, 3−severe or abundant) following Handlinger et al 2006.

2.5.3. Haemocyte counts

To count the number of haemocyte as a measure of body condition, 1 ml of haemolymph was collected aseptically, usually from ventral sinus on the base of the fifth walking leg, or the pericardial sinus in smaller animals. A haemocytometer chamber was immediately filled for total haemocyte counts and the remainder used for bacterial culture. Photographs were taken of the haemocytometer chamber and the number of cells graded according to shape and the number of cells counted.

2.6. Bioeconomic analysis

Performance of the operations was assessed through bioeconomic analysis. A detailed description of the structure and model used is provided in the final report and publications from project 2006/220 (Gardner et al., submitted a & b; Green et al., 2012). The objective of these analyses in the context of commercial scale operations was to provide a framework for management decisions in the combination with translocation. This enabled outcomes to be modelled and integrated with other management changes, such as setting of the TAC or changes to management of the east coast fishery.

The bioeconomic model consisted of a population dynamics model, which represented the underlying resource, and an economic model, which calculated annual discounted profits. The population model was fitted to research and commercial sampling data, including length-frequency measurements and compulsory catch and effort data for the commercial sector. The population model provided estimates of the population sizes of undersize lobsters, which were critical for predicting the outcomes of translocation.

2.6.1. Population dynamics model structure

The population dynamics model was used to represent the sex- and size-structure of the stock in a number of sub-zones, to account for spatial heterogeneity in biological traits (Fig. 2), and changes in this structure over time due to the impact of fishing, natural mortality, growth and variation in recruitment. The biological model had eight quasi-monthly time steps, and the lobster population was represented using 5 mm carapace-length size bins; both of these specifications were also required for economic modelling because price varies with time of year and size of lobster.

Projections of the outcome of the fishery with and without translocation were also run using the biological model. The number of juveniles recruiting to the population in future years was selected from data from 1998 to 2007. This time period was selected because it coincided with the duration of ITQ management in the fishery and thus reduced risk of bias from change in fishing practices.

The spatial areas of most interest for translocation were those off western Tasmania (sub-zones 5-11; Fig 2.), which is where translocation operations were planned. Three options for translocations were considered:

1. *southern translocation*: moving lobsters from slow growth, deep-water areas (>35 fathoms) directly inshore,
2. *broad translocation:* moving lobsters from the same areas inshore but also northwards, thereby benefiting from the latitudinal trend in growth (Punt et al., 1997; Gardner et al., 2006; Gardner and van Putten 2008);
3. *northern translocation:* moving lobsters from the same areas as far north as possible (sub-zone 5), thereby maximising the benefit from the latitudinal trend in growth (Gardner and van Putten 2008).

The third scenario, *northern translocation*, was included as an example of the maximal economic benefit, the second scenario, *broad translocation*, was the strategy implemented over the last two years through the course of this project. This scenario was selected by industry vote and was driven by the desire to provide access to translocated lobsters to a larger number of fishers.

Industry consultation resulted in a plan to translocate 100,000 lobsters from sub-zones 9, 10 and 11 (Figure 2), although ultimately all lobsters were taken from sub-zone 11 due to weather and fishing conditions. Whilst translocation operations only took place on the west coast of Tasmania, changes in the biological state of the resources and the associated fishery on the east coast were expected and of interest because both the fleet and quota can shift among sub-zones. Movement of the fleet was modelled using an effort dynamics model that allowed the allocation of catch among sub-zone to respond to the biomass in each sub-zone as well as the allocation of the catch among area in the previous time-step and in the current time-step in the previous year. This implied that the fleet movement responded to the catch rate, but with inertia based on where effort was expended in the previous year.

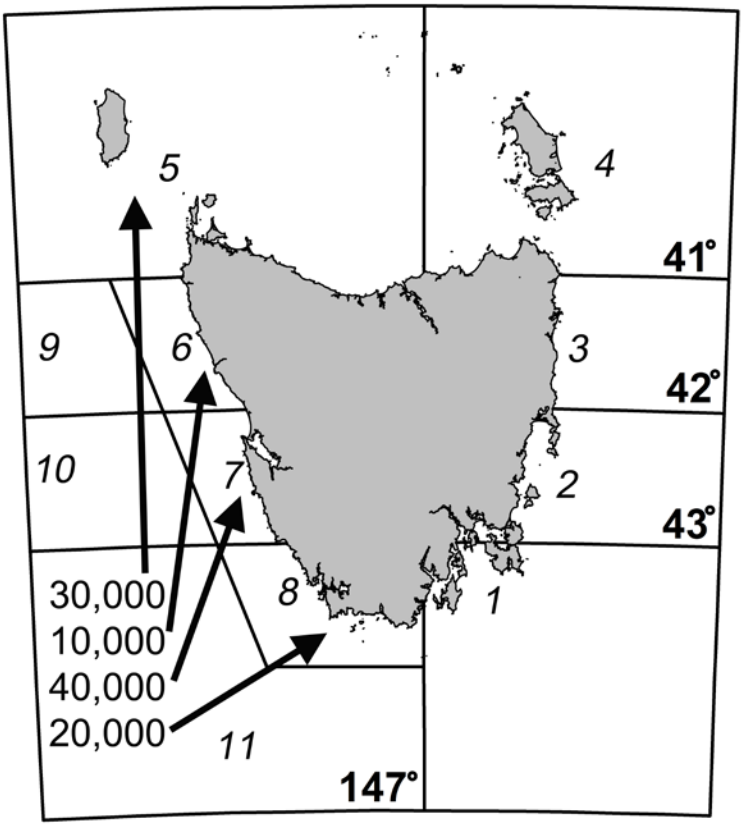


Figure 2. The Tasmanian fishery region showing the sub-zones used for modelling the fishery (1 to 11) with sub-zones 9-11 separated from adjacent inshore sub-zones by the 35 fathom contour. Three alternate options for translocation were evaluated; Southern translocation involved moving 100,000 lobsters directly inshore from sub-zone 11 to 8; broad translocation involved moving 100,000 lobsters as illustrated; and northern translocation involved moving 100,000 lobsters from sub-zone 11 to 5.

2.6.2. Specification of translocation population dynamics

The population dynamics of translocated animals generally followed those of non-translocated animals in terms of their contribution to spawning and the likelihood of capture during fishing. Translocated animals were selected at random (from undersized lobsters) from the sub-zone in which they were sourced and became indistinguishable from the animals in the sub-zone to which they are translocated after two years. There were however several differences between these two categories of lobster for the two years after release:

(i) An additional mortality rate of 0.02 yr^{-1} for translocated animals for the first two years. This assumed increase in mortality exceeded the observed rate of release mortality and was thus conservative (Green and Gardner, 2009);
(ii) Females did not produce eggs (even if they were mature) for the first year after being translocated. This is conservative compared to an expected 30% foregoing spawning (Green et al., 2009).
(iii) For the second year following translocation, egg production transitioned between that for the sub-zone from which the animal was taken and that to which it was relocated according to:

$$Q_l = (\chi^{\text{mat}})^t Q_l^{\text{From}} + (1-\chi^{\text{mat}})^t Q_l^{\text{To}}$$

where $Q_l^{\text{From/To}}$ is egg production for animals in size-class *l* in the sub-zone from which the animal is taken (From) and to which it has been relocated (To), *t* is the time since the relocation occurred, and χ^{mat} is a parameter equal to 0.5 which determines the length of the transition period.

(iv) Growth of male translocated lobsters was indistinguishable from that of animals in the destination area (Chandrapavan et al., 2010). In contrast, female translocated lobsters experienced initial enhanced growth of approximately 5mm per year relative to the animals in the destination area. In the two years following translocation female growth changed from the initial enhanced growth to that of the resident population. The transition in growth for female translocated lobsters is given by:

$$X_i^{female} = \left(\chi^{grow}\right)^t X_i^{female,Enhanced} + \left[1 - \left(\chi^{grow}\right)^t\right] X_i^{female,resident}$$

where X_i^{female} are the female size-transition matrices (which specifies the probability of growing from one size-class to the other size-classes) for time-step *i*. *Enhanced* denotes the enhanced size transition matrix immediately following translocation and *resident* denotes the matrix for animals in the destination area. The parameter controlling the rate of transition in the growth matrices, χ^{grow} was set to 0.5.

2.6.3. Economic feasibility of translocation

The assumed implementation model for translocation was for the commercial fishing industry to fund the movement of lobsters by means of an annual levy applied to all catch shares. Benefits in terms of allocation of catch would then also be shared equally amongst all catch shares. This system was agreed by industry by vote in November 2011 with initial operations funded by a levy of AUD$10 applied to each of the 10,507 catch shares, generating an annual fund of AUD$105,070 to charter commercial vessels to undertake the translocations. Given the objective of moving 100,000 lobsters below the minimum legal size per annum, this equated to AUD$1.05 for translocation of each undersize lobster. At that time the actual cost of moving lobsters was unknown but was subsequently established by a process of public tender. That provided market based costs of AUD$0.60 per lobster for *southern translocation*; AUD$1.50 per lobster for *broad translocation;* and AUD$2.00 per lobster *northern translocation,* which were used in our bioeconomic model.

The preliminary analysis of translocation conducted prior to any field tests included two methods of translocation (Gardner and van Putten, 2008). One involved the capture of undersize lobsters by commercial fishers during normal fishing operations that could be later released when the fishing vessel was inshore. This approach involved negligible marginal cost because costs were sunk in normal harvesting operations. The second approach involved chartering vessels to fish exclusively for the purpose of collecting animals for translocation. Although this second approach had a higher cost, it was favoured by Government and by the commercial industry because of the greater control over the scale and location of operations.

Projection scenarios with and without translocation were compared on the basis of net present value (NPV) which was the sum of annual discounted profits for a period of 15 years and with a real discount rate of 7.5% based on average business lending rates in the five years prior.

The annual discounted profit from commercial fishing for year *y* was the difference between the costs and revenues for year *y*, discounted to the first year of the projection period. Costs here are economic cost, and include items such as capital and unpaid labour, hence profit as measured here is effectively economic yield:

$$P_{\mathrm{y}} = \frac{1}{(1+\beta)^{y-y_S}}\left[\sum_{z}\sum(R^{\mathrm{z}}_{\mathrm{y,i}} - \tilde{\mathrm{C}}^{\mathrm{z}}_{\mathrm{y,i}}) - T_{\mathrm{y}}\right]$$

where P_y is the (discounted) profit or rent during year *y*, β is the discount rate (0.075), y_S is the first year of the projection period (2012), $R^z_{y,i}$ is the revenue generated from commercial fishing in sub-zone *z* during time-step *i* of year *y*, $\tilde{C}^z_{y,i}$ is the (variable) cost of commercial fishing in sub-zone *z* during time-step *i* of year *y*, and T_y is the cost of translocation or vessel charter for the whole state (zero in non-translocation scenarios) during year *y*.

The revenue from commercial fishing in Area *z* during time-step *i* of year *y* is given by:

$$R^z_{y,i} = \sum_l p^z_{y,i,l} \sum_s \tilde{S}^{s,z}_{y,l} V^s_i F^z_{y,i} N^{s,z'}_{y,i,l} e^{-Mt_i/2}$$

where $N^{s,z}_{y,i,l}$ is the number of animals of sex *s* in size-class *l* in sub-zone *z* at the start of time-step *i* of year *y*, $\tilde{S}^{s,z}_{y,l}$ is the selectivity of the gear on animals of sex *s* in size-class *l* in sub-zone *z* during year *y* given the implications of the legal minimum length, V^s_i is the relative vulnerability of males to females during time-step *i*, M is instantaneous rate of natural mortality (assumed to be independent of sex, size, sub-zone, and time), t_i is the duration of time-step *i*, $F^z_{y,i}$ is the exploitation rate on fully-selected (i.e. $\tilde{S}^{s,z}_{y,l} = 1$) animals in sub-zone *z* during time-step *i* of year *y*, and $p^z_{y,i,l}$ is the price of a lobster in size-class *l* and sub-zone *z* during time-step *i* of year *y* (Gardner et al., 2013).

The costs of commercial fishing in sub-zone *z* during time-step *i* of year *y* is given by:

$$\tilde{C}^z_{y,i} = c^z_i C^{\mathrm{Comm},z}_{y,i} / (q^z_i B^{e,z}_{y,i})$$

where c^z_i is the cost for a single potlift during time-step *i* in sub-zone *z* (Gardner et al., submitted a), q^z_i is the catchability coefficient for time-step *i* and sub-zone *z*, $C^{Comm,z}_{y,i}$ is the commercial catch in sub-zone *z* during time-step *i* of year *y* (the projections allow for commercial, recreational, and illegal catches), and $B^{e,z}_{y,i}$ is the exploitable biomass in Area *z* in time-step *i* of year *y* (the biomass available to the fishery less half of the catch during this time-step).

2.7. Development of framework for ongoing operations beyond the life of the CRC.

The effect of translocation on governance and fishery management plans required consideration for translocation to become an ongoing commercial-scale operation. In

particular, current fishery performance measures and associated limit and reference points were based on model projections under different quota scenarios and these needed to incorporate the change in management. Translocation affected these outcomes so there was a need for a formal process for dealing with this in current fishery management (the consequence is that the catch would be kept needlessly low because productivity gains from translocation would be ignored).

This component of the project involved review of existing policy and integrated translocation within the management plan. There was also a need for developing a long-term process for industry funding operations through the license system.

3. Results and Discussion

3.1. Governance

3.1.1. Steering committees

A steering committee, titled the Translocation Governance Committee, was established in November 2011 to oversee all operations of the commercial scale Southern Rock Lobster translocation. The committee comprised of industry representatives (Rodney Treloggen, John Sansom, Peter Atkins Stephen Glover, Chris Parker, Rob Rex, Rob Royle, David Wyatt and Mal Maloney), fisheries managers (Hilary Revill, DPIPWE) and scientists (Caleb Gardner, Klaas Hartmann and Emily Ogier, IMAS).

The role of the Translocation Governance Committee was to

- oversee all operations of the Southern Rock Lobster translocation
- define translocation details including catch/release areas and specific sites within (criteria of sites?), numbers to be moved between sites, timing of the translocations
- define the requirements for tenders –
    - Vessel, survey, capacity observer hosting
    - Operator - experience, crew
    - Gear/pot numbers
    - Lobster characteristics for translocation
    - Logistic constraints – counting, transporting
    - Coordinate permits
- Define translocation details – Areas, sites numbers, catch and release points,
- Construct a contract for professional services.

Translocation Tender Selection Sub-committee comprised
David Llewellyn, Rob Rex, Rodney Treloggen, John Sansom (TRLFA), Mal Maloney (TRLFA), Caleb Gardner (IMAS), and Mark Natoli (IMAS).

All lobsters moved were under-sized and thus remained the property of the state throughout the operation. After they were released they returned to the pooled stock until they are ultimately harvested or die through natural processes. There is no chain of ownership with the benefits of increased productivity shared by all fishers who have catch share allocations in the Tasmanian lobster fishery.

3.1.2. Tenders

Tenders were advertised in the mercury Newspaper (Appendix 5).

3.1.3. General tender requirements

Tenders were successfully conducted within the requirements detailed below. In general, finding vessels to complete the tenders was more difficult than originally anticipated. The following problems were encountered:

1. In the first offer of tenders a large number of applications were received but most were unsuitable. This is because either the tenderer was unsuitable (eg they did not own a boat); the price was extravagantly high (often because fishers based their estimate on their total daily revenue for lobster fishing, not the ex-quota lease price); or they requested payment as a daily rate rather than a price per lobster as required in the tender offer.
2. Successful tenderers had no obligation to proceed with the operation.
3. There was pressure from other fishers to not apply for tenders, and those operators who did accept tenders were abused, which made others reluctant to participate.

Description of the tender

The University of Tasmania is conducting a pilot scale evaluation of the commercialisation of Southern Rock Lobster translocation. This project is being run in collaboration with the Department of Primary Industry, Parks, Water and Environment and the Tasmanian Rock Lobster Fishermen's Association.

The objective of this tender is to translocate Southern Rock Lobsters from offshore West Coast locations in Areas 6, 7 and 8 to inshore locations in Areas 5, 6, 7 and 8.

Translocation of lobsters will occur over about six weeks.

The University will accept tenders for the entire operation, or approximately half on a north-south geographical split.

The completion of the contract is to be measured by the number of lobsters translocated. The number of lobsters moved is to be estimated by counting lobsters in a subsample of the pots deployed and extrapolating from this sub-sample. A minimum of 20% of pots are to be marked before hauling (to remove selection bias) and all lobsters to be from counted these marked pots[1]. Observers will be responsible for collecting information on counts of lobsters and will report back on a daily basis to the project committee.

The Vessel used for the tender is and will be maintained by the Operator in Marine and Safety Tasmania (MAST) Survey class 2B and 3B survey throughout the Charter Period.

The Vessel will be required to have high quality facilities suitable for transporting large numbers of lobsters without impacting the health and vitality of lobsters.

The Vessel is required to provide accommodation and access to a satellite phone for an observer. Victualling costs for the observer will provided separately to the observer and are thus not covered by the tender.

The Operator will procure and maintain insurance in full force and effect throughout the Charter Period at its sole cost and expense in respect of:

[1] This plan to only count lobsters in a subsample of pots was replaced by the successful tenderer with a system to count all lobsters, which provided a more accurate count than in this plan.

i. Loss or damage to the Vessel, the Equipment and the Safety Gear for their respective full replacement values.
ii. Workcover and any other accident or other compensation insurance required by any applicable law of any State in which any voyage may be undertaken during a Charter Trip and the Commonwealth in respect of the Skipper and Crew.
iii. Third Party/Public Risk Liability Insurance for at least $20,000,000

All undersize lobsters are to be translocated, that is, there is no grading. Legal sized lobsters will be released rather than translocated where possible.

Operations will be conducted by research permit and the number of pots that can be used is only limited by the vessel survey requirement.

IMAS pots and buoy lines may be used by the tenderer where available with any lost gear replaced by the tenderer.

Other gear can be modified to increase retention of undersize lobsters, particularly the meshing up of escape gaps.

Sites are described in an annex to the contract.

Force Majeure – If the University of Tasmania determines that a chosen tenderer is unable to complete the tender as contracted for any reason, including boat or equipment failure, illness or inefficiency, the University of Tasmania may re-allocate the outstanding balance of the tender to another operator nominated by the Translocation Governance Committee.

3.2. Translocation

Translocation of lobsters totalled 61,000 in 2011/2012 and 100,000 in 2012/13 (Table 1). Lobsters could not be caught in planned northern removal sites in year 1with an exploratory shot of 60 pots yielding only 90 lobsters, in contrast to daily catches of up to 6000 lobsters in southern sites. The industry steering committee was reconvened and altered the removal sites to southern areas. This was controversial but did have the useful outcome of emphasizing the need for contingency planning for this situation in future years. Prior to 2013 we didn't think this situation was possible with the sites identified for removal in the north famous as high density "rat patches". Nonetheless, the unexpected occurred and animals in these regions failed to enter traps, perhaps due to some environmental situation such as a pulse of natural food (this often occurs when oceanic salps are pushed inshore).

The effect of the change of location on fishery management outcomes was interesting in the context of needing to adapt during the course of translocations. Over two years we moved 160K lobsters rather 200K but movements were over larger distances. The benefit from larger movement cancelled out the effect of smaller number so that fishery outcomes were essentially identical.

Table 2. Estimates of the number of Southern Rock Lobsters captured and released at sites for 1st translocation Feb-Mar 2012

	Site	Area	No. of Lobsters
Capture			
	Telopea Point	8	12,578
	Snevor Point	8	11,621
	Coffee Pot Reef	8	600
	South Cape	8	4,207
	Wilsons Bight	8	1,006
	Wedge Island	8	469
	East Pyramids	8	6,615
	North Head	8	11,416
	Maatsuyker Island	8	3,558
	Davey Reef	8	4,467
	South Head	8	4,622
Release			
	Clydes Margos	7	8,129
	Condor/Bird Island	7	8,175
	The Shank	7	8,041
	Low Rocky Point	7	8,114
	Maatsuyker Island	8	10,027
	Red-Bridge Point	8	10,000
	Flat Witch Island	8	1,192
	Condor/Bird Island	7	7,108

Figure 3. Deckwork during translocation operations. The pot being handled here was a standard IMAS research pot, supplied to the tenderer to increase the number of pots available for each shot.

Figure 4. Deckwork during translocation operations. Large numbers of undersize lobsters were collected from removal sites in each pot. Here the crew grades the catch with undersize retained for translocation and legal-sized lobsters released if any were captured (typically very few lobsters). The observer on the right collects data including size, sex, damage and tag details for a sub-set of the catch.

Figure 5. Catch in one of the pots illustrating the large number of small, slow-growing and pale lobsters that were captured at the removal sites when escape gaps were closed. Catches of up to 6000 lobster per day were taken by the vessel that conducted the translocations.

Figure 6. Translocated lobsters after having been lifted from the wet-wells and immediately prior to release. Releases occurred at night to reduce post-release predation by finfish.

Figure 7. Translocated lobsters being released at night to reduce post-release predation by finfish. IMAS observers were present on all trips, in this case Chris McKinlay on the left.

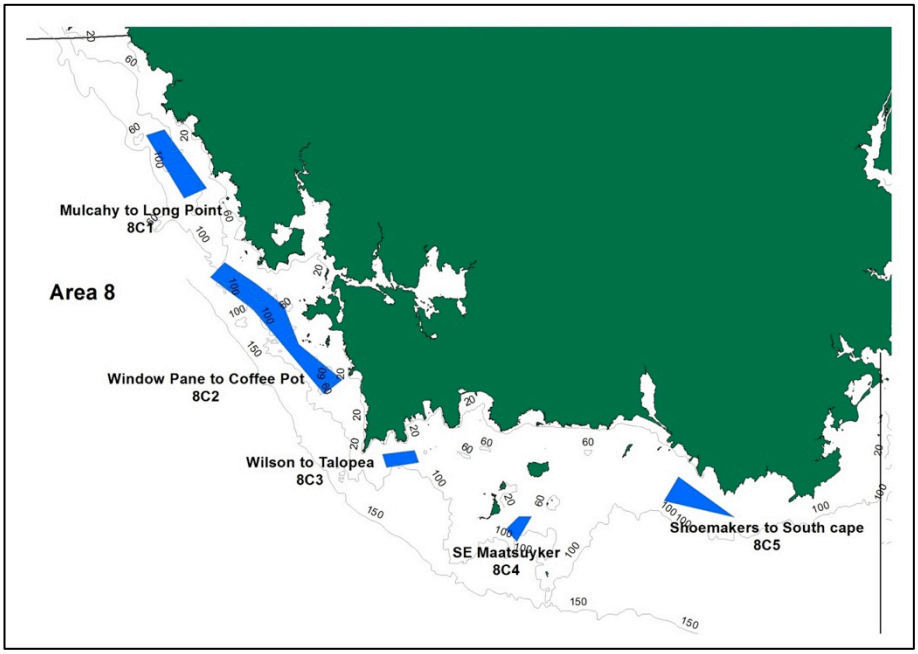


Figure 8. Capture sites for Area 8 (SW) translocations, 2012 and 2013.

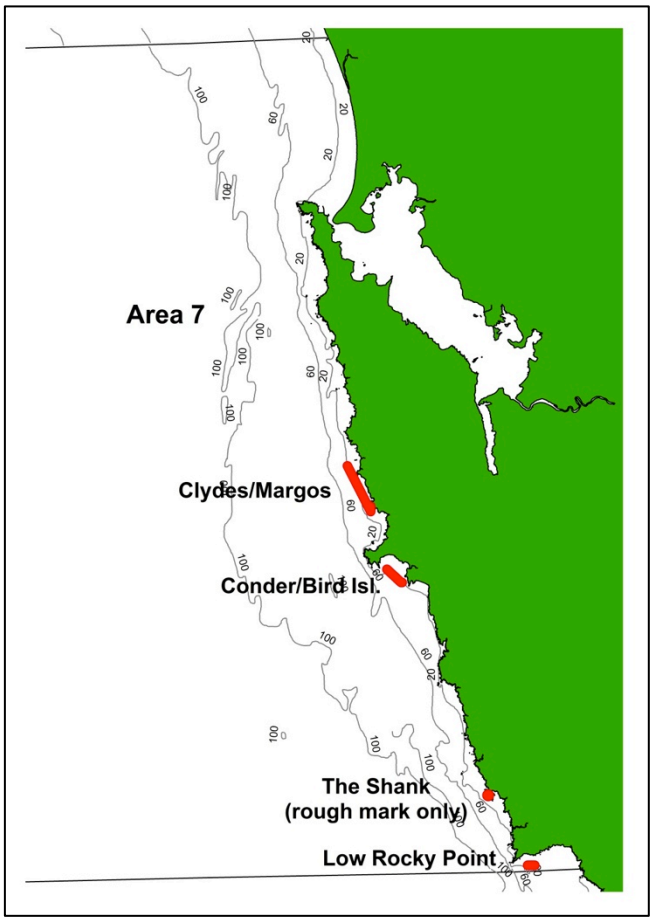


Figure 9. Area 7 release sites for round one translocation Feb-Mar 2012

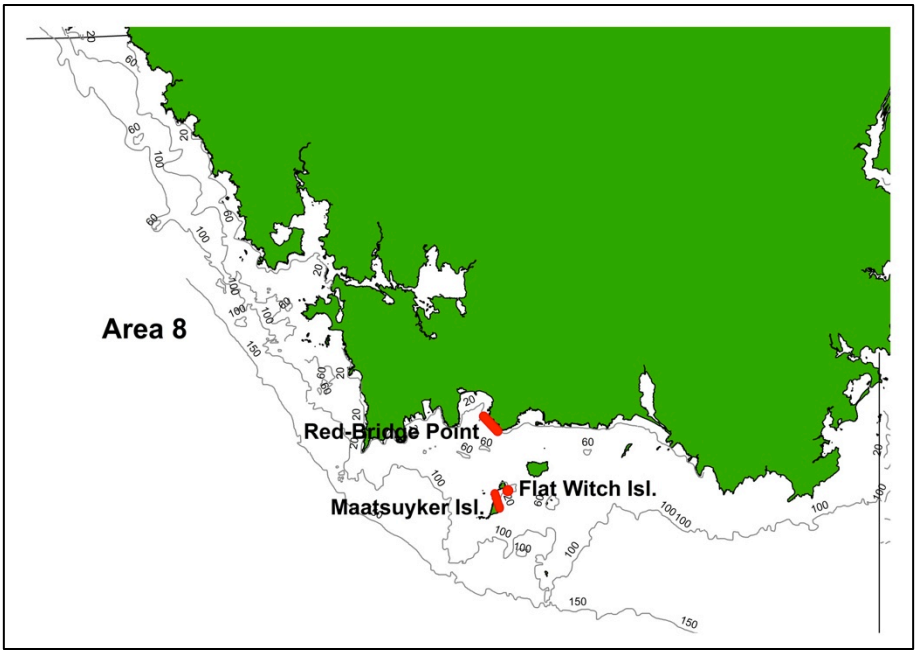


Figure 10. Area 8 release sites for round one translocation Feb-Mar 2012

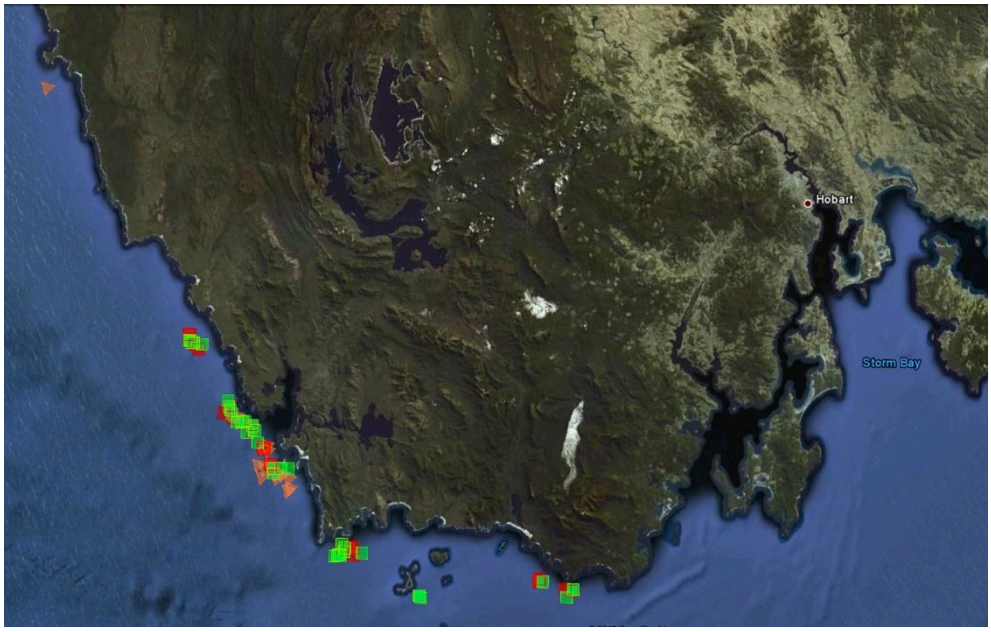


Figure 11. Removal sites in the south. Green cells are sites from year 1, red / orange are sites from year 2. Squares are sites sampled as per original plans, triangles are sites shifted south in response to low catch rates in the north.

Figure 12. Detail of sites in the Port Davey region. Green cells are sites from year 1, red / orange are sites from year 2. Squares are sites sampled as per original plans, triangles are sites shifted south in response to low catch rates in the north.

Figure 13. Detail of sites on the south coast. Green cells are sites from year 1, red / orange are sites from year 2. Squares are sites sampled as per original plans, triangles are sites shifted south in response to low catch rates in the north.

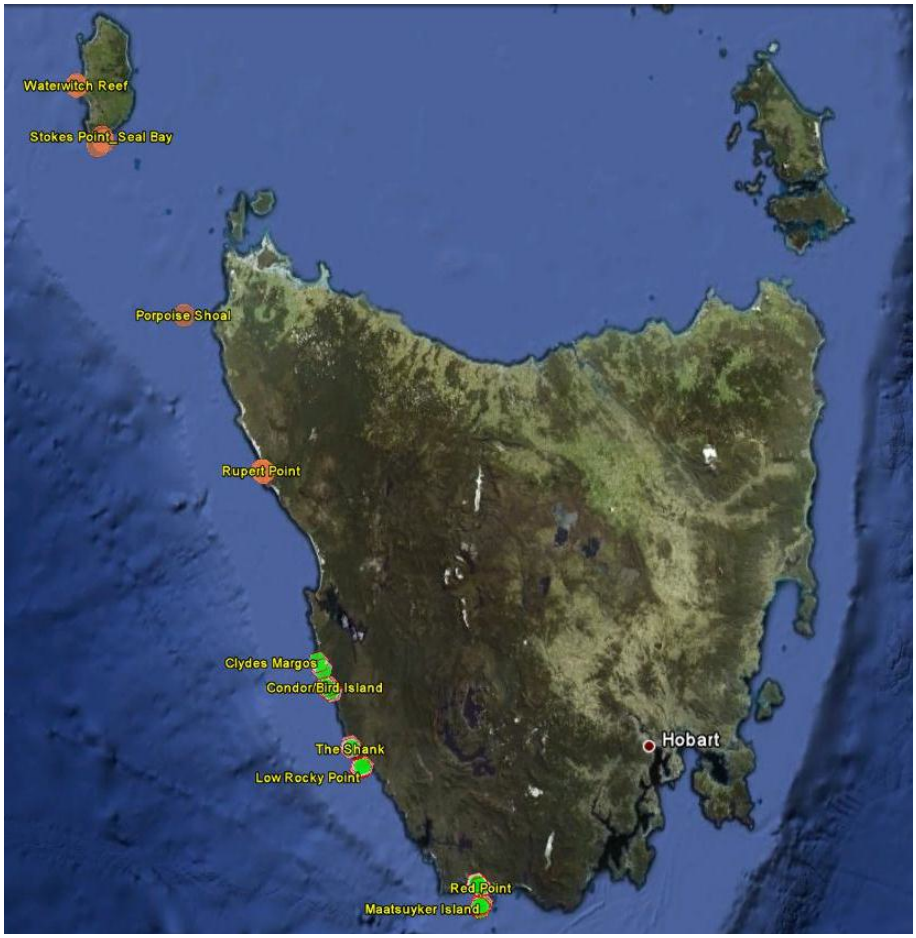


Figure 14. Statewide release sites.

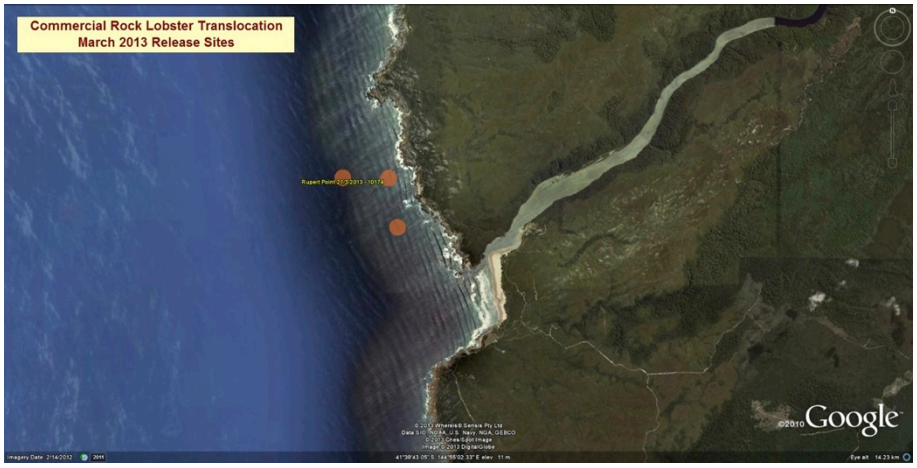


Figure 15. Detail of the Rupert Point release site.

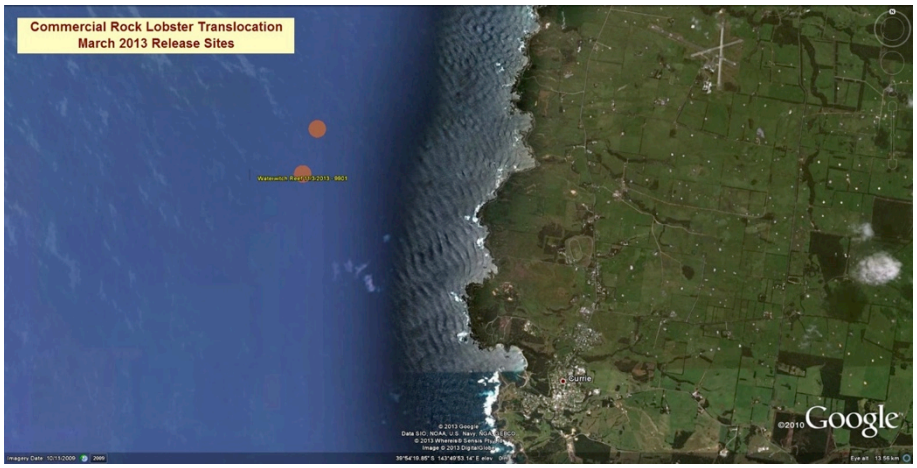


Figure 16. Detail of the Water Witch release at King Island, our most northerly translocation and site of greatest growth benefit.

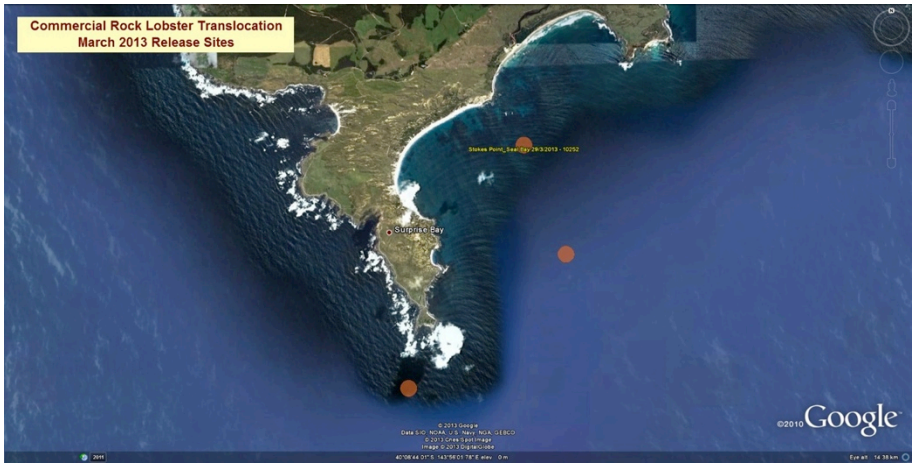


Figure 17. Detail of the Seal Bay release site, King Island. This site was included by the steering committee during the course of translocations in response to a letter from fishers at King Island. They wanted two sites at King Island to suit operators with different businesses.

Figure 18. Detail of south coast release sites. These involved very short movements from deep to shallow.

