Introduction

Translocations: The human-mediated movement of a species to maintain population number, connectivity and genetic diversity.

Uses: Conservation, agriculture, repopulation/restocking [1, 2].

Risks: Misinterpretation of biological, behavioural or genetic backgrounds, leading to replacement of local populations, population competition and size reduction, introduction of disease, loss of localized adaptations (fitness) and loss of genetic diversity [3, 4].

Many marine species are assumed to be panmictic, meaning a single population with random mating, having no physical, behavioural or genetic barriers to connectivity. However, recent research is showing finer scale population subdivision is more common than previously assumed [5, 6, 7, 8]. Translocations have already been undertaken by commercial industry for the southern rock lobster, Jasus edwardsii, to maintain populations for fishing [9, 10]. Around Tasmania, lobsters are translocated from deeper water to shallow water areas currently over-exploited by agriculture. There are important phenotypic (or physical) differences between shallow and deep water populations, where shallow water phenotypes are more desirable due to a rich red shell colour, larger size and faster growth rate (Figure 1). These lobsters exhibit phenotypic plasticity, being able to change phenotype based on their environment, as translocated individuals change to the more desired red phenotype after their first moult.

This study aims to use microsatellite markers, or variations in short tandem repeats of DNA sequences, to investigate genetic differentiation among Tasmanian populations of the southern rock lobster. This study will determine whether assumptions made by the fishing industry of a panmictic population is true, and reveal potential patterns in connectivity across larger oceanic distances.

Methodology

Lobsters were sampled from six sites across the southern Tasmanian coast (Figure 2), three from shallow water (<30m) sampling the red phenotype, and three deep areas (>60m) targeting pale phenotype. One population was sampled from New Zealand, to provide a larger scale of genetic connectivity. Sampling was conducted by taking a clip from the pleopod (swimming limb) of lobsters for genetic analysis. The Institute for Marine and Antarctic Studies (IMAS), provided capture-release permits as per the Australian Government National Health and Medical Research Council code of practice for care of animals for scientific purposes.

DNA was extracted from a large sample of 460 lobsters, using 8 microsatellite markers designed for Jasus edwardsii [11]. DNA was amplified using Polymerase Chain Reaction, and PCR products were sent to the Australian Genome Research Facility (AGRF) for separation into microsatellite repeat lengths.

Results

Table 1 showed a consistent significant genetic difference between New Zealand and Tasmanian sites of around 0.03. Overall, populations of Tasmania showed no genetic differences either between shallow and deep water sites, or between geographically separate sites, however, on a larger scale, a clear genetic difference exists between populations of lobsters around Tasmania compared to the population from New Zealand.

Table 2 shows the rate of migration between now combined populations of Tasmania and the population in New Zealand, based on microsatellite frequencies. 32% of New Zealand lobsters sampled were migrants from Tasmania. Alternatively, 99% of Tasmanian lobsters were self recruited, or originated from Tasmanian populations. Gene flow was in the order of 10 to 30 times more common from Tasmania to New Zealand, than in the reverse direction.

Discussion

Translocations of lobsters from deep to shallow water sites around Tasmania have already been conducted and shown to be biologically beneficial [10, 14]. Assumptions about what is biologically meaningful should be treated with great care, as small levels of statistically significant genetic difference found in some marine species may not be a true reflection of an entire population structure [5]. F-statistics suggest translocating lobsters in this manner is viable on a genetic level, as no significant genetic differences were found between Tasmanian lobsters of different phenotypes. Therefore, assumptions of a panmictic population of the southern rock lobster around Tasmania is true.

Large scale patterns of genetic difference based on isolation by oceanic distance have been found in marine species like the southern rock lobster [4, 5, 8]. This study was limited by a single New Zealand population sampled, indicating further exploration of population connectivity across greater oceanic distances would better reveal migration patterns and genetic connectivity. The most complicated barrier to migration for marine species is ocean currents, with 2,000 kilometres of open ocean between Tasmania and the population in New Zealand, based on microsatellite statistics across all populations. Bold indicates significant values of p value <0.002.

Conclusion

No significant genetic difference was identified between Tasmanian populations of different phenotypes, suggesting small scale translocation of lobsters from deep to shallow waters around Tasmania are genetically viable. Analysis rejects the assumption of a panmictic population over larger geographical distances, highlighting the biggest limitation and the best direction forward, to use a wider number of genetic measures to investigate population genetic structure of the southern rock lobster across larger oceanic distances.

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References

7. Elizabeth; EP, East Pyramids; NZ, New Zealand HI, Hobbs Island; MAT, Maatsyuker Island; CQE, Cape Queen Elizabeth; EP, East Pyramids; NZ, New Zealand
8. TAR, Taroona Reserve; MBI, Mutton Bird Island;
9. The good, the bad and the recovery in an assisted migration of a population. Data analysis was considered significant at the level of p<0.002, with Fst values above 0.004 demonstrating genetic difference between marine populations [13].Computer analysis determined genetic connectivity as well as the level and directionality of migration or gene flow.
10. The population genetics of the Southern Rock Lobster: Is Translocation Genetically Viable? Erin Morgan