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Genetic subdivision of Australian and New Zealand populations of *Jasus verreauxi* (Decapoda: Palinuridae)—preliminary evidence from the mitochondrial genome

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INTRODUCTION

The commercially important rock lobster, *Jasus verreauxi* (H. Milne Edwards), occurs principally along the New South Wales coast of Australia (where it is known as the eastern rock lobster), and the north-east coast of the North Island of New Zealand (green or packhorse rock lobster) (Kensler 1967). Possible transport of phyllosoma larvae from Australia to New Zealand, most probably via an east-directed flow of water around 34°S from the east coast of Australia (Booth 1986), led to the suggestion that the breeding stock of Australian *J. verreauxi* could be a larval source for the New Zealand stock (Silas 1967; Williamson 1967). Investigations to ascertain the discreteness of these stocks are required for efficient management of this resource.

Restriction endonuclease analysis of mitochondrial DNA (mtDNA) provides a high resolution technique with which to study the microevolutionary processes operating within species (Avise et al. 1987). As the genome is strictly maternally inherited and does not recombine during meiosis (Lansman et al. 1983), clusters of animals with similar patterns of mtDNA nucleotide sequence variation are interpreted as being genetically related and, at least partially, reproductively isolated from other such groups. Using this technique, several marine species have been shown to consist of more than one genetically discrete population (Ovenden 1990).

A recent study of the mtDNA of *J. edwardsii* from southern and south-eastern Australia and from eastern New Zealand did not invalidate the hypothesis of widespread genetic homogeneity, most likely mediated by extensive larval dispersal (Ovenden et al. 1992). In another test of the possibility of gene flow via widespread larval dispersal in this genus, we have extended mtDNA analysis to Australian and New Zealand populations of *J. verreauxi*.

Abstract The palinurid rock lobster, *Jasus verreauxi*, has a disjunct distribution, occurring on the east coast of Australia and in New Zealand. Oceanic currents flowing across the Tasman Sea from Australia towards New Zealand and the long life of phyllosoma larvae suggests larval mixing and, consequently, genetic similarity between these populations. However, restriction endonuclease analysis of the mitochondrial DNA (mtDNA) of 25 late juvenile and adult lobsters showed that Australian and New Zealand haplotype assemblages are defined by two restriction sites, one confined to each locality. Genetic differentiation between Australian and New Zealand *J. verreauxi* was also supported by gene diversity analysis (G_{ST}). In contrast to the results from a similar study of a congeneric species with an analogous distribution (*J. edwardsii*), these preliminary results suggest that larval exchange between adult populations across the Tasman Sea may be limited.

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METHODS

Late juvenile and adult *J. verreauxi* were collected from Era Beach, New South Wales, Australia ($n = 8$, 34°11'S 151°04'E, October 1989), and North Cape ($n = 8$, 34°26'S 173°07'E, February 1990) and Matakaoa Point ($n = 9$, 37°34'S 178°20'E, February 1990), North Island, New Zealand. Antennal glands were removed and stored in liquid nitrogen. Mitochondrial DNA was extracted, cleaved with restriction endonucleases, radioactively end-labelled, and visualised by agarose electrophoresis (Brasher et al. in press).

Haplotypes were generated for each lobster by designating a letter from A to C for each unique fragment pattern, or morph, for each of the six restriction endonucleases used (Table 1). Restriction site presence or absence for each genome was binary-coded for computer analysis and converted to estimates of nucleotide sequence diversity between pairs of genomes using the maximum likelihood method of Nei & Tajima (1983). Haplotypes were grouped according to sequence diversity using the unweighted pair group method (UPGMA, Nei 1987). Gene diversity analysis (G_{ST}) was performed by treating nucleotide substitutions as alternate alleles (Takahata & Palumbi 1985). The significance of G_{ST} values was assessed by comparison to pseudo-values obtained from random re-arrangements of the raw data (Palumbi & Wilson 1990).

RESULTS

Of the 25 specimens involved in the study, 20 were analysed with the six restriction endonucleases. The remaining five specimens were scored for five or less of the endonucleases and are not included in the following analyses. Among the 45 restriction sites surveyed from the 20 specimens (*Afl*III, 7 [sites]; *Ava*I, 4; *Ban*I, 7; *Bst*YI, 14; *Eco*RV, 3; *Hind*III, 10), 35 were invariant between haplotypes (Table 2). Each haplotype was defined by the presence of between 36 and 39 restriction sites. Haplotypes 2, 3, 4, 5, and 7 differed from the most common haplotype (AAAAAA; 7/20 individuals) by one restriction site gain or loss (Table 1). The remaining haplotypes differed from the common haplotype by two (Haplotypes 6, 8, and 9) and three (Haplotype 10) restriction sites.