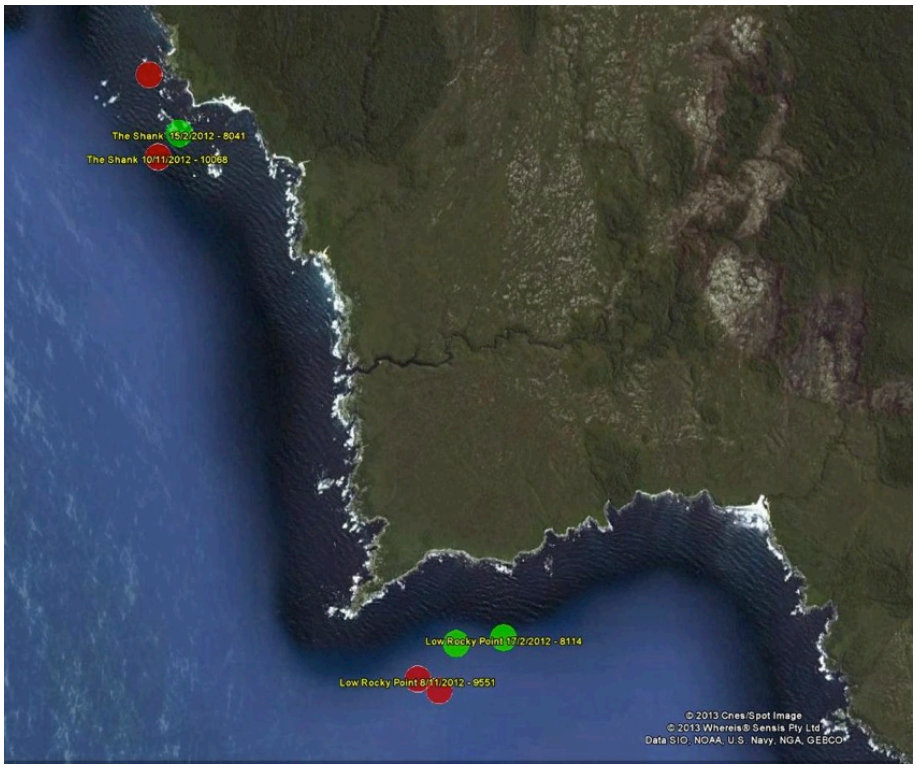


Figure 19. Detail of releases at Low Rocky Point on the mid-west coast.

Figure 20. Detail of releases at Point Hibbs on the mid-west coast.

3.3. Monitoring and data collection

Monitoring was required to assess the sensitive issue of change in catch rate at removal sites. This was tracked through the course of the project by comparison between removal sites and adjacent sites that were not included in translocations. Results are shown in Figure 16. This illustrates that catch rates are highly variable between months, years and sites – which means it's difficult to determine any trend at removal sites.

Our interpretation of this data is that there was no evidence of any change in catch rate from removal sites. This was not unexpected because of the small proportion of total lobsters removed from any one site. Despite these results and the clear problem in ascribing change in catch rate to any one factor (such as translocation), rather than several other factors (such as fisher removals, weather, month, year) some commercial fishers insisted that translocation removals had affected their catch rates. This was managed by asking them to participate in site selection for future work.

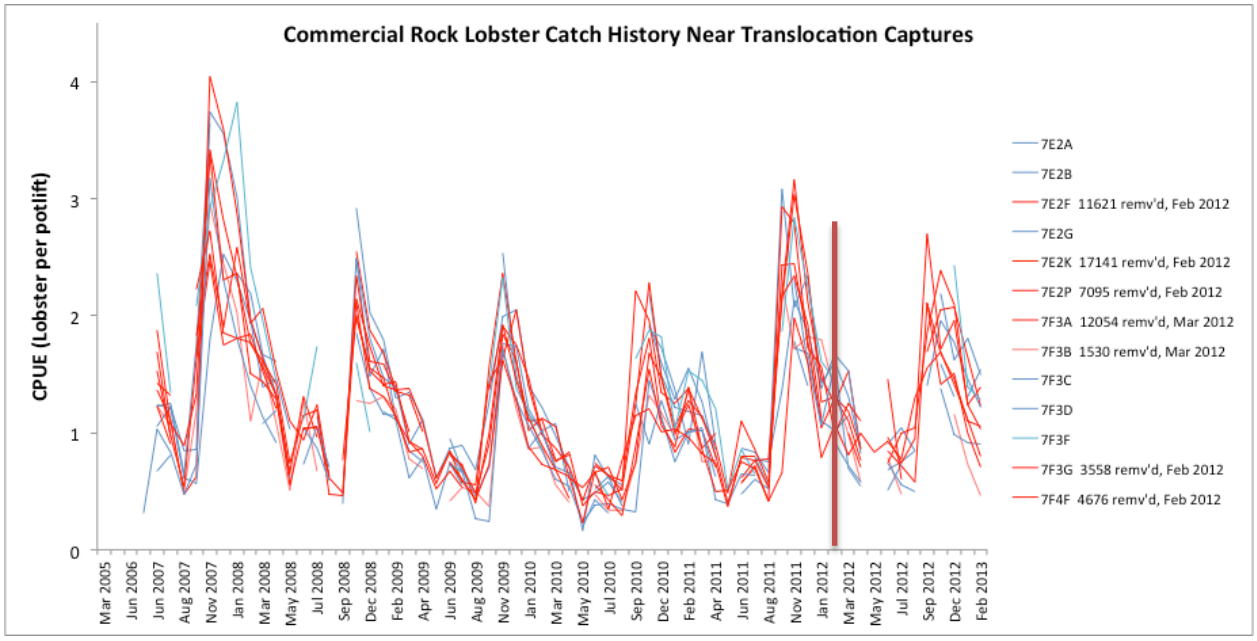


Figure 21. Trends in catch rate at removal sites and adjacent fishing reporting blocks. The red vertical line represents the point in time where removals occurred. Catch rate in removal sites (red) has remained similar to that of adjacent blocks (blue). There is no evidence of an effect of translocation on fishers who continue to operate in these areas.

3.4. Population genetics

Genetic analysis did not identify any scale of population structure that would suggest any genetic differences between shallow (red) phenotypes and deep (pale) phenotypes. There is a significant level of genetic differentiation between Tasmania and New Zealand, and therefore the assumption of widespread population panmixia can be rejected. Although large scale translocations are genetically viable in this region of Tasmania, it is important to understand that if the indications of asymmetric gene flow and population differentiation found are transferable across the rest of this species range, then translocations should only be undertaken on the scale of jurisdiction. Similarly, finding significant genetic structure in an important fishery species, where previously none had been identified, means a much more detailed assessment of lobster connectivity across the range may find more unique genetic stocks, and important source sink relationships which will have important implications for successful translocations and stock structure management schemes.

3.5. Health screening

There were no signs of transmissible disease in translocated lobsters, or risk of disease transmission following translocation, from either external examination of whole lobsters or histopathological examination of dissected lobsters. A small portion of lobsters (20%) had low grade inflammation under the carapace, which was considered incidental. Microorganisms were not evident within the inflammation. Two sites were sampled, Port Hibbs and Port Davey, Tasmania. Lobsters from Port Davey generally had less damage, less inflammation and were in better condition than lobsters from Port Hibbs.

3.5.1. External examination

We examined 23 females and 32 males from Port Hibbs and 13 and 17 females and males respectively from Port Davey (**Table 3**). Most lobsters have external evidence of minor lesions, and a one quarter had limb or antennae loss (Table 1). This is within the range of normal Southern Rock Lobster fishing practices (Emery et al. in review).

Table 3. Summary of external examination of lobsters from deep-water translocation sites. A. Port Hibbs. B. Port Davey

	Port Hibbs		Port Davey	
Category	**Female**	**Male**	**Female**	**Male**
Number	23	32	13	17
Mean carapace length (mm)	84	90	83	91
Minimum CL (mm)	76	16	76	76
Maximum CL (mm)	92	111	91	110
Mean weight (g)	288	375	280	379
Number of lobsters with lost legs	11	10	6	8
Number of lobsters with missing antenna	6	9	3	4
Number of animals with lesions	23	30	11	12
Mean haemocyte count	32	33	60	47
Mean histopath score	0.83	1.47	0.62	0.76

3.5.2. Histopathological findings

Findings described here were from Graeme Knowles, Veterinary Pathologist, Animal Health laboratory DPIPWE.

Diagnosis
Mild and incidental findings

Comment
Overall the microscopic findings are low grade and generally incidental. In the sections of tissues examined there were NO histopathological findings consistent with the notifiable disease Crayfish plague (*Aphanomyces astaci*).

Similar to the findings of Handlinger et al (2006) there are no significant disease findings in these samples, submitted for histopathology, which are a risk for disease transmission following translocation.

There were no gill inflammatory reactions related to the incidental free living small (generally 100um diameter) free−crawling crustaceans or the low numbers of goose barnacles or turbellaria (tube worms), which more commonly occur towards the end of the intermoult period.

Four lobsters had mild focal chronic inflammation of skeletal muscle. A small crustacean was the cause for inflammation in one. In the three lobsters without a degenerate crustacean within the inflammation (see the three listed above), micro−organisms are not evident.

Port Hibbs
Low numbers of lobsters have turbellaria (5/55), small crustaceans generally 100um diameter− (3/55) between filaments of gills or occasional Goose barnacles (2/55) attached to their gill arches. Some lobsters have inflammation expanding under the carapace (12/55) and others have rare small crustaceans (3/55) over their surface. In three lobsters there are bacilli bacteria within the inflammation below the carapace. Micro−organisms are not evident within the inflammation under the carapace of the other lobsters. Inflammation within the hepatopancreas is rare and only low grade focal inflammation is seen in one lobster (1/55). Micro−organisms are not evident within the inflammation of the hepatopancreas. Inflammation is also rare in the tail skeletal muscle. In one lobster there was a focal mild inflammation surrounding a degenerate crustacean (1/55).

Port Davey
There are fewer findings in lobsters from Port Davey. Low numbers have mild inflammation under the carapace (6/30), focal inflammation within the hepatopancreas (1/30) and inflammation of the skeletal muscle of the tail (3/30). Micro−organisms are not evident within the inflammation under the carapace, in the hepatopancreas or skeletal muscle. Please note that all microscopic findings described above were mild (grade 1). Those tissues not described are unremarkable.

3.5.3. Haemocyte count

Lobsters with low haemocyte counts did not have any negative reports on their histopathology. Haemocyte counts ranged between individual lobsters, from 9 to 52 at Port Hibbs and 18 to 80 at Port Davey.

3.6. A framework for ongoing operations beyond the CRC

The following text is the document used by the industry to agree a process for future management of commercial scale translocation in Tasmania.

3.6.1. Background

For the two-year, pilot scale, project that began in 2011 TRLFA committees were formed to manage operations and 160,000 lobsters were moved. This immediately increased productivity, allowing the TACC to be raised 5 kg per unit higher than it would have been otherwise. These operations were largely funded by quota owners at the rate of $10 per unit or $2 per kg of TACC generated. These industry funds were augmented by research funding of observers and other research services.

The industry now needs to consider its next progressive step. This document outlines a system that industry can use to do this.

3.6.2. Review periods

Beginning in 2013/14, translocation will be conducted in three-year blocs. This means that a decision to conduct translocation would be reviewed every three years by the TRLFA, but not within the three-year period.

Operating over a three-year period will provide much-needed flexibility, which is particularly important if the TACC is to continue be adjusted in advance of planned annual translocations.

There may, for example, be situations where conditions ranging from adverse weather to fluctuations in funds require annual translocation totals to be amended. In such cases a three year program would allow funds to be carried across from one year to another, allowing additional lobsters to be moved in a following year.

3.6.3. Funding

At the TRLFA's direction, funds for translocation will continue to be provided by licence-owners annually via a levy collected by DPIPWE at re-licensing. In the past two years this levy has been $10 per quota unit. In terms of the TACC this generated an immediate increase of five kg of quota per unit, at a cost of $2 per kg.

While this TACC benefit can be expected to continue, we must acknowledge that industry funding in the past two years was boosted with external funds from the CRC, FRDC and IMAS. For the future, this means an increased levy would be necessary.

The current proposal is to increase the levy to $3 per extra kilogram of TACC allocated. This means that if translocation were to remain at a level where 5kg per quota unit is generated, then the annual levy per quota unit would be $15. If the scale were increased by 50% so that an additional 7.5 kg of quota were allocated to each unit, then the cost per unit would be $22.50. Some points to note:

- The levy paid by industry only covers the cost of moving lobsters to areas where they will grow faster.

- The TRLFA translocation committee will attempt to minimise costs by seeking cost-effective transfers.
- There have been offers of volunteer vessels – vessels that are travelling up the west coast and could move lobsters at minimal cost. The translocation committee will investigate volunteer potential to reduce the levy amounts quoted above.
- Observers/taggers will be funded through existing IMAS projects, provided funding of fisheries research at IMAS is maintained.
- The levy options above are based on maximising the benefits by translocating lobsters northwards, where growth is faster and the return on your translocation investment is greater.
- Levies are not used to pay executive officers or committee members.

3.6.4. Governance

Permits will be issued by DPIPWE.
IMAS will be responsible for tagging.

3.6.5. TRLFA committee systems

As in the past two years the TRLFA will establish a translocation committee to:

- Oversee project governance
- Determine release sites
- Call tenders for translocation and issue contracts

3.6.6. Costs and benefits

The following general guide on cost and benefits uses indicative numbers and areas to suggest a scale of gains. In reality, it would not be possible to sustainably move the number of lobsters indicated from deep-water area 7 every year.

NUMBERS
To increase the TACC by 5 kg/unit and still meet the CPUE, biomass and egg production targets, the following number of undersize lobsters (60-104 mm CL) would need to be translocated (data from 2011/12 assessment).

Deep water capture area	Shallow water release area			
	8	7	6	5
8	225,000	110,000	80,000	50,000
7	-	175,000	90,000	55,000
6	-	-	150,000	60,000

The key points here are that gains in productivity are possible with movement from deep to shallow water but not to the scale that occurs with northward translocations.

COSTS
Cost for translocation of each lobster based on experience with commercial tenders 2012-13 are estimated as:

Deep water capture area	Shallow water release area			
	8	7	6	5
8	$0.70	$1.10	$1.60	$2.00
7	-	$0.85	$1.50	$1.75
6	-	-	$0.85	$1.50

Cost per kg of additional quota under the 5 kg extra quota scenario

Deep water capture area	Shallow water release area			
	8	7	6	5
8	$157,000	$121,000	$128,000	$100,000
7	-	$148,000	$135,000	$96,250
6	-	-	$127,000	$90,000

3.6.7. On water operations

- As per the last two years
- Open call for tenders, evaluated by TRLFA committee (using UTAS legal guidelines)
- Vessels required to be of high standard for live transport and to be approved by the TRLFA committee
- Observers on the vessel (funded through standard IMAS at sea sampling operations)
- Small proportion to be tagged (~ 2%)
- Sites determined by TRLFA committee with release sites to be rotated each year where possible.

3.7. Integration with DPIPWE's TACC setting process

Progression towards an operational plan required review of the commercial scale operations conducted over the previous two years. There was substantial difference between the planned vs actual operations which highlighted issues likely to arise in future and the need for flexibility / contingency planning.

- As per the last two years, model projections to incorporate the scale and location of translocations so that the TACC can be adjusted with respect to existing reference points. Of most relevance is the CPUE target, which is met with a higher TACC in the presence of translocation.

- Survival and growth of translocated lobsters has been measured by previous trials. If the biology changes from what occurred, the solution is the same as per normal TACC setting, which is monitoring using tagging data.

The TACC setting process in the presence of translocation is illustrated by the probability tables of fishery reference points below. These describe the likelihood of the fishery meeting biological or economic reference points at a defined time in the future, usually 2020. Limit reference points relate to sustainability and require a high certainty of being met, that is, a probability of at least 90%. Target reference points are used for economic performance and can be met at a lower probability of 70%.

The performance of the fishery in relation to different reference points is shown in Table 4, Table 5 and Table 6. These illustrate the TACC setting process with different outcomes depending on the TACC allocated. The general pattern is that reference points are more likely to be met by lower TACCs. It is also apparent that the most challenging reference point in this fishery is the economic target (Table 6).

The process of TACC setting in the Tasmanian lobster fishery is important in the context of translocation and has become political in recent years with campaigning by ENGOs and even academic marine ecologists against the process. These statements require some commentary because they affect the future prospects for incorporating translocation into TACC setting. Criticism of the process has been on two issues / misunderstandings. These are that: (i) the process assumes constant recruitment (so TACCs are set too high if recruitment is below average); and (ii) that the use of economic targets promotes higher TACC than would be set if the fishery were managed for ecological sustainability. To illustrate, the Tasmanian Conservation Trust wrote to the Australian Government's Standing Committee on Agriculture, Resources, Fisheries and Forestry in 2012 stating that "*the level of recruitment used in the model is the average from the last 10 year*s" and this was also repeated in articles by UTAS academics in 2014 plus the claim that there is "*an over-reliance of fisheries managers on computer models that attempt to maximise economic returns with little margin for error in an era of change when model variables increasingly fall outside known bounds*."

The process below illustrates how these claims are incorrect. First, recruitment is assumed to be stochastic rather than constant, which gives rise to probability based reference points shown in Table 4 to Table 6. There is a substantial safety margin in these with the reference points for sustainability based on very high probability of meeting the target: a 90% probability is used for limit reference points rather than 50%, which would be applied if decisions were based on average recruitment with "little margin for error". Table 6 shows the target reference point related to economic performance for the fishery. This reference point is more difficult to meet than sustainability limits and forces the TACC lower than would occur if reference points were only based on ecological sustainability.

Summaries of reference points for the fishery both with and without translocation, at 100,000 lobsters p.a. including northward movement by one assessment area, are shown in Table 7 and Table 8. In Table 8 where there is no translocation, the economic CPUE target reference point could only be met with a TACC of 95 kg per quota unit. However, in the presence of translocation, this same target is met with a higher TACC of 100 kg per unit (Table 7).

Table 4. The probability of the stock remaining above the Legal Sized Biomass Limit Reference Point in the presence of translocation, under three different TACC scenarios. In this case the outcome is not sensitive to the TACC. Statewide and for most areas there is a high probability for meeting this limit. One exception is area 4 which remains below the limit regardless of the TACC. This area requires other management changes to address the limit.

	110kg/pot	105kg/pot (SQ)	100kg/pot
Area 1	100	100	100
Area 2	78	84	90
Area 3	88	92	94
Area 4	19	27	31
Area 5	98	99	99
Area 6	81	89	96
Area 7	94	97	99
Area 8	100	100	100
Statewide	95	99	100

Table 5. The probability of the stock remaining above the Legal Sized Biomass Target Reference Point in the presence of translocation, under three different TACC scenarios. Conclusions are similar to those for the limit reference point illustrated in Table 3.

	110kg/pot	105kg/pot (SQ)	100kg/pot
Area 1	54	73	86
Area 2	79	90	96
Area 3	58	76	89
Area 4	24	35	47
Area 5	99	100	100
Area 6	51	65	82
Area 7	36	49	68
Area 8	76	90	96
Statewide	76	91	96

Table 6. The probability of the stock remaining above the Catch Rate Target Reference Point in the presence of translocation, under three different TACC scenarios. This target point is used as a proxy for economic performance as the catch rate target was based on that at estimated MEY. The economic target is more challenging to meet and drives the TACC setting.

	110kg/pot	105kg/pot (SQ)	100kg/pot
Area 1	37	56	73
Area 2	66	78	87
Area 3	40	53	62
Area 4	15	22	28
Area 5	100	100	100
Area 6	26	42	58
Area 7	26	44	59
Area 8	55	70	86
Statewide	63	80	93

Table 7. Summary of fishery performance against reference points in the presence of translocation (as applied for setting the TACC in 2014/15).

	Level	Year	95kg/pot	100kg/pot	105kg/pot
Exploitable Biomass Limit	90%	2016	100	100	100
Exploitable Biomass Target	70%	2019	95	90	72
CPUE Target	70%	2021	90	74	48
Egg Production Limit	90%	2016	100	100	100

Table 8. Summary of fishery performance against reference points in the absence of translocation (as applied for setting the TACC in 2014/15). Note the lower probability of meeting the CPUE target with a quota allocation of 100 kg / pot.

	Level	Year	95kg/pot	100kg/pot	105kg/pot (12/13)
Exploitable Biomass Limit	90%	2016	100	100	98
Exploitable Biomass Target	70%	2021	93	78	62
CPUE Target	70%	2019	66	43	21
Egg Production Limit	90%	2016	100	100	100

3.8. Economic outcomes

Translocations on the scale conducted through the project and planned for the future were found to increase legal-sized biomass and thus catch rates, with gains in catch rate achieved by *broad translocation* comparable to a 4.5% reduction in the TACC, or from 105 to 100 kg per catch share, as based on comparable trajectories in catch rate (Figure 17) and exploitable biomass. Similarly the more effective *northern translocation* achieved a catch rate trajectory comparable to a 7% reduction in TACC.

The increase in catch rate when translocation is combined with a constant TACC implies that catching costs decline for the same revenue. The discounted cash flow effect of this change was estimated at $17 million for *southern translocation* ($1,637 for each of the 10,507 catch shares), $26 million for *broad translocation* ($2,487 per catch share) and $38 million for *northern translocation* ($3,648 per catch share). Note that these values include costs of translocation. These equate to an increase in NPV above that achieved without translocation of 4.9%, 7.4% and 10.9% respectively. The NPV achieved by northern and broad translocation exceeds the maximum economic yield achievable by fine-tuning the TACC in the absence of translocation.

Improvements in catch rate and thus economic yield were distributed throughout the fishery, not only in the west coast sub-zones that received translocated lobsters (Figure 17). This occurred because the fleet moved towards sub-zones with high catch rates on the west coast, resulting in lower harvest rates and stock rebuilding. The exceptions to this are sub-zones 1, 2 and 3, which have a catch cap and consequently the catch taken from these sub-zones is constrained independently of translocation outcomes.

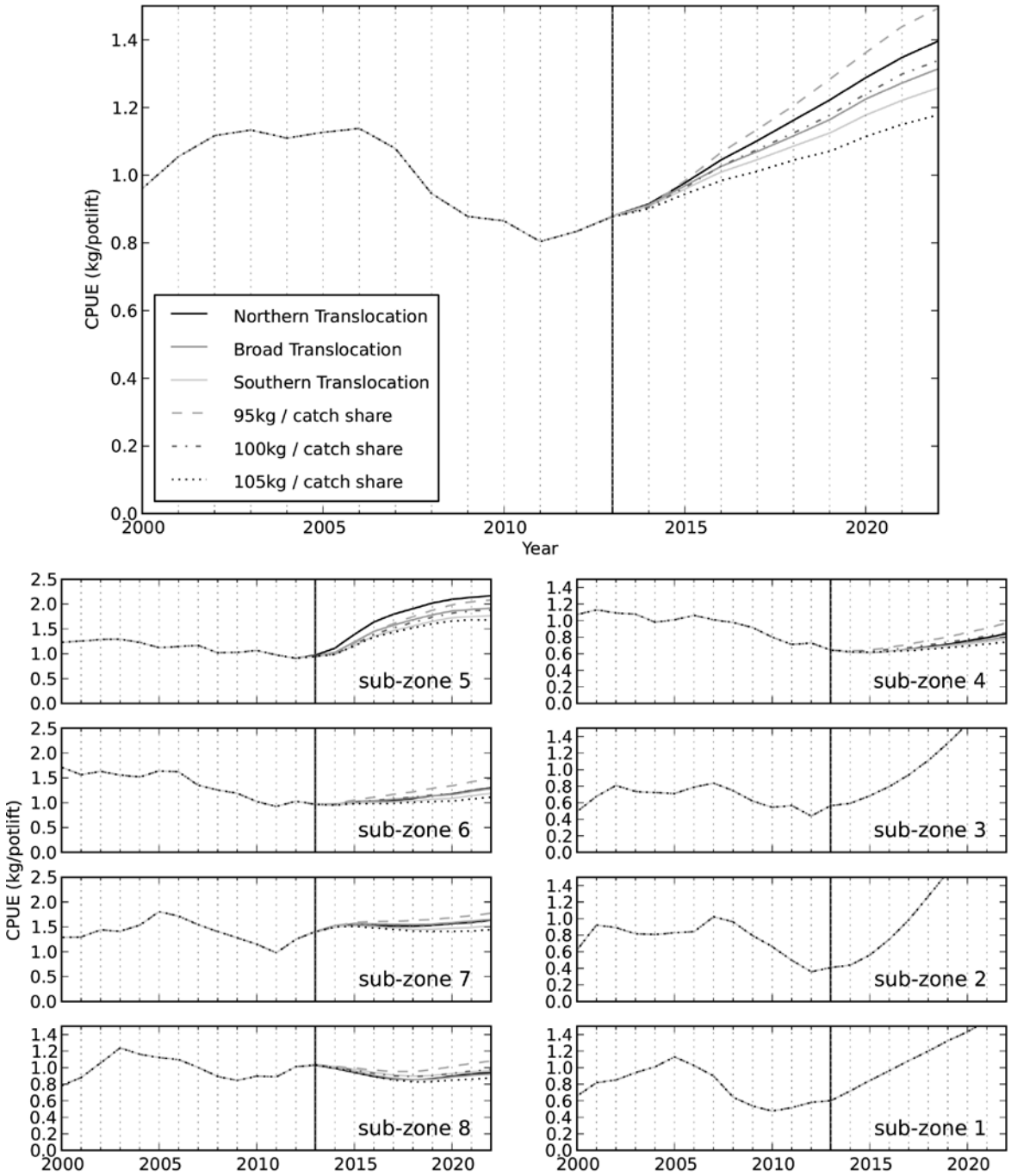


Figure 22. Median projections of catch rate (kg/ potlift) under various scenarios for Statewide (upper) and by sub-zone (lower). The rapid change in stock in sub-zones 1-3 is a consequence of the introduction of a constraining catch cap in this region in 2013, which was unrelated to translocation.

3.9. Sustainability and ecosystem indicators

The effect of translocation of 100,000 lobster p.a. on egg production was complex due to the interaction between the following processes: (i) translocated females grow faster and larger so become available for harvest at an earlier age; (ii) more eggs per female were produced

each spawning season because females were a larger size; (iii) a portion of translocated females skip egg production in the first spawning season after translocation; and (iv) the harvest rate on the entire stock is reduced as a consequence of greater productivity and stock abundance after translocation. The combined effect of these processes was a modest decline in total egg production for the first few years after translocation commenced, followed by a modest improvement in egg production as stock rebuilding accelerated. Total egg production is of less interest for management than regional egg production, with most concern around depleted egg production in faster growing northern areas (Hartmann et al., 2012). The translocation scenarios examined here improved egg production in these depleted northern areas (sub-zones 4 and 5), although only modestly, and to an insufficient level to resolve all management concerns in those areas (Figure 18).

Measures of ecosystem impacts from fishing also improved in scenarios with translocation, with higher levels of both total biomass and large (>145 mm CL) lobster biomass although only modestly and as per egg production, this would not be an important management outcome of translocation in the current structure. Nonetheless, we note that management is currently attempting to increase levels of both these measures of biomass for ecosystem health (DPIPWE, 2013) and translocation would slightly assist rather than hinder attempts to meet these goals.

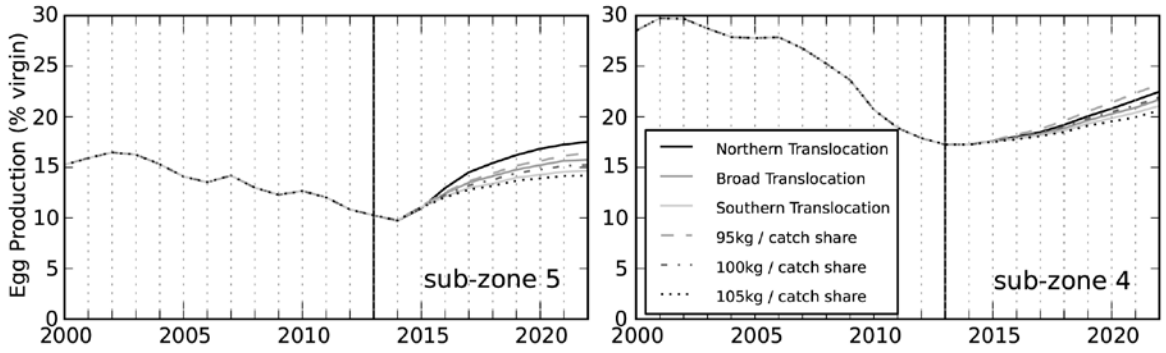


Figure 23. Median projections of egg production under various translocation scenarios for northern areas of the Tasmanian Southern Rock Lobster fishery where egg production is of concern.

4. Benefits and Adoption

This project moved translocation from pilot scale research operations to commercial operations. It followed previous research on translocation and was directly entirely at adoption. The main risk to the project at the commencement was resistance from a portion of the industry to the process. This was highlighted by a large number of Tasmanian commercial fishers signing a petition calling for an end to Southern Rock Lobster translocation, and then presenting this to the CRC. In that instance the response of the CRC was to simply point out that the project was initiated at the request of industry and the fate of future research and adoption lay entirely in the hands of industry, not the CRC. Nonetheless, this event illustrated the passion that translocation generated. Of particular concern was that the criticism was largely based on rumour and misunderstanding.

To address barriers to progress, the project focused on communication, which was most effective at the level of direct conversations at industry meetings and port visits. There were also three issues identified that led to additional research in this project, which was more information on health and genetic risks from translocation, plus monitoring of removal sites.

An industry committee was formed to oversee commercial scale translocations with many of the members of this committee having previously signed the petition against the project. This mix of people helped resolve many of the issues, although misinformation remained an issue at the end of the project and is always an issue when dealing with such a large group. Evidence of this is that there are many incorrect ideas that continue to circulate, such as claims that large numbers of legal-sized lobsters were moved, despite the presence of an observer on all trips.

At the conclusion of the project the industry voted to continue commercial scale operations using the approach developed in 2012 and 2013. They will now collect funds and manage operations through an industry committee. At this meeting the industry also rejected a proposal to increase production by this method by a further 50% to 78 tonnes per annum.

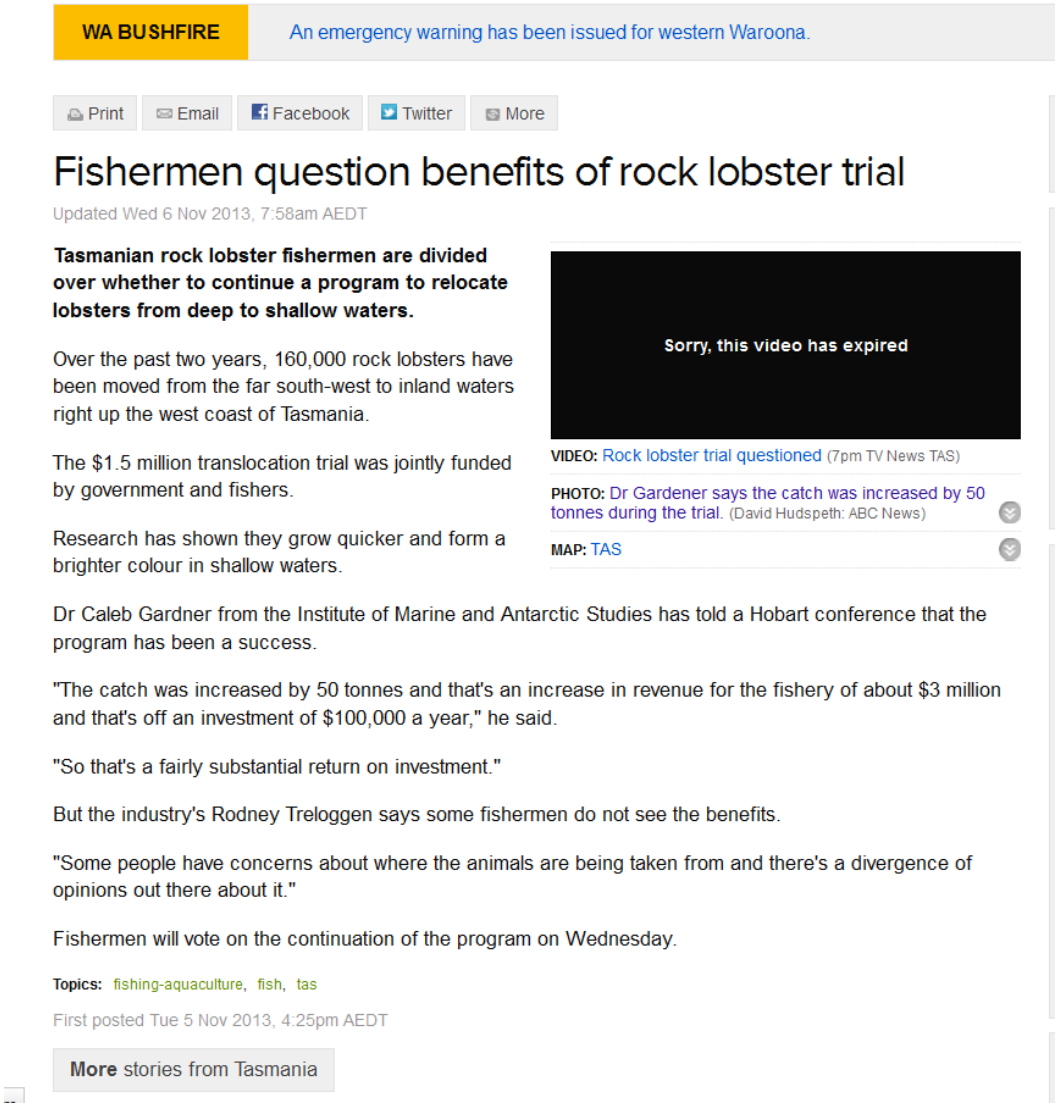
The benefit of this project is readily quantified in terms of increase in production, revenue, and asset value.

The project moved an average of 80,000 lobsters per annum, which resulted in an increase in the allowable commercial catch of 52 tonnes each year. This is an approximate increase in revenue of $6 million over the two years of the project, assuming an average market price of $60/kg.

Each kilogram of additional production was obtained at a cost to industry of $2, which is only 9% of the current lease price of $22. For future translocations the levy paid by fishers has been increased to $15 per unit. This increases the allocation at a cost of $3/kg, clearly a better prospect financially than leasing in quota at the current rate of $22/ kg.

Quota unit values reflect cash flow from lease payments to the units. These cash flows increase with translocation so that approximately $1300 of the market value of each quota

unit is attributable to translocation (based on current market yield of 7.7%) or $13.6 million capitalisation across the fishery.



WA BUSHFIRE An emergency warning has been issued for western Waroona.

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Fishermen question benefits of rock lobster trial

Updated Wed 6 Nov 2013, 7:58am AEDT

Tasmanian rock lobster fishermen are divided over whether to continue a program to relocate lobsters from deep to shallow waters.

Over the past two years, 160,000 rock lobsters have been moved from the far south-west to inland waters right up the west coast of Tasmania.

The $1.5 million translocation trial was jointly funded by government and fishers.

Research has shown they grow quicker and form a brighter colour in shallow waters.

Sorry, this video has expired

VIDEO: Rock lobster trial questioned (7pm TV News TAS)

PHOTO: Dr Gardener says the catch was increased by 50 tonnes during the trial. (David Hudspeth: ABC News)

MAP: TAS

Dr Caleb Gardner from the Institute of Marine and Antarctic Studies has told a Hobart conference that the program has been a success.

"The catch was increased by 50 tonnes and that's an increase in revenue for the fishery of about $3 million and that's off an investment of $100,000 a year," he said.

"So that's a fairly substantial return on investment."

But the industry's Rodney Treloggen says some fishermen do not see the benefits.

"Some people have concerns about where the animals are being taken from and there's a divergence of opinions out there about it."

Fishermen will vote on the continuation of the program on Wednesday.

Topics: fishing-aquaculture, fish, tas

First posted Tue 5 Nov 2013, 4:25pm AEDT

More stories from Tasmania

5. Further Development

At the time of completion of this report, three issues require further action.

1. The first and most significant is to shift the timing of fund collection and translocation operations to a more manageable time frame. This was an issue in 2012 and 2013 where funds were collected through the license process in March, at around the same time as catch rates began to decline. The quota had been set by this stage with the expectation that translocation would occur within a few weeks. As a result, each year there was a narrow window of only a month between funds being collected and catch rates starting to decline. This created a risk that the translocations could not be completed.

The solution to this is to collect funds in March for translocations scheduled later that year, through late spring and summer. This shift in timing of operations is underway using savings created in the project (from salary infalls). Translocations will occur with residual project funds in March 2014 so that funds collected from industry with their license fees in March 2014 can be used to pay for operations commencing November 2014. This provides adequate time for planning and flexibility in timing of operations. It is anticipated that this greater flexibility will reduce the cost of translocation because it should increase competition in the tender process and also better enable operators to target periods of highest catch rates and good weather.

	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar
Quota Year			←	—	—	—	—	—	—	—	—	—	—	—	→
High Catchability															
Funds collected			X												X
TACC advice provided to minister										X					

2. Despite efforts through the project to discuss and manage resistance of fishers who operate in removal areas, this issue remained and affected the scale of adoption of translocation. At the final vote in November 2013, fishers approved maintaining operations at the level that increases catch by 52 tonnes p.a. but did not support a modest increase in the scale of operations to 78 tonnes. This represents an opportunity cost of at least $1 million per annum. Our assessment was that this increase was trivial in terms of stock so resistance to even this small amount signals that translocation may never be adopted to its full potential in Tasmania, which appears to be in the order of 200 tonnes per annum.

Solutions here clearly include ongoing monitoring and communication, however during 2013 we also began to explore translocation with behavioural economic techniques. This involves a simulated fishery with players (fishers) competing in a fishery for cash payments. The main topic of interest is to see if cooperation and resistance to change is affected by stock rebuilding which is anticipated in the fishery. This is low cost research conducted through operational support for PhD students and will conclude mid 2014.

3. Further communication of translocation to National and International audiences is warranted because the project was a rare case of a novel approach to fishery management leading to improvements in production. Fisheries management needs examples like this to promote a culture where new ideas can be seriously explored. There tends to be resistance to new approaches such as translocation and enhancement. This project shows that very high returns on investment are possible with relatively simple changes to management.

6. Planned Outcomes

Public Benefit Outcomes

- increased productivity of recruits, which assists stock rebuilding of the fishery which is being pursued for ecosystem goals
- increase in tax receipts from more profitable commercial fishers. This is approximately $343,000 p.a. based on the marginal increase in yield of 52 t, the economic yield of $22 / kg (i.e. the lease price) and company tax rate of 30%.

Private Benefit Outcomes

- higher catch and catch rates increases economic yield from the commercial fishery, which results in higher payments to quota owners
- 5% of the state's population have both the capacity to fish recreationally for lobsters and desire to purchase a recreational Southern Rock Lobster license. These individuals benefit because commercial effort is drawn away from areas important to recreational fishers.

Linkages with CRC Milestone Outcomes

1.2 - Enhanced yields from wild-harvest innovations – complete. Additional production of 52 tonnes p.a. of Southern Rock Lobster @ cost of $3/ kg with expansion only limited by industry voting.
1.2.2 - Production interventions implemented in at least one fishery – complete in the Tasmanian SRL fishery.
1.2.3 - Annual production characterised and interventions optimised in at least one fishery – intervention initiated but not yet optimized in the fishery. TACC setting in the fishery based on natural recruitment has been optimized separately through an associated CRC project and incorporates translocation.

7. Conclusion

This project moved translocation from pilot scale research operations to full commercial operations. Previous research had examined a range of biological issues and concluded that translocating lobsters to areas of higher growth was a feasible option for increasing production in the Tasmanian fishery. Moving to commercial scale operations through this project involved collecting funds from commercial fishers through the annual quota renewal process. The project moved an average of 80,000 lobsters per annum, which resulted in an

increase in the allowable commercial catch of 52 tonnes each year. This is an approximate increase in revenue of $6 million over the two years of the project, assuming an average market price of $60/kg.

Governance processes were developed and will continue to be applied in the fishery as translocation continues into the future as a commercial operation managed through the peak industry body, the TRLFA.

Genetic testing confirmed previous studies and showed that the jurisdiction contained a single stock, as expected with such long lived larvae that disperse over wide areas. This showed that translocation would not harm genetic diversity of SRL.

Health testing confirmed advice from the Chief Veterinary Officer, which was that the operations were minimal risk.

Some parts of industry remain concerned about translocation. Although there is support for ongoing operations at a level that is commercial and provides a high return on investment, the scale of operations is still well below what could be achieved in this fishery. As a result, there is a foregone opportunity to obtain all the benefits associated with higher production which include stock rebuilding, increasing egg production, improving ecosystem function and increasing economic yield.

Translocation of lobsters in Tasmania is just one example of the challenge in improving fisheries management where beneficial change tends to be resisted. This is an ongoing challenge and although translocation has not yet been developed to an optimal level, it does provide an example of change and successful introduction of novel management.

8. References

Chandrapavan, A., Gardner, C. and Green, B.S. (2010). Growth rate of adult rock lobsters Jasus edwardsii increased through translocation, *Fisheries Research (Amsterdam)*, **105:** 244-247.

DPIPWE (2013). Department of Primary Industry, Water and the Environment Tasmanian Rock Lobster Fishery – New East Coast Management Arrangements, Tasmanian Government, 2013.

Emery TJ, Hartmann K, S.; GB, Gardner C, Tisdell J (in review). Handle with care: an analysis of the effects of appendage damage on the growth and productivity of the southern rock lobster (*Jasus edwardsii*)

Gardner, C., Frusher, S.D., Barrett, N., Haddon, M. and Buxton, C. (2006) Spatial variation in size at onset of maturity of female southern rock lobster Jasus edwardsii around Tasmania, Australia, *Scientia Marina*, **70:** 423-430.

Gardner, C., Hartmann, K., Punt, A. and Jennings, S. (submitted a). Estimating economic yield in an ITQ managed lobster fishery. Journal of Environmental Economics and Management.

Gardner, C., Hartmann, K., Punt, A. Jennings, S. and Green, B.S. (submitted b). A bioeconomic evaluation of translocation as a fisheries management tool. Journal of Environmental Economics and Management.

Gardner, C., Larkin, S. and Seijo, J.C. (2013). Systems to Maximize Economic Benefits from Lobster Fisheries., in: B. Phillips (Ed.) Lobsters: Biology, Management Aquaculture and Fisheries., Wiley-Blackwell, UK, pp. 113-132.

Gardner, C. and Van Putten, E.I. (2008) Biological Modeling of Translocation as a Management Tool for a Rock Lobster Fishery, *Reviews in Fisheries Science*, **16:** 81-90.

Green, B.S. and Gardner, C. (2009). Surviving a sea-change: survival of southern rock lobster (Jasus edwardsii) translocated to a site of fast growth, *ICES Journal of Marine Science*, **66:** 656-664.

Green, B.S., Gardner, C. and Kennedy, R.B. (2009). Generalised linear modelling of fecundity at length in southern rock lobsters, Jasus edwardsii, *Marine Biology*, **156:** 1941-1947.

Green, B.S., Gardner, C., Linnane, A.J., Hobday, D., Chandrapavan, A., Punt, A.E., McGarvey, R., Hartmann, K., Treloggen, R., Revill, H., Hoare, M. and Hawthorne, P. (2012). Australian Seafood CRC Project No. 2006/220. Spatial management of southern rock lobster fisheries to improve yield, value and sustainability.

Hartmann, K., Gardner, C. and Hobday, D. (2012). Tasmanian Rock Lobster Fishery 2010/11, in: IMAS Fishery Assessment Report, University of Tasmania. 2011.

Handlinger, J., Carson, J., Gardner, C., Pyecroft, S. and Sammons, J., (2006). Rock lobster enhancement and aquaculture sub-program: health assurance of southern rock lobsters. 77 pp. FRDC Report 2001/094.

Punt, A.E., Kennedy, R.B. and Frusher, S.D. (1997) Estimating the size-transition matrix for Tasmanian rock lobster, Jasus edwardsii, *Marine and Freshwater Research*, **48:** 981-992.

9. Appendices

9.1. Appendix 1: Intellectual Property

Data were collected on the catch during translocation operations and also recaptures of tagged lobsters. All governance and operational information on translocation is freely available.

9.2. Appendix 2: Staff

IMAS
Caleb Gardner
Klaas Hartmann
Bridget Green
Gary Carlos
Chris McKinlay
Alina Bermejo

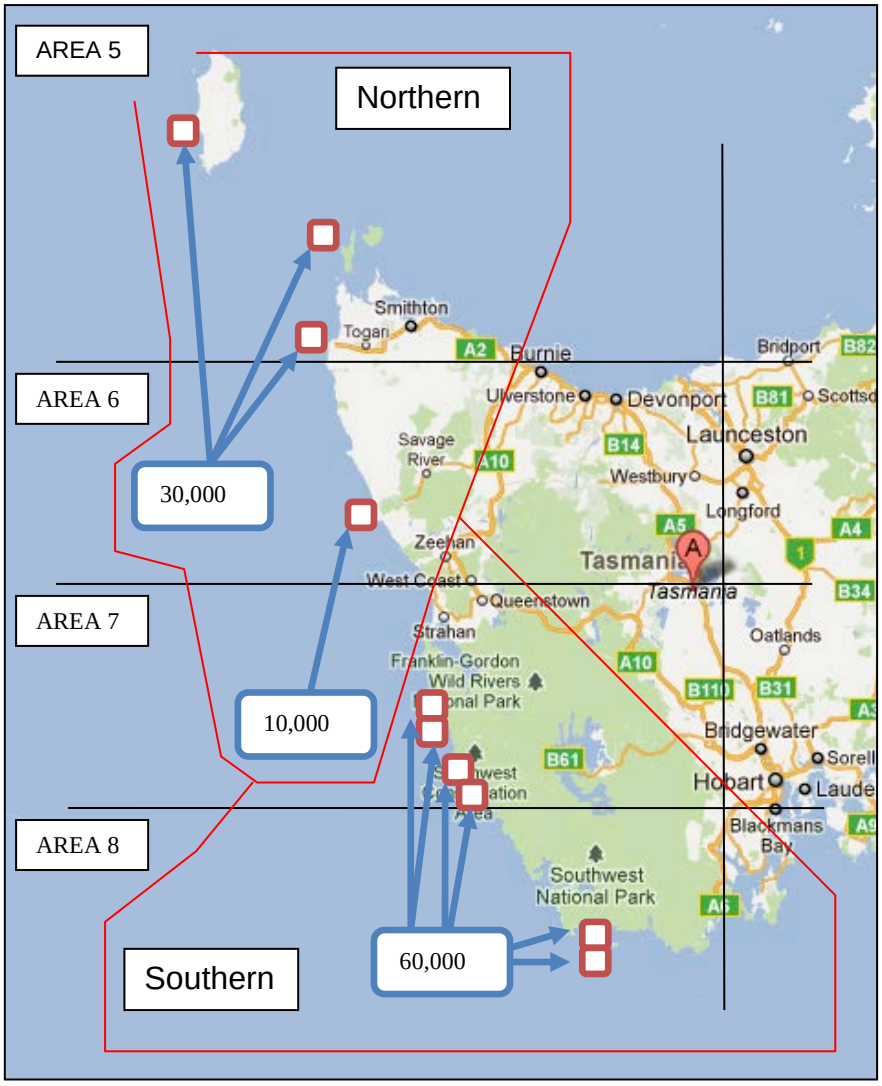
DPIPWE
Hilary Revill
James Parkinson

TRLFA
Rodney Treloggen

9.3. Appendix 3: Detail of Removal and Release Sites

UNIVERSITY'S REQUIREMENTS

1. The objective of this tender is to translocate Southern Rock Lobsters from offshore West Coast locations in Areas 8 to inshore locations in Areas 7 and 8.
2. The completion of the contract is to be measured by the number of lobsters translocated. The number of lobsters moved is to be estimated by counting lobsters in a subsample of the pots deployed and extrapolating from this sub-sample. A minimum of 20% of pots are to be marked before hauling (to remove selection bias) and all lobsters to be from counted these marked pots. Observers will be responsible for collecting information on counts of lobsters and will report back on a daily basis to the project committee.
3. All undersize lobsters are to be translocated, that is, there is no grading. Legal sized lobsters will be released rather than translocated where possible.
4. Lobsters to be released at night or dusk or dawn.
5. Sites are as described below.



Summary of translocation operations. Blue boxes show the number of lobsters to be moved from capture to release sites. Tenders can be for the Northern, Southern, or entire operations.

Latitudes and longitudes will be provided to the successful tenderer(s).

AREA 5
Release: target release is total of 30,000 lobsters from Area 6 with 10,000 into each of

- Waterwitch Reef, < 10 fm
- Albatross Island, <12 fm
- Porpoise Shoal, <12 fm

Capture: none

AREA 6
Release: target release is total of 10,000 lobsters from Area 7 into

- North Pieman, <12 fm

Capture: target capture is total of 30,000 lobsters from the following site. These are moved to block 5.

- Conicals, >25 fm

AREA 7
Release: target release is total of 40,000 lobsters from Area 8 with 10,000 into each of

- Margos to Clydies, <12 fm
- Bird Island to Condor, <12 fm
- Low rocky point reef, <12 fm
- The Shank, <12 fm

Capture: target capture is total of 10,000 lobsters from one of the following sites. These are moved to block 6.

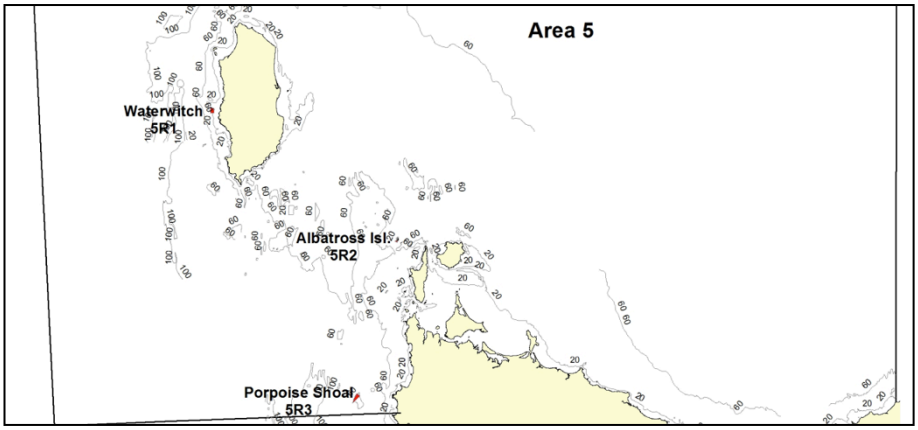
- Sth Hibbs, 28-38 fm
- Top Side High Rocky, 28-38 fm
- Hibbs, 28-38 fm

AREA 8
Release: target release is total of 20,000 lobsters from Area 8 with 10,000 into each of

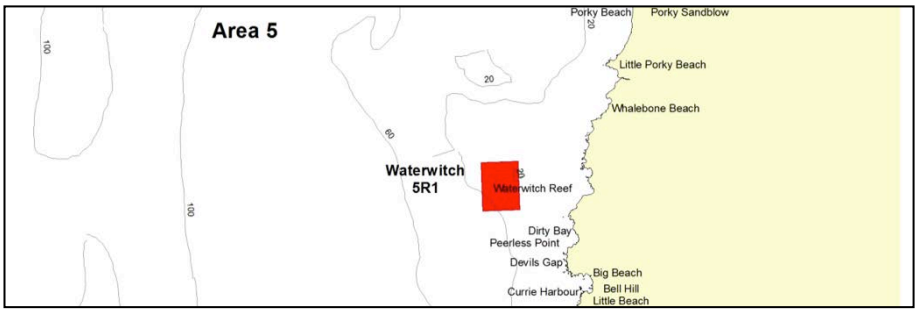
- Bridget to Red Point, <12 fm
- Walkers Island, <12 fm

Capture: target capture is total of 60,000 lobsters from the following sites. These are moved to block 7 and 8.

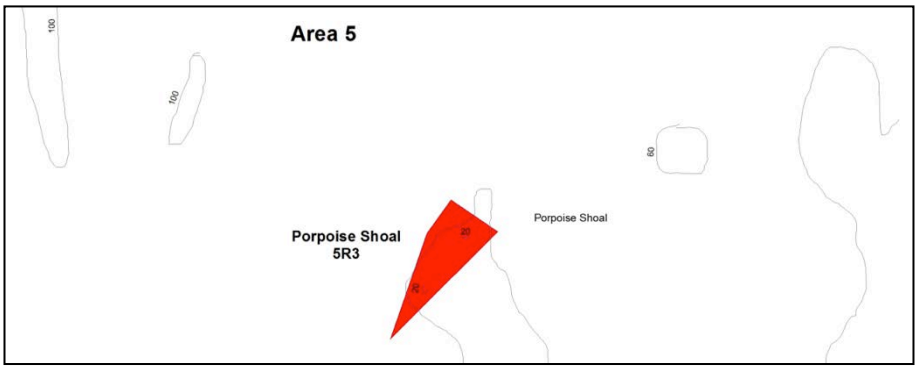
- Max 10,000 from Shoemakers to South cape, 28-38 fm
- Max 10,000 from SE Maatsuyker, 28-38 fm
- Max 10,000 from Wilson to Talopea, 28-38 fm
- Max 30,000 from Window Pane to Coffee Pot, 28-38 fm
- Max 10,000 from Mullochy to Long Point (excluding stripey patch), 28-38 fm



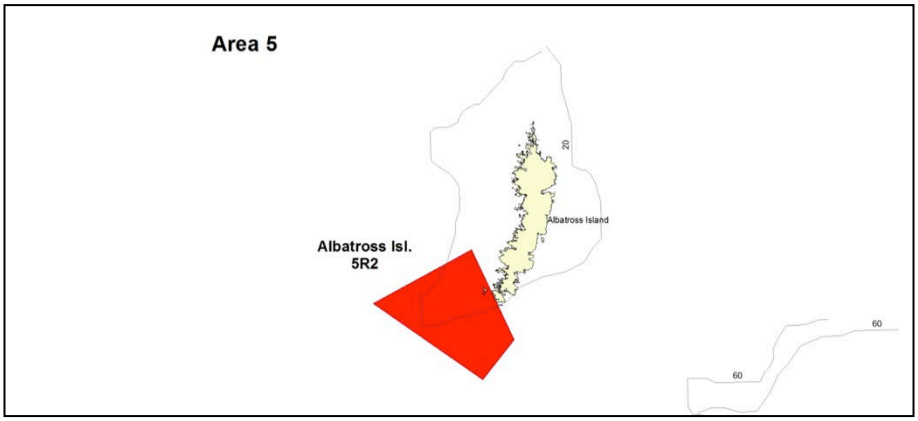
Area 5. Release sites. Three sites with 10,000 lobsters released into each.



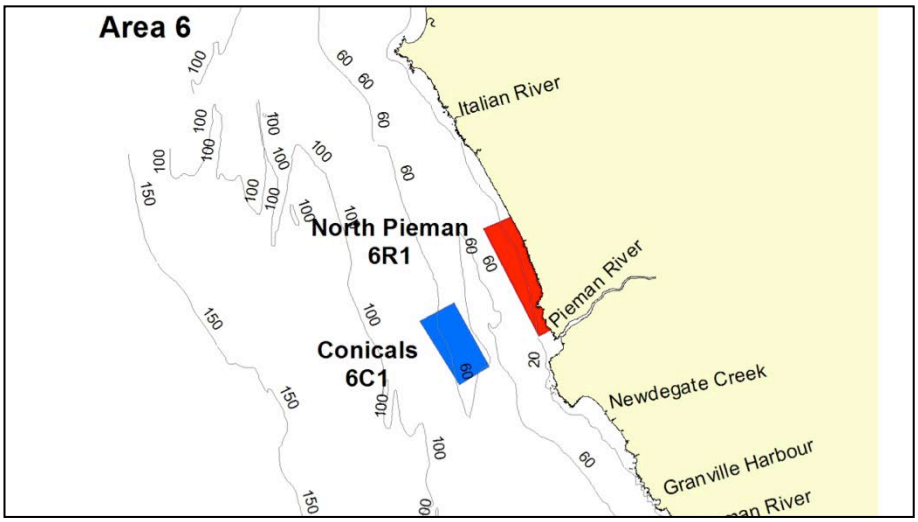
Area 5, Detail of the Waterwitch Reef release site.



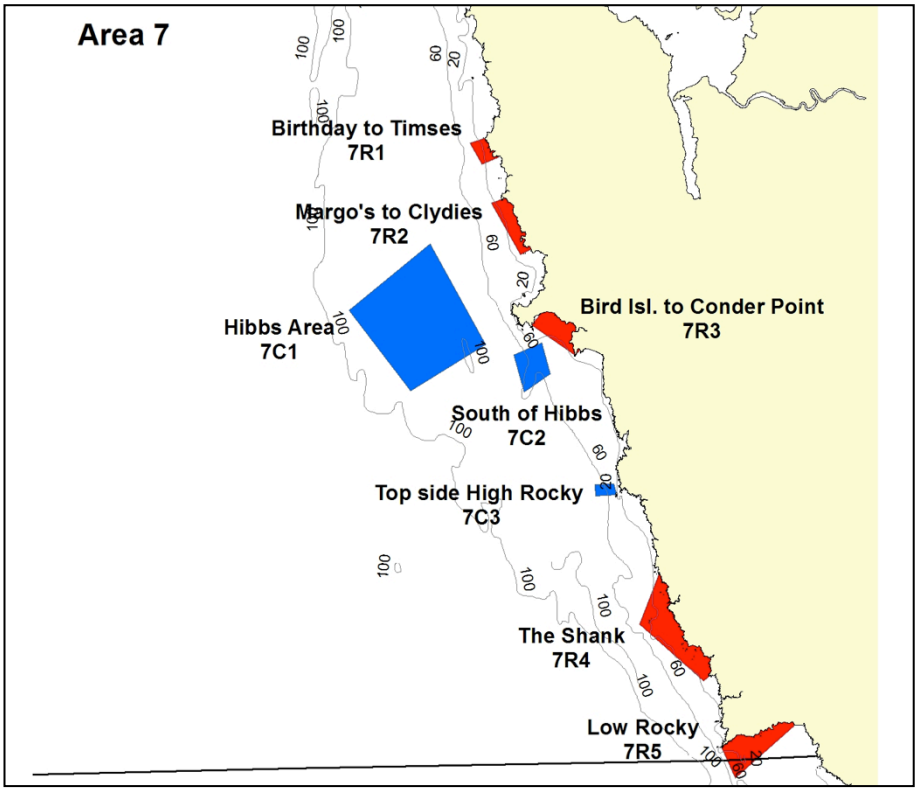
Area 5, Detail of the Porpoise Shoal release site.



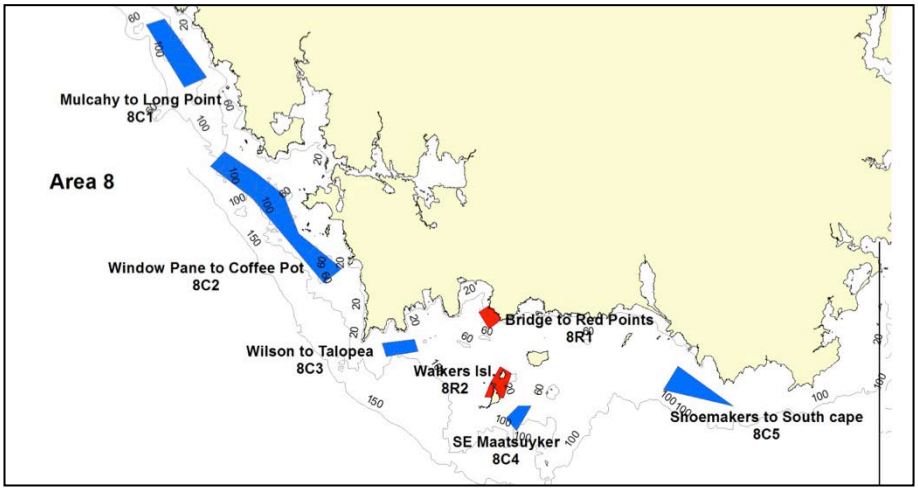
Area 5, Detail of the Albatross Island release site.



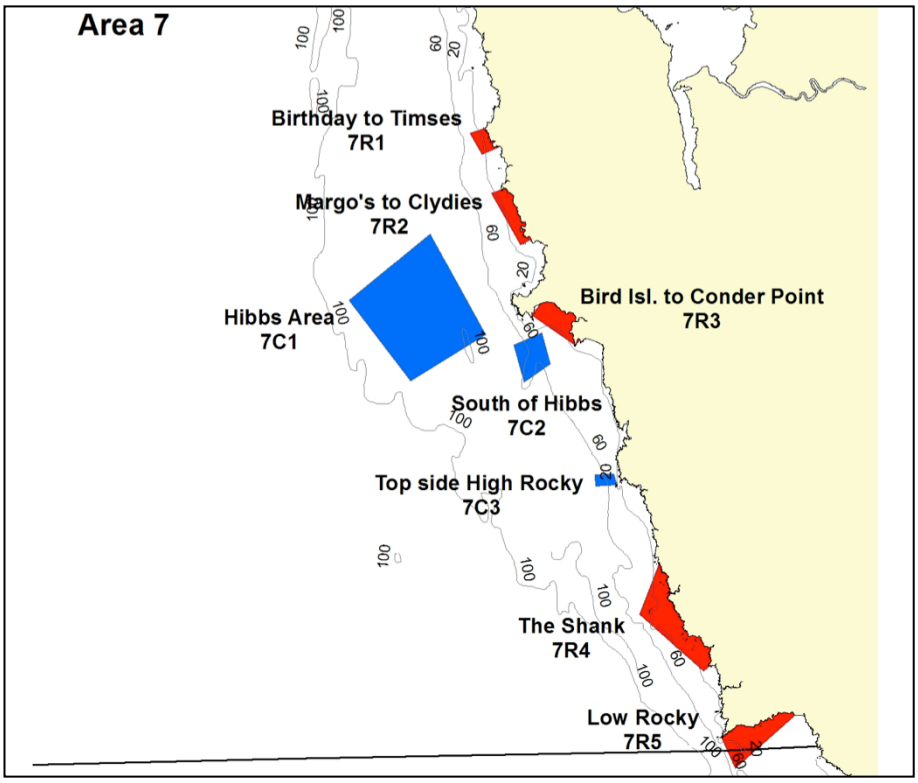
Area 6. Collection site at Conicals. Release site north of Pieman River in < 12 fm.



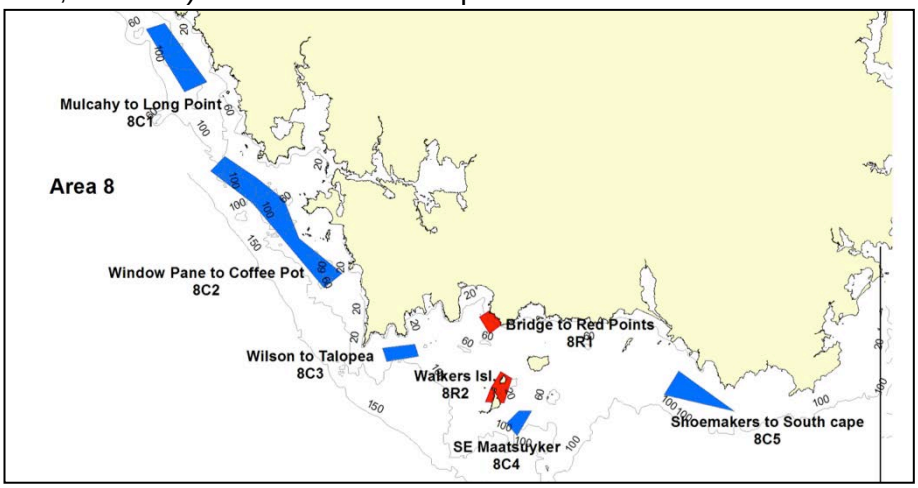
Area 7. Capture sites (blue) and release sites (red). Note that only four of the five release sites are to be used.



Area 8. Capture sites (blue) and release sites (red).



Area 7. Release sites (red). Note that only four of the five release sites are to be used. Blue sites (7C1, 7C2, and 7C3) are translocation capture sites unrelated to this tender.



Area 8. Capture sites (blue) and release sites (red).

Area	Block	Points	Nearest area of land - approximate only	Longitude (Degrees)	Longitude (Decimal Minutes)	Latitude (Degrees)	Latitude (Decimal Minutes)
7	Margos to Clydies	NE corner	Bay insisde Penerowne Point	145	15.48780	-42	31.34220
7	Margos to Clydies	SE corner	Point North Hibbs Bay	145	17.18100	-42	33.98220
7	Margos to Clydies	SW corner	Slightly SW direction out from Point North Hibbs Bay	145	16.42620	-42	34.25100
7	Margos to Clydies	NW corner	Slightly SW direction out from Penerowne Point	145	14.48460	-42	31.57860
7	Bird Island to Conder Point	NE corner	Red Reef Cliff	145	17.76780	-42	37.24260
7	Bird Island to Conder Point	SW corner	Conder Point	145	20.02705	-42	39.46786
7	Bird Island to Conder Point	NW corner	Leelinger Island	145	16.97323	-42	38.04757
7	The Shank	NE corner		145	25.61340	-42	50.55840
7	The Shank	SE corner	Just NE of Veridian Point	145	29.02740	-42	55.82820
7	The Shank	SW corner	SW of Veridian Point	145	28.51200	-42	56.12880
7	The Shank	NW corner	Out from Acacia Rocks	145	24.15720	-42	53.17200
7	Low Rocky Point Reef	NE corner	Western Side Big Beach	145	34.73460	-42	58.37160
7	Low Rocky Point Reef	SE corner	Almost Due South NE corner	145	34.73100	-42	58.51020
7	Low Rocky Point Reef	SW corner	SE direction from Low Rocky Point	145	30.61680	-43	1.07700
7	Low Rocky Point Reef	NW corner	Just SE of Low Rocky Point	145	29.65380	-42	59.50200
8	Bridge to Red Point	NE corner	Slightly North of Bridge Point	146	16.11240	-43	31.43580
8	Bridge to Red Point	SE corner	Red Point	146	17.34600	-43	32.64120
8	Bridge to Red Point	SW corner	SW of Red Point	146	15.99900	-43	33.36720
8	Bridge to Red Point	NW corner	SW of Bridge Point	146	14.87820	-43	31.99740
8	Walkers Island	NE corner	NE of Flat Witch Island	146	18.49980	-43	37.00020
8	Walkers Island	SE corner	East of Maatsuyker Island	146	17.58360	-43	39.00000
8	Walkers Island	SW corner	West of Maatsuyker Island	146	15.22020	-43	38.90460
8	Walkers Island	NW corner	NW of Flat Witch Island	146	17.21640	-43	36.45000
8	Shoemakers to South Cape	SE corner	South of Soldier Bluff	146	43.43340	-43	39.79980

8	Shoemakers to South Cape	SW corner	Further SE of Prettys Point	146	35.53320	-43	38.43360
8	Shoemakers to South Cape	NW corner	SE of Prettys Point	146	37.16640	-43	36.49980
8	SE Maatsuyker	NE corner	SE of Maatsuyker Island	146	19.24980	-43	39.64980
8	SE Maatsuyker	SE corner	SE of Maatsuyker Island	146	20.22900	-43	40.29960
8	SE Maatsuyker	SW corner	SE of Maatsuyker Island	146	19.00020	-43	41.68320
8	SE Maatsuyker	NW corner	SE of Maatsuyker Island	146	17.80020	-43	40.66680
8	Wilson to Talopea	NE corner	SE of Talopea Point	146	7.61640	-43	34.16640
8	Wilson to Talopea	SE corner	Further SE of Talopea Point	146	8.06640	-43	35.14980
8	Wilson to Talopea	SW corner	Further South of Wilson Rocks	146	4.45800	-43	35.54100
8	Wilson to Talopea	NW corner	South of Wilson Rocks	146	4.02300	-43	34.45380
8	Window Pane to Coffee Pot	NE corner	SE Coffee Pot Reef	145	46.63320	-43	18.66660
8	Window Pane to Coffee Pot	NE intermediate point	SSE of North Head	145	50.10000	-43	20.43360
8	Window Pane to Coffee Pot	NE intermediate point	NE of Hilliard Head	145	53.16660	-43	22.24980
8	Window Pane to Coffee Pot	NE intermediate point	Near Sugarloaf Rock	145	54.79980	-43	25.43340
8	Window Pane to Coffee Pot	SE corner	SE Flying Cloud Point	145	59.59980	-43	28.33320
8	Window Pane to Coffee Pot	SW corner	Further SE Flying Cloud Point	145	57.55020	-43	29.50020
8	Window Pane to Coffee Pot	intermediate NW point	Slightly NE Hiliard Head (approx 7.5 km to sea)	145	49.66680	-43	22.50000
8	Window Pane to Coffee Pot	NW corner	>5 km to SW of Coffee Pot Reef	145	45.00000	-43	19.83360
8	Mulcahy to Long Point (excluding Stripy Patch)	NE corner	ESE of Mulcahy Bay	145	40.16580	-43	7.74180
8	Mulcahy to Long Point (excluding Stripy Patch)	SE corner	SE of Svenor Point	145	44.76420	-43	12.59820
8	Mulcahy to Long Point (excluding Stripy Patch)	SW corner	More SE of Svenor Point	145	42.24780	-43	13.37580
8	Mulcahy to Long Point (excluding Stripy Patch)	NW corner	More ESE of Mulcahy Bay	145	38.11920	-43	8.20260

9.4. Appendix 4: Advertisement, Request for Tender

Example for the northern component of the translocation operations

Rock lobster translocation

Applications are invited from suitably licensed, equipped and experienced fishers to tender for the translocation of southern rock lobsters from offshore West Coast locations in Areas 6 and 7 to inshore locations in Areas 5 and 6.

Translocation of about 40,000 lobsters will occur within a period of five weeks, beginning on or about 15th February 2013.

Tender documents and further information are available in hard copy or email from Caleb Gardner (caleb.gardner@utas.edu.au), phone 03 62277233, or mobile 0409 427 366

Applications close: 5pm Friday, 8 February 2013.

9.5. Appendix 5: Requirements provided to operators for translocation tenders

Capturing Lobsters.

1. All potting for capture of lobsters is to be in the depth 28- 38 fathoms.
2. Capture sites are within the areas defined below.
3. The number of lobsters per capture site is 10,000
4. The intent is to capture pale, slow growing lobsters
5. Both sexes are to be translocated.
6. Sized lobsters are to be returned to the water where possible.
7. Recognising that it's difficult to count such a large number of lobsters, the number captured can be estimated by marking 20% of pots, counting the lobsters in this subset of pots, and then multiplying up to the rest of the pots.
8. The observers duty is to tag lobsters, doing 200 per day and measure a further 200 animals. This is their priority above all other tasks and the main reason they're getting paid to be aboard. We need to know where each of these lobsters are released so if one translocation trip involves two different release sites – please don't mix up the tagged lobsters! You'll need to ensure the tagged lobsters are kept separated.
9. The location of pots sets to capture lobsters must be recorded. This is the normal process for observer sampling.
10. If you become aware of other possible capture sites that have large numbers of slow growing, pale or wedgetail lobsters that are moving - it may be possible to include these locations. Please contact IMAS and we'll seek approval from the industry committee.

Releasing lobsters

1. All releases are to be into less than 12 fathoms of water
2. Release sites are within the areas defined below.
3. Releases are to be done at dusk or at night wherever possible.
4. Releases should be in piles rather than spread out along the coast and ideally in the middle of the release site. It's fine to release 10,000 lobsters into a single spot if this is done at night to provide protection from predators.

Keeping lobsters for health checks

This time we're going to do health checks on lobsters. We need 100 lobsters kept for us and these will be sent to the Fish Health Lab for testing. Ideally you'd keep any sick looking lobsters found during the trip (if you're able to keep these separate??). If not, just keep 100 lobsters from the last trip.

General

Please provide a daily update to IMAS of progress.

9.6. Appendix 6: Genetic Analyses of Translocated Lobsters

This research has been published previously as "Morgan, DE and Green, BS and Murphy, NP* and Strugnell, JM*, "Investigation of genetic structure between deep and shallow populations of the southern rock lobster, Jasus Edwardsii in Tasmania, Australia", PLOS One, **8** (10) Article e77978. ISSN 1932-6203 (2013)"*

Investigation of genetic structure between deep and shallow populations of the southern rock lobster, Jasus Edwardsii in Tasmania, Australia

Abstract
The southern rock lobster, *Jasus edwardsii*, is a commercially important species, worth $200 million to the Australian economy. There are clear phenotypic differences between shallow water (red coloured) and deeper water (pale coloured) individuals. Translocations of individuals from deeper water to shallower waters are currently being trialled as a management strategy to facilitate a phenotypic change from lower value pale colouration, common in deeper waters, to the higher value red colouration found in shallow waters. Although panmixia across the J. edwardsii range has been long assumed, it is critical to assess the genetic variability of the species to ensure that the level of population connectivity is appropriately understood and translocations do not have unintended consequences. Eight microsatellite loci were used to investigate genetic differentiation between six sites (three shallow, three deep) across southern Tasmania, and one from New Zealand. Analyses rejected the assumption of panmixia, revealing small levels of genetic differentiation across southern Tasmania, significant levels of differentiation between Tasmania and New Zealand, and high levels of asymmetric gene flow in an easterly direction from Tasmania into New Zealand. These results suggest that translocation among Tasmanian populations are not likely to be problematic, however, a re-consideration of panmictic stock structure for this species is necessary.

Keywords: Translocation, microsatellites, larval dispersal, population genetics, southern rock lobster, *Jasus*

Introduction
Human-mediated movement of species, known as translocation or assisted migration, is increasing in popularity as a strategy to maintain species abundance, connectivity and diversity. Translocation has been used commonly throughout agricultural history, and it is currently also an important conservation strategy for threatened species [1,2]. Successful translocation of individuals is reliant on a number of biological, behavioural and genetic factors. If translocation programs between populations fail to recognise genetic differences between prospective populations, the process can have serious effects on the species in question, including partial or complete replacement of the local population, competition resulting in population size reduction, inbreeding depression, outbreeding depression and consequent loss in fitness, 'swamping' or disease introduction, or loss of localized adaptations [3]. Understanding genetic connectivity between populations is key for effective species management and successful translocations between populations [4].

Pilot translocations were trialled in the commercially important southern rock lobster (*Jasus edwardsii*), to determine if it was possible to improve value and productivity of the Australian stock [5,6]. Between 2004 and 2008, lobsters were translocated from deeper water

(>60 metres depth) locations in Tasmania and released in shallower water locations (0-30 m depth) [5,7]. Importantly, there are clear phenotypic differences between these shallow and deep water populations of southern rock lobster. The shallow water phenotype is characterised by a darker red shell colour, larger body size and shape, higher vitality for live transport and faster growth rate, as compared to the deep water phenotype [6,8,9]. These pilot translocations of 30,000 individuals were a biological proof of concept, and now there is a commercial scale of 100,000 to determine if it may be commercially viable [5].

It is assumed that phenotypic differences between shallow and deep populations of the southern rock lobster are due to differences in habitat, and are not genetic, as pilot studies have shown that translocated, pale individuals change to the more desired phenotype after a single moult [5,8]. In cases of phenotypic plasticity such as this, there are species (aquatic and terrestrial) that show adaptive variation due to both phenotypic plasticity as well as genetic differentiation [10]. Morphological variation in pumpkinseed sunfish was explained by both genetic and phenotypically plastic characteristics [10]. The idea that genetic differentiation could be present between populations demonstrating phenotypic plasticity, is central to this study, as this may require consideration for conservation of populations with differential genetic characteristics across phenotypic divides.

Like many marine species with long larval phases, the southern rock lobster has been assumed to be panmictic throughout the range of Australasia [11-13]. Knowledge of genetic stock structure is based upon a single genetic study of nucleotide sequence polymorphisms in the mitochondrial genome [11] and a few allozyme studies [12,13]. Recent research of marine species is increasingly showing finer scale population subdivision than previously thought [14-16]. This includes the southern rock lobster around New Zealand [16], where significant population subdivision and dispersal patterns have been demonstrated, countering these assumptions of panmixia. Additionally, larval transport models via ocean currents also suggest that population structure is likely to be complex [17,18]. As microsatellite markers were recently developed for the southern rock lobster [19], the tools are available to assess population connectivity for this species at a level appropriate to identify genetic structure.

This study aims to use microsatellite markers to investigate genetic differentiation among Tasmanian populations of the southern rock lobster, where translocations are under consideration as an ongoing management strategy. Analysis of genetic structure will occur at different levels, including between 1) phenotypically different populations of shallow water (red phenotype) and deep water (pale phenotype) lobsters, 2) fine scale geographic separation of Tasmanian populations, 3) regional geographic separation in east and west Tasmanian populations, and 4) the oceanic divide of Tasmania and a New Zealand site. This will help to determine if current translocation efforts stand to negatively impact the southern rock lobster, and if there is significance in the scale and directionality of connectivity for this species. Potential patterns in connectivity and source-sink recruitment relationships may be important in the appropriate management and success of translocation for this species in the future.

Materials and Methods

Sample Collection

Lobsters were sampled from six sites with different phenotypes across the southern coast of Tasmania (Fig. 1). Baited traps deployed and collected from research and commercial vessels were used to catch lobsters. Three shallow water sites sampled (Taroona Reserve [TAR], Mutton Bird Island [MBI, South of Port Davey] and Hobbs Island [HI, North of Port Davey]), were between 0 and 30 metres water depth, and comprised of lobsters with red

coloured phenotypes. Three deep water sites sampled (Maatsyuker Island [MAT, translocated into Taroona Reserve between 2004 and 2008], Cape Queen Elizabeth [CQE] and East Pyramids [EP, Port Davey]) were greater than 60 metres in depth, and were largely populated by pale coloured lobsters. Distances between sample sites (by sea) range from 10 km (between EP and MBI) to 220 km apart (between HI and TAR). We will consider the effects of geographic and oceanic distance as well as phenotypic difference, and any potentially resulting genetic patterns on subsequent translocations within the stock.

Samples of rock lobster in Taroona reserve were collected on 1-4 February 2012 (including translocated individuals from Maatsyuker Island). A clip of tissue from the pleopod was stored in 95% ethanol, and the lobster released. Pleopod tissue samples from other Tasmanian sites were collected from 15 January to 15 February 2012. In addition, tissue samples were taken from lobsters collected from Taieri Mouth, Otago Harbour and Moeraki on the south island of New Zealand (NZ) (Fig. 1) during August 2011. All pleopod samples were assigned unique ID tags and stored individually in 95% ethanol at -20°C.

DNA Extraction, PCR Amplification and Genotyping

DNA was extracted from a total of 460 individuals using the high salt extraction method [20]. Nine microsatellite loci identified by Thomas and Bell [19] for use on *J. edwardsii* (Table 1), were assigned unique fluorophores (FAM, NED, VIC, PET) [21], for fluorescent tagging of DNA in a PCR reaction. PCR reactions were performed to amplify selected DNA fragments with MyTaq RedMix (Bioline) in 11µl PCR reaction mixtures using the PCR protocol recommended by Thomas and Bell [19]. Each mix contained 5.43µl of MyTaq RedMix, 0.07µl of 10mM forward primer, 0.22µl of 10mM reverse primer, 0.17µl of 5pmol/µl fluorescent dye (FAM, NED, VIC, PET), 4.11µl of H_2O and 1µl of concentrated DNA product.

PCR products were sent to the Australian Genome Research Facility Ltd (AGRF) for capillary separation. Results were visualised in GENEIOUS PRO version 5.6.4 [22], using the microsatellite analysis external plug-in [23]. PCRs were repeated for those individuals for which unclear or missing signals were obtained for up to 3 more times before being classed as missing data.

Genetic Polymorphism

Binned genotypes scored were formatted in GENALEX version 6.4 [24]. MICRO-CHECKER version 2.2.3 [25], was used to check allelic data for negative, zero or out of range values. Null allele frequencies were estimated in FREENA [26]. Due to a significant portion of null alleles found (>10% at any locus) in FREENA, false homozygote frequencies were used to adjust the number of null alleles by re-naming potential nulls as 999 [27]. Further analysis of data used both the adjusted allele frequency data and raw data to assess the effect of null alleles on results. GENEPOP version 4.1.3 [28,29], FSTAT version 2.9.3 [30], and GENALEX were used to analyse basic descriptive statistics within and between populations. Allelic diversity, observed versus expected levels of heterozygosity and levels of inbreeding (using the Fixation index estimate) were calculated in GENALEX. FSTAT was used to calculate allelic richness. GENEPOP was used to test for significant departures from Hardy Weinberg Equilibrium. The number of private alleles for each population and linkage disequilibrium between loci were assessed using GENEPOP.

Genetic Connectivity and Population Subdivision

Pair wise F-statistics (Fst's) were calculated in FSTAT between assigned groups of individuals. Fst's were tested by hierarchical comparisons between: 1) all populations, 2) shallow water and deep water groups, 3) paired groups of east Tasmanian coast and west Tasmanian coast, and 4) paired groups of Tasmania and New Zealand.

Population Structure

STRUCTURE version 2.3.4 [31], was used to cluster individuals. The admixture model was used to assume some level of connection between populations. A burn-in length of 100,000, 500,000 MCMC replicates, 3 iterations and a search for the number of clusters (K) between 1 and 10 (the assumed number of populations present plus 3) were used. STRUCTURE HARVESTER online version 0.6.92 [32], was used to evaluate results using the Evanno method [33]. Discriminant analysis of principle components (DAPC) was used to assess data using the program R version 2.15.1 [34], run via R STUDIO version 0.96.331 [35]. PCA was performed in R using ADEGENET version 1.3-4 [36,37]. 60 principle components were retained as predictors for discriminant analysis.

Migration and Directionality of Gene Flow

BAYESASS version 3.0.1 [38] was used to assess admixture [39]. Raw genotype data was converted for input analysis into BAYESASS using FORMATOMATIC version 0.8.1 [40]. Trace output convergence was assessed using TRACER version 1.5 [41]. 21,000,000 iterations and 5,000,000 burn in length were used to produce convergent trace outputs. The data was tested in a hierarchical manner between different geographic distances.

Results

DNA Extraction, PCR Amplification and Genotyping

A total of 460 individuals were genotyped for eight microsatellite loci. Despite numerous attempts to optimise PCR conditions for the locus JE_05 [19] it was successful in less than 10% of reactions, and so was excluded from this study.

Genetic Polymorphism

A significant frequency of null alleles were detected from loci JE_01, JE_LZ, JE_17, JE_40 and JE_07 using MICRO-CHECKER [25]. In addition, 3 of these loci, JE_01, JE_17 and JE_07, were suggested to have 'possible stuttering', most likely due to null allele effects [25]. Null allele frequencies for these five loci were quantified by the EM algorithm [42] (Table S1) and adjusted using FREENA [26], to correct for a homozygote excess by random re-labelling of homozygote null alleles with the unique number 999, using estimates of false homozygote frequencies. No large allele dropout was detected, and loci JE_NS, JE_9M and JE_JM had non-significant (less than 10%) null alleles. For the adjusted dataset, all populations were accepted as under HWE. All loci were found to be in linkage equilibrium.

Allelic richness for each population is similar (~17 alleles) (Table 2). TAR, HI and NZ populations have a lower number of private alleles (6-9), compared with EP, which has a slightly higher number of private alleles (19). No significant difference in allelic richness was detected between populations (~18 across all populations). After correction for null alleles, the observed levels of heterozygosity are consistent with the expected (~0.9/~0.9), showing that populations are under HWE. Populations had neither a homozygote (inbreeding) or heterozygote (outbreeding) excess (-0.032 to -0.007) indicating populations conformed to HWE once corrections for null alleles were considered.

Genetic Connectivity and Population Subdivision

F-statistics were used to compare across 1) all populations, 2) solely between Tasmanian populations, 3) between red (shallow) and pale (deep) populations of Tasmania, and 4) between east Tasmania and west Tasmania. After Bonferroni correction, the data set indicated a significant difference between NZ and the other six Tasmanian populations, the largest oceanographic distance compared (Fst=0.0290-0.0342) (Table 3). Fst analysis of the data set indicated a $p<0.05$ significant difference between shallow and deep populations of MBI and CQE (Fst=0.0021) (additionally separated across east and west Tasmania), between the west coast populations of shallow populations of HI and MBI (Fst=0.001) and between the deep population of MAT and the shallow population HI (Fst=0.003). The dataset was also analysed without locus JE_07, due to an unusual repeat motif flagged early on in analysis. Most results were consistent to those with the locus included, and overall significant differences noted between Tasmania and New Zealand did not change (Table S2).

Table 1. Microsatellite loci characteristics modified from Thomas and Bell [19]

Locus	GenBank Accession Number	Repeat motif	Ta	$Size_M$ (bp)
JE_01	JN806248	$(CA)_{62}$	70–60	121-261
JE_17	JN806249	$(ATAC)_{13}$	70–60	165-253
JE_NS	JN806252	$(CAG)_{50}$	70–60	286-553
JE_JM	JN806253	$(TTAGG)_3$ $(TA)_2$ $(GGTTA)_{25}$	70–60	190-389
JE_05	JN806254	$(TACCT)_{20}$	70–60	Na
JE_LZ	JN806255	$(GGTTA)_{33}$	70–60	263-568
JE_40	JN806250	$(GTAG)_{62}$	60–50	357-509
JE_07	JN806251	$(CGT)_{52}$	60–50	398-465
JE_9M	JN806256	$(ACCTA)_9$ $(ACCAA)_3$ $(ACCTA)_7$	60–50	187-322

Ta, Touchdown PCR protocol annealing temperature; ($Size_M$), modified base pair range from Thomas and Bell estimates [19].

Table 2. Descriptive statistics across all populations

Population:	N	N_A	N_{PA}	AR	H_O	H_E	F_{IS}
TAR	98	29.875	9	18.095	0.924	0.908	-0.018
MBI	68	28.000	12	17.805	0.921	0.907	-0.014
HI	59	25.750	6	17.720	0.913	0.906	-0.007
MAT	73	28.500	10	18.245	0.926	0.905	-0.022
CQE	67	27.875	11	18.058	0.922	0.903	-0.021
EP	70	29.250	19	18.351	0.928	0.911	-0.018
NZ	25	17.125	6	16.542	0.866	0.846	-0.032

N, number of individuals per population; N_A, average number of alleles across all loci per population; AR, average allelic richness across all loci per population; H_O, observed level of heterozygosity; H_E, expected levels of heterozygosity; F_{IS}, Fixation index (inbreeding coefficient). TAR, Taroona Reserve; MBI, Mutton Bird Island; HI, Hobbs Island; MAT, Maatsyuker Island; CQE, Cape Queen Elizabeth; EP, East Pyramids; NZ, New Zealand.

Table 3. F-statistics across all populations

	TAR	MBI	HI	MAT	CQE	EP
MBI	0.0002					
HI	0.0005	**0.0010**				
MAT	0.0016	0.0024	**0.0030**			
CQE	0.0003	**0.0021**	0.0015	-0.0004		
EP	0.0012	0.0026	-0.0005	0.0008	0.0002	
NZ	**0.0292***	**0.0320***	**0.0342***	**0.0342***	**0.0290***	**0.0312***

Data set of Fst values, bold indicates significant values of p value <0.05, ***** significant values after Bonferroni correction of p<0.002381. TAR, Taroona Reserve; MBI, Mutton Bird Island; HI, Hobbs Island; MAT, Maatsyuker Island; CQE, Cape Queen Elizabeth; EP, East Pyramids; NZ, New Zealand.

Table 4. Percentage contribution of each population to assigned clusters (K=6) using STRUCTURE

Population:	**Contribution to Clusters (Percentage):**					
	1	**2**	**3**	**4**	**5**	**6**
TAR	17	17	16	16	17	17
MBI	19	15	13	19	19	15
HI	16	18	16	17	17	16
MAT	16	17	16	18	17	17
CQE	18	16	18	17	16	16
EP	15	19	16	17	17	17
NZ	18	12	29	12	17	13

TAR, Taroona Reserve; MBI, Mutton Bird Island; HI, Hobbs Island; MAT, Maatsyuker Island; CQE, Cape Queen Elizabeth; EP, East Pyramids; NZ, New Zealand.

Table 5. Percentage contribution of each population to the clusters assigned by DAPC

Population:	**Contribution to Clusters (Percentage):**			
	1	**2**	**3**	**4**
TAR	29	38	17	16
MBI	47	22	7	24
HI	36	32	15	17
MAT	34	34	19	12
CQE	27	31	24	18
EP	26	37	17	20
NZ	0	16	12	72

TAR, Taroona Reserve; MBI, Mutton Bird Island; HI, Hobbs Island; MAT, Maatsyuker Island; CQE, Cape Queen Elizabeth; EP, East Pyramids; NZ, New Zealand.

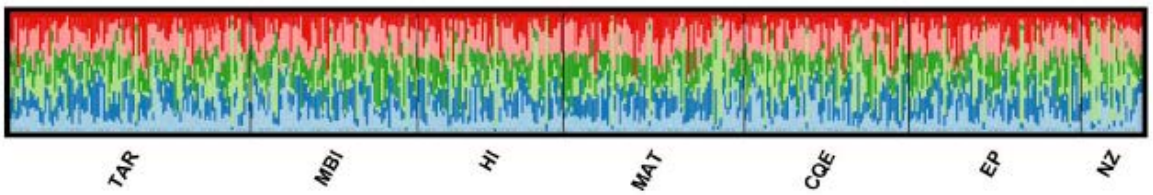
Table 6. Migration rates (posterior probabilities) between Tasmania and New Zealand

	TAS	NZ
TAS	***0.9987*** (0.0012)	0.0013 (0.0012)
NZ	0.3208 (0.0121)	***0.6792*** (0.0121)

Bold/italicised values indicate self recruitment, values in parentheses indicate standard deviation, left column indicates where migrants travelled to, top row indicates where migrants originated from. TAS, Tasmania; NZ, New Zealand.

When Tasmanian populations were combined and compared to the NZ population in a pair wise Fst test, analysis showed significant levels of differentiation (Fst=0.0305) over this large scale distance. When populations from Tasmania only were compared by grouping the three shallow populations and the three deep populations in a pairwise analysis, no significant difference was detected. Similarly, when comparing populations on the east coast of Tasmania (TAR, CQE) with populations on the west coast of Tasmania (MBI, HI, MAT, EP) no significant difference was found. Overall, F-statistics indicated a significant difference between Tasmanian and New Zealand individuals, and a small but less significant level of differentiation among some populations of Tasmania, with no clear pattern in differentiation and phenotype or geographical distance.

Figure 2. Structure assignment of individuals across all populations into clusters of best fit at K=6. Colours indicate percentage contribution of individuals to assigned clusters (y axis), individuals represented by each line (x axis), black lines separate populations from which individuals belong. TAR, Taroona Reserve; MBI, Mutton Bird Island; HI, Hobbs Island; MAT, Maatsyuker Island; CQE, Cape Queen Elizabeth; EP, East Pyramids; NZ, New Zealand.

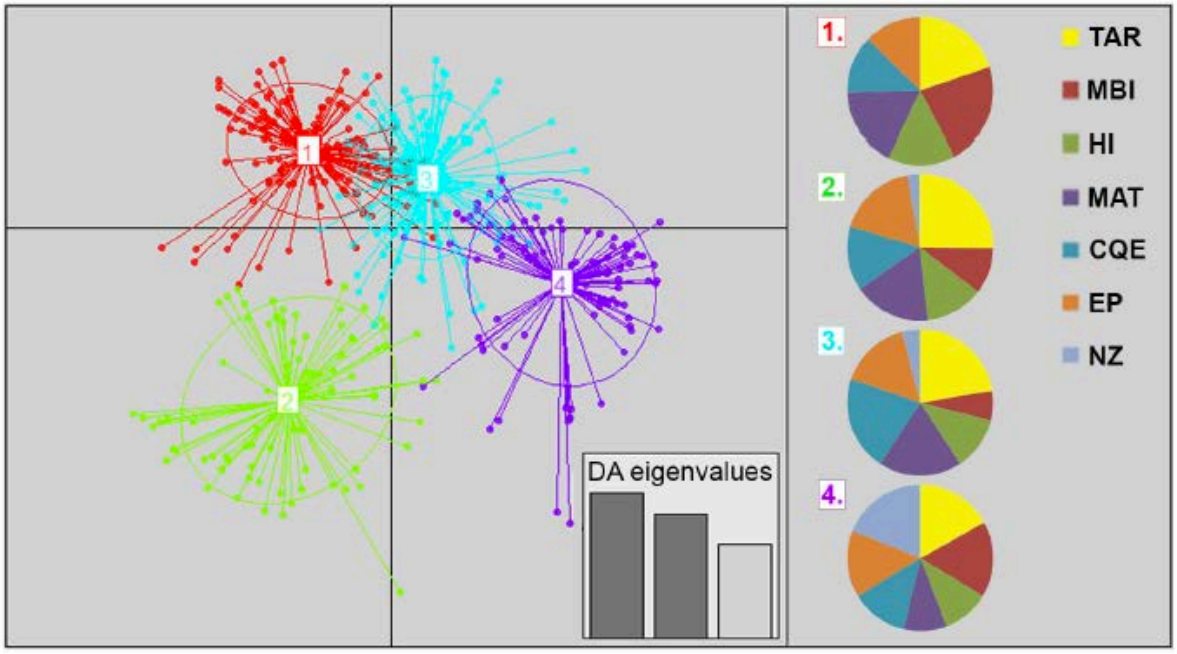


Population Structure

An analysis of clusters in STRUCTURE revealed no clear grouping of individuals sampled (Fig. 2). Grouping the six populations around Tasmania and the one population in New Zealand suggested a K of best fit as six clusters, however, no clear assignment of individuals to singular clusters can be visualised. The site of New Zealand shows individuals with a very minor difference to the remaining grouping of Tasmanian sites, with a slightly larger contribution of individuals to cluster three (~13% increase), and a lower contribution to clusters two (~5% less) and four (~5% less), potentially suggesting small differences in genetic character between New Zealand and Tasmanian populations (Table 4). Other comparisons show no more than a maximum of four percent difference between the percentage proportion of any one site assigned to a cluster, most averaging only a one percent difference. A hierarchical subdivision in STRUCTURE was created from individuals of Tasmania, with New Zealand removed to reveal potential substructure on a finer scale. STRUCTURE determined a best fit of five population clusters (K = 5), however, no clear assignment of individuals to any clusters was evident (data not shown).