Ten different mtDNA haplotypes were observed among the 20 *J. verreauxi* collected from Australia and New Zealand (Table 1). The most common haplotype (1) was found at all three sampling localities (1/5 [individuals], North Cape; 4/9, Matakaoa Point, New Zealand; and 2/6 Era Beach, Australia). The remaining three haplotypes represented in the Australian sample (5, two individuals; 6 and 10, one individual each) were not shared by lobsters sampled from New Zealand. Two of these Australian haplotypes (5 and 6) shared the same restriction site (E3, Table 2). This site, not found in any haplotypes

Table 1 Differences between haplotypes, expressed as restriction site gains and losses relative to the common haplotype AAAAAA, and haplotype distribution among the three sample sites. Morph designations, from left to right, were assigned for the following restriction endonucleases: *Afl*III (F) [recognition sequence: CTTAAG], *Ava*I (A) [CPyCGPuG]; *Ban*I (B) [GGPyPuCC]; *Bst*YI (Y) [PuGATCPy]; *Eco*RV (E) [GATATC]; and *Hind*III (H) [AAGCTT]. Numbers with restriction endonuclease denotations indicate specific enzyme site changes (Table 2).

		Site changes from common haplotype		Locality			Total
		Gain	Loss	North Cape N.Z.	Matakaoa Point N.Z.	Era Beach Aust.	
1	AAAAAA	—	—	1	4	2	7
2	ABAAAA	A3	—	1	0	0	1
3	ACAAAA	A4	—	0	1	0	1
4	BAAAAA	—	F4	0	1	0	1
5	AAAABA	E3	—	0	0	2	2
6	AAABBA	E3, Y13	—	0	0	1	1
7	AAAAAC	H10	—	3	1	0	4
8	CAAAAC	H10	F5	0	1	0	1
9	AACAAC	H10, B7	—	0	1	0	1
10	BAACAB	H9, Y14	F4	0	0	1	1

Table 2 Presence (1) or absence (0) of restriction endonuclease recognition sites in 10 mitochondrial DNA haplotypes (enzyme order: *Afl*III; *Ava*I; *Ban*I; *Bst*YI; *Eco*RV; *Hind*III) identified amongst 20 *Jasus verreauxi*.

Site Name	Haplotype									
	AAAAAA	AAAAAC	ABAAAA	BAAAAA	CAAAAC	ACAAAA	AACAAC	BAACAB	AAAABA	AAABBA
<i>Afl</i> III										
F1	1	1	1	1	1	1	1	1	1	1
F2	1	1	1	1	1	1	1	1	1	1
F3	1	1	1	1	1	1	1	1	1	1
F4	1	1	1	0	1	1	1	0	1	1
F5	1	1	1	1	0	1	1	1	1	1
F6	1	1	1	1	1	1	1	1	1	1
F7	1	1	1	1	1	1	1	1	1	1
<i>Ava</i> I										
A1	1	1	1	1	1	1	1	1	1	1
A2	1	1	1	1	1	1	1	1	1	1
A3	0	0	1	0	0	0	0	0	0	0
A4	0	0	0	0	0	1	0	0	0	0
<i>Ban</i> I										
B1	1	1	1	1	1	1	1	1	1	1
B2	1	1	1	1	1	1	1	1	1	1
B3	1	1	1	1	1	1	1	1	1	1
B4	1	1	1	1	1	1	1	1	1	1
B5	1	1	1	1	1	1	1	1	1	1
B6	1	1	1	1	1	1	1	1	1	1
B7	0	0	0	0	0	0	1	0	0	0
<i>Bst</i> YI										
Y1	1	1	1	1	1	1	1	1	1	1
Y2	1	1	1	1	1	1	1	1	1	1
Y3	1	1	1	1	1	1	1	1	1	1
Y4	1	1	1	1	1	1	1	1	1	1
Y5	1	1	1	1	1	1	1	1	1	1
Y6	1	1	1	1	1	1	1	1	1	1
Y7	1	1	1	1	1	1	1	1	1	1
Y8	1	1	1	1	1	1	1	1	1	1
Y9	1	1	1	1	1	1	1	1	1	1
Y10	1	1	1	1	1	1	1	1	1	1
Y11	1	1	1	1	1	1	1	1	1	1
Y12	1	1	1	1	1	1	1	1	1	1
Y13	0	0	0	0	0	0	0	0	0	1
Y14	0	0	0	0	0	0	0	1	0	0
<i>Eco</i> RV										
E1	1	1	1	1	1	1	1	1	1	1
E2	1	1	1	1	1	1	1	1	1	1
E3	0	0	0	0	0	0	0	0	1	1
<i>Hind</i> III										
H1	1	1	1	1	1	1	1	1	1	1
H2	1	1	1	1	1	1	1	1	1	1
H3	1	1	1	1	1	1	1	1	1	1
H4	1	1	1	1	1	1	1	1	1	1
H5	1	1	1	1	1	1	1	1	1	1
H6	1	1	1	1	1	1	1	1	1	1
H7	1	1	1	1	1	1	1	1	1	1
H8	1	1	1	1	1	1	1	1	1	1
H9	0	0	0	0	0	0	0	1	0	0
H10	0	1	0	0	1	0	1	0	0	0

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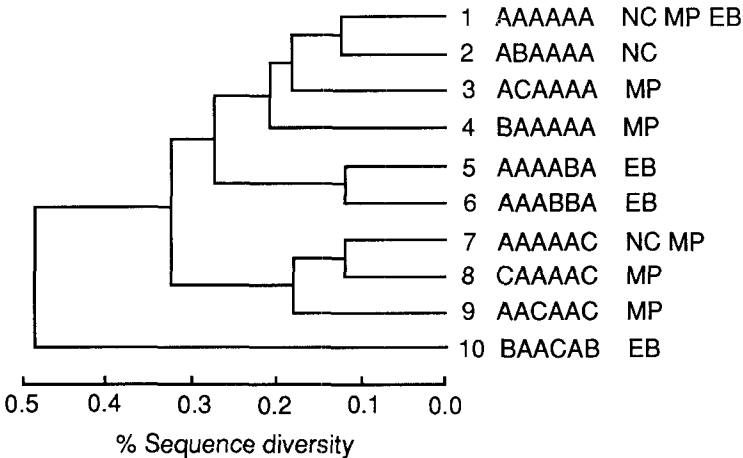


Fig. 1 Phenogram of *Jasus verreauxi* mtDNA haplotypes generated by UPGMA analysis of nucleotide sequence diversity estimates. Haplotypes are numbered according to Table 1 and their collection locale is included (NC, North Cape and MP, Matakaoa Point, New Zealand; and EB, Era Beach, Australia).

from New Zealand, grouped Haplotypes 5 and 6 in the UPGMA (Fig. 1). Three of the six haplotypes found only in New Zealand (7, four individuals; 8 and 9, one individual each) constitute a branch on the phenetic tree (Fig. 1); these share the restriction site H10, which was not found in any Australian haplotypes.

The amount of gene diversity (G_{ST}) as a result of genetic subdivision between lobsters sampled from Australia (Era Beach) and from New Zealand (North Cape and Matakaoa Point combined) was 0.29, a value that was greater than 99.6% of 500 pseudo-values.

Genetic subdivision between the New Zealand locales was not indicated by haplotype, restriction site distributions, or gene diversity analysis.

Although five *J. verreauxi* (North Cape, three individuals; Era Beach, two individuals) were excluded from the main analysis on the basis of incomplete restriction site data, the distribution of the two diagnostic sites (when scored) is consistent with the above results; that is, restriction site E3 is unique to Australian individuals and H10 was observed only in New Zealand.

DISCUSSION

In an extensive study of the mitochondrial genomes of 132 late juvenile and adult *J. edwardsii*, phenetic clustering, gene diversity analyses, and pairwise comparison of sequence diversities of specimens from each, or grouped, locales did not detect genetic subdivision across c. 4600 km of southern ocean habitats from Western Australia to New Zealand

(Ovenden et al. 1992). In contrast, 6 of 14 *J. verreauxi* collected from New Zealand and 3 of 6 Australian *J. verreauxi* could be separated into two haplotype assemblages on the basis of two restriction sites: H10, which occurred exclusively in New Zealand individuals; and E3, which was restricted to Australia. Gene diversity analysis provided additional evidence for genetic differentiation between New Zealand and Australian *J. verreauxi*. The absence of genetic differences between the two widespread locations from New Zealand is consistent with tagging studies (Booth 1986), which suggests a single *J. verreauxi* stock within New Zealand.

The mtDNA data presented here for *J. verreauxi* is preliminary, however. Confirmation of these results will depend upon a more extensive mtDNA analysis, which should include specimens from more widespread sampling. Moreover, genetic results will need to be incorporated with ecological and oceanographic studies before the stock status of *J. verreauxi* can be comprehensively evaluated.

If there is indeed population subdivision between Australian and New Zealand *J. verreauxi*, as the present results suggest, how is this maintained given the generally eastward flow in the Tasman Sea (Stanton 1973) and the long life of phyllosomas, estimated to be at least 8 months (Booth 1986)? An explanation may lie in recent studies of circulation in the Tasman Sea (e.g., Hamilton 1990) which show that the flow originating from the east coast of Australia near 34°S crosses in a north-easterly, rather than easterly, direction and departs the Tasman Sea well north of New Zealand. Because breeding *J. verreauxi* in Australia seldom occur south of 33°S (Booth