DAPC was tested on all individuals with a best fit for clusters found at K = 4 (Fig. 3). The majority of individuals across the Tasmanian sample sites were assigned to genetically distinct clusters of 1 and 2 (58-69%), with a lesser contribution to clusters 3 and 4 (31-42%) (Table 5). Some number individuals from each of the Tasmanian sample sites belong to each of the clusters. The New Zealand population has the majority of individuals (72%) assigned to cluster 4, with less contribution to clusters 2 and 3 and no individuals assigned to cluster 1 (indicating this cluster as unique to Tasmania) (Table 5). A hierarchical analysis from DAPC, removing the New Zealand population to reveal more refined Tasmanian population substructure, again clustered individuals into a K = 4 grouping. The percentage of individuals in each Tasmanian population assigned to the four clusters, indicated that the same four clusters were formed (as that when NZ was included) with similar percentages of individuals from each population assigned. This revealed no new population sub structure within the Tasmanian sites, but rather confirmed that the Tasmanian individuals are assigned to each these four clusters in some degree.

Figure 3. Assignment and subsequent grouping of individuals with optimum cluster of K=4. Plot of DAPC for four assigned genetic clusters, each indicated by different colours. Dots represent different individuals, bottom right inset shows eigenvalues of principle components in relative magnitude.



Analysis using STRUCTURE and DAPC suggested that there was some level of differentiation present between individuals from Tasmania compared to New Zealand, however, no fine scale structuring was noted amongst populations of Tasmania, suggesting a high level of admixture between populations.

Migration and Directionality of Gene Flow

Evaluation of migrants or admixture between populations was analysed using BAYESASS on hierarchical levels of 1) between all populations and 2) between combined populations of Tasmania and New Zealand. BAYESASS permits migration rates to be asymmetric but they must be small, migrants per generation must not exceed a third, and scenarios with low genetic differentiation (Fst<0.02), or the program struggles to define resulting migration

patterns [39]. A pair wise comparison of each of the six Tasmanian populations and the New Zealand population therefore struggled to define levels of migration between Tasmanian populations. This was because Tasmania potentially had more than one third of migrations per generation, and Fst values between populations of Tasmania were noted as low (0.002). BAYESASS failed to distinguish which populations across Tasmania were exchanging an accurate number of migrants, as significant levels of migration in any one population changed between other Tasmanian populations each time the test was replicated (Table S3). Importantly, migration levels between the six Tasmanian populations and New Zealand were always consistent, despite the inaccuracy observed amongst Tasmanian populations (Table S3). A comparison between grouped populations of Tasmania and the New Zealand population (Table 6) was therefore more accurate and reproducibly consistent, as Fst values between the two populations were adequate (~0.03), migration levels were thought to be less than a third, and decreasing the number of populations increases the accuracy of estimations of migration rates [39]. This comparison suggested that 32% of New Zealand individuals sampled were migrants from Tasmania, where as less than 1% of Tasmanian individuals were from New Zealand (Table 6).

To take into consideration any effects of unequal number in sample sizes, pair wise comparisons of each individual Tasmania population were run against the New Zealand population. Results showed no differences except that New Zealand was shown to realistically contribute closer to 1-3% of migrants to Tasmania (Table S4). BAYESASS indicates that although migration rates are high amongst Tasmanian populations, they are lower between Tasmania and New Zealand, and in the order of 10 to 30 times more frequent from Tasmania to New Zealand than in the reverse direction.

Discussion

Genetic Viability of Translocation in Tasmania

Pilot scale translocations of lobsters from deep to shallow waters around the southern coast of Tasmania and Southern Australia were financially and biologically beneficial [5,7,8,43]. This current study suggests that the translocation of lobsters collected from deep water locations and released in shallow water around southern Tasmania is also potentially viable on a genetic level. With no significant genetic differences between the shallow (red) phenotypes and the deep (pale) lobster populations, and a high level of migration (and subsequent gene flow) between all Tasmanian populations, translocation of lobsters in southern Tasmania is unlikely to lead to any genetic problems.

There is minor evidence of some population structure, with low, yet significant individual pairwise comparisons between some Tasmanian sites. With Fst values <0.003, it is probable that these values are not biologically significant [44,45], however, a number of marine species have weaker values of genetic differentiation between populations that are still highly biologically significant and likely to represent important levels of unique stock structure [46,47] Therefore low levels of statistically significant structure in *J. edwardsii* should not be disregarded completely. Rather, more complete sampling across the Tasmanian coast and Australia in general is required for a more definitive conclusion on genetic stocks. Incredibly, detailed studies of population structure have not yet investigated patterns of genetic structure across Australia. The need for further study on Tasmanian populations, and the genetic stock structure of J edwardsii across Australia is emphasised by the recent study of New Zealand populations [16]. Thomas (2010) determined that J edwardsii was not homogeneous throughout its range in NZ, and rejected the null hypothesis of panmixia [16], although, like

the present study, Thomas's conclusions are based on small, yet significant population differences.

Nevertheless, finding statistically significant differences in pair wise comparisons of populations is not sufficient enough to confidently conclude that such populations are demonstrating an important level of genetic sub-structuring [46]. Statistical power will be high when using multiple and highly variable markers such as microsatellites on a large dataset such as this [44,48]. Therefore, small levels of difference in allele frequencies that are potentially unrelated to the true population structure (and hence not meaningful on a biological level) can be presented as statistically significant [44,48]. For this reason, assumptions about what is biologically meaningful genetic differentiation should be interpreted with a degree of care [44]. What is truly decided as meaningful should be interpreted with an understanding of the biological question in mind [46], as well as with a number of different statistical methods and an understanding of the limitations of each. In an evaluation of potential genetic differences between shallow and deep water phenotypes across Tasmania, no tests supported any significant genetic differences between the two phenotypes, hence, it can be understood that small levels of differentiation noted between these individual locations is not due to differences in phenotype, and translocation is likely to have no negative consequences for southern Tasmania.

Evidence for Large Scale Population Subdivision

Whilst there was little evidence for population structure among Tasmanian populations, assumptions of population panmixia between Australia and New Zealand [11] appear to be incorrect. Significant genetic structuring is evident between Tasmania and New Zealand, similar to that found by Thomas [16] in a comparison of a South Australian population and New Zealand. These results are in contrast to previous assumptions of a mixed New Zealand and Australian stock of *J. edwardsii* that are supported by models of larval trajectories that suggest trans-Tasman dispersal from Australia to New Zealand [17]. The understanding about population connectivity in lobsters between Australia and New Zealand populations has changed over time. These two populations were historically thought of as separate species, *J. edwardsii* and *J. novaehollandiae* (based on minor differences in morphology) [49], until electrophoretic analysis concluded that the level of differentiation was like that of different populations, not species, and the two populations formed one stock [13]. As some level of gene flow was evident, with supporting evidence from biological, biochemical, oceanography reports, life history characteristics and mtDNA analysis [11,12], the two species became known as one continuous population. The results of the present study, whilst not predicting a return species status, suggest the two countries do not share a single population.

Whilst clearly only a preliminary study of *J. edwardsii* connectivity across its entire range, there is evidence that gene flow between distant populations does not occur equally in both directions; with both the results of this study and those of Thomas 2012 [16], suggesting a significantly larger number of migrants travelling to New Zealand, than from New Zealand in the opposite direction. This suggests Australia is a potential source of new migrants and subsequent gene flow into New Zealand, acting as a source of stock recruitment. Clearly more populations are needed to be included to determine the full extent of asymmetric gene flow, not only across the Tasman Sea but also along the coast of Australia. If these results stand up in further study, then the health of the New Zealand populations may be dependent on the supply of Australian genetic material.

Given the significant influence ocean currents have been suggested to have on population differentiation between Tasmania and New Zealand, they may also play a significant role in determining population connectivity amongst Australian populations. Migration rates were unable to be appropriately resolved between the sampled populations across Tasmania, clearly indicating important gaps in sampling that could have led to a determination of the level of self recruitment, or source stocks for southern Tasmania. Hydrological and gene flow modelling suggests a dominant eastward flow of the transport of larvae between populations [18], which for Tasmania to New Zealand, results support [16,17]. Details of localised patterns in ocean eddies, currents and associated depths, strengths and directions, are not well studied enough to understand patterns in local source-sink relationships on a fine a scale as that across any one (or two) management zones (like that of sites across Southern Tasmania).
There are a number of large currents across the expanse of southern Australasia that have been able to be used to suggest source-sink relationships and have suggested that an easterly pattern of step wise recruitment via these currents is what drives gene flow in this species [18]. Given the results presented here suggest a source-sink relationship between Australia and New Zealand (respectively), clearly a larger scale study is required to confirm the influence of ocean currents on population structure. For example the most westerly (WA) and northerly limits (NSW) of the range of this species may serve as important source populations for those in South Eastern Australia and New Zealand and therefore should be targeted in future studies. If an eastern flow in stock source recruits throughout the range of the southern Australian coast is confirmed, this may have an important effect on the viability of translocations between populations. Over-exploitation of a source population may therefore have a serious effect not on the stock exploited but on the population to the east which may rely on this stock for recruits.

Conclusion

This analysis did not identify any scale of population structure that would suggest any genetic differences between shallow (red) phenotypes and deep (pale) phenotypes. There is a significant level of genetic differentiation between Tasmania and New Zealand, and therefore the assumption of widespread population panmixia can be rejected. Although large scale translocations are genetically viable in this region of Tasmania, it is important to understand that if the indications of asymmetric gene flow and population differentiation found are transferable across the rest of this species range, then translocations should only be undertaken on the scale of jurisdiction. Similarly, finding significant genetic structure in an important fishery species, where previously none had been identified, means a much more detailed assessment of lobster connectivity across the range may find more unique genetic stocks, and important source sink relationships which will have important implications for successful translocations and stock structure management schemes.

References

1. Rout TM, Hauser CE, Possingham HP (2007) Minimise long-term loss or maximise short-term gain? Ecological Modelling 201: 67-74.
2. Vitt P, Havens K, Kramer AT, Sollenberger D, Yates E (2010) Assisted migration of plants: changes in latitudes, changes in attitudes. Biological Conservation 143: 18-27.
3. Eldridge WH, Naish KA (2007) Long-term effects of translocation and release numbers on fine-scale population structure among coho salmon (*Oncorhynchus kisutch*). Molecular Ecology 16: 2407-2421.
4. Cowen RK (2000) Connectivity of marine populations: open or closed? Science 287: 857-859.

5. Green BS, Gardner C, Linnane A, Hawthorne PJ (2010) The good, the bad and the recovery in an assisted migration. PLoS One 5: e14160.
6. Chandrapavan A, Gardner C, Linnane A, Hobday D (2009) Colour variation in the southern rock lobster *Jasus edwardsii* and its economic impact on the commercial industry. New Zealand Journal of Marine and Freshwater Research 43: 537-545.
7. Green BS, Gardner C (2009) Surviving a sea-change: survival of southern rock lobster (*Jasus edwardsii)* translocated to a site of fast growth. ICES Journal of Marine Science 66: 656-664.
8. Chandrapavan A, Gardner C, Green BS (2010) Growth rate of adult rock lobsters Jasus edwardsii increased through translocation. Fisheries Research 105: 244-247.
9. Chandrapavan A, Gardner C, Green BS, Linnane A, Hobday D (2011) Improving marketability through translocation: a lobster case study from southern Australia. ICES Journal of Marine Science 68: 1842-1851.
10. Robinson BW, Wilson DS (1996) Genetic variation and phenotypic plasticity in a trophically polymorphic population of pumpkinseed sunfish (*Lepomis gibbosus*). Evolutionary Ecology 10: 631-652.
11. Ovenden JR, Brasher DJ, White RW (1992) Mitochondrial DNA analyses of the red rock lobster *Jasus edwardsii* supports an apparent absence of population subdivision throughout Australasia. Marine Biology 112: 319-326.
12. Booth JD, Street RJ, Smith PJ (1990) Systematic status of the rock lobsters *Jasus edwardsii* from New Zealand and *Jasus novaehollandiae* from Australia. New Zealand Journal of Marine and Freshwater Research 24: 239-249.
13. Smith PJ, McKoy JL, Machin PJ (1980) Genetic variation in the rock lobsters *Jasus edwardsii* and *Jasus novaehollandiae*. New Zealand Journal of Marine and Freshwater Research 14: 55-63.
14. Temby N, Miller K, Mundy C (2007) Evidence of genetic subdivision among populations of blacklip abalone (*haliotis rubra* leach) in Tasmania. Marine and Freshwater Research 58: 733-742.
15. Elphie H, Raquel G, David D, Serge P (2012) Detecting immigrants in a highly genetically homogeneous spiny lobster population (*Palinurus elephas*) in the northwest Mediterranean Sea. Ecology and Evolution 2: 2387-2396.
16. Thomas L (2012) Population genetics of the red rock lobster, *Jasus edwardsii*. New Zealand: Victoria University of Wellington. In press.
17. Chiswell SM, Wilkin J, Booth JD, Stanton B (2003) Trans-Tasman sea larval transport: is Australia a source for New Zealand rock lobsters? Marine Ecology Progress Series 247: 173-182.
18. Bruce B, Griffin D, Bradford R (2007) Larval transport and recruitment processes of southern rock lobster. CSIRO Marine and Atmospheric Research.
19. Thomas L, Bell JJ (2011) Characterization of polymorphic microsatellite markers for the red rock lobster, *Jasus edwardsii* (Hutton 1875). Conservation Genetics Resources 4: 319-321.
20. Animal Genomics Laboratory (2001) Extraction of DNA from tissue: high salt method.
21. Blacket MJ, Robin C, Good RT, Lee SF, Miller AD (2012) Universal primers for fluorescent labelling of PCR fragments--an efficient and cost-effective approach to genotyping by fluorescence. Molecular Ecology Resources 12: 456-463.
22. Drummond AJ, Ashton B, Buxton S, Cheung M, Cooper A, et al. (2005-2012) GENEIOUS v5.6.4. 5.6.4 ed. Auckland, New Zealand: Biomatters Ltd.
23. Biomatters Ltd. (2012) Geneious Microsatellite Plugin for Geneious Pro 5.6 or later.
24. Peakall R, Souse PE (2006) GENALEX 6: genetic analysis in excel, population genetic software for teaching and research. Molecular Ecology Notes 6: 288-295.

25. Van-Oosterhout C, Hutchinson WF, Wills DP, Shipley P (2003) MICRO-CHECKER: software for identifying and correcting genotyping errors in microsatellite data. Molecular Ecology Notes 4: 535-538.
26. Chapuis MP, Estoup A (2007) Microsatellite null alleles and estimation of population differentiation. Molecular Biology and Evolution 24: 621-631.
27. Sun JT, Lian C, Navajas M, Hong XY (2012) Microsatellites reveal a strong subdivision of genetic structure in Chinese populations of the mite *Tetranychus urticae Koch (Acari: Tetranychidae)*. BMC Genetics 13.
28. Raymond M, Rousset F (1995) GENEPOP (version 1.2): population genetics software for exact tests and ecumenicism. Journal of Heredity 86: 248-249.
29. Rousset F (2008) GENEPOP'007: a complete re-implementation of the GENEPOP software for windows and linux. Molecular Ecology Resources 8: 103-106.
30. Goudet J (2001) FSTAT, a program to estimate and test gene diversities and fixation indices (version 2.9.3). Lausanne, Switzerland: University of Lausanne.
31. Pritchard JK, Stephens M, Donnelly P (2000) Inference of population structure using multilocus genotype data. Genetics 155: 945-959.
32. Earl DA, vonHoldt BM (2012) STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the evanno method. Conservation Genetics Resources 4: 359-361.
33. Evanno G, Regnaut S, Goudet J (2005) Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. Molecular Ecology 14: 2611-2620.
34. R Core Team (2012) R: a language and environment for statistical computing. Vienna, Austria: R Foundation for Statistical Computing.
35. RStudio (2012) RStudio: integrated development environment for R (version 0.96.331). Boston, MA.
36. Jombart T (2008) Adegenet: a R package for the multivariate analysis of genetic markers. Bioinformatics 24: 1403-1405.
37. Jombart T, Ahmed I (2011) Adegenet 1.3-1: new tools for the analysis of genome-wide SNP data. Bioinformatics 27: 3070-3071.
38. Wilson GA, Rannala B (2003) Bayesian inference of recent migration rates using multiocus genotypes. Genetics 163: 1177-1191.
39. Faubet P, Waples RS, Gaggiotti OE (2007) Evaluating the performance of a multilocus bayesian method for the estimation of migration rates. Molecular Ecology 16: 1149-1166.
40. Manoukis N (2008) Formatomatic: population genetic file creator and converter.
41. Rambaut A, Drummond AJ (2007) Tracer v1.5.
42. Dempster A, Laird N, Rubin D (1977) Maximum likelihood from incomplete data via the EM algorithm. J R Stat Soc B 39: 1-38.
43. Gardner C, Van Putten EI (2008) The economic feasibility of translocating rock lobsters to increase yield. Reviews in Fisheries Science 16: 154-163.
44. Waples RS (1998) Separating the wheat from the chaff: patterns of genetic differentiation in high gene flow species. The Journal of Heredity 89: 438-450.
45. Waples RS, Punt A, Cope JM (2008) Integrating genetic data into management of marine resources: how can we do it better? Fish and Fisheries 9: 423-449.
46. Knutsen H, Olsen EM, Jorde PE, Espeland SH, Andre C, et al. (2011) Are low but statistically significant levels of genetic differentiation in marine fishes 'biologically meaningful'? A case study of coastal Atlantic cod. Molecular Ecology 20: 768-783.
47. Wolfram K, Mark FC, John U, Lucassen M, Portner HO (2006) Microsatellite DNA variation indicates low levels of genetic differentiation among cuttlefish (*Sepia*

officinalis L.) populations in the English Channel and the Bay of Biscay. Comparative Biochemistry and Physiology Part D Genomics and Proteomics 1: 375-383.
48. Ryman N, Palm S, Andre C, Carvalho GR, Dahlgren TG, et al. (2006) Power for detecting genetic divergence: differences between statistical methods and marker loci. Molecular Ecology 15: 2031-2045.
49. George RW, Kensler CB (1970) Recognition of marine spiny lobsters of the *Jasus lalandii* group (*Crustacea : Decapoda: Palinuridae*). New Zealand Journal of Marine and Freshwater Research 4: 292-311.
50. Google Inc. (2012) Google Earth. 6.2 ed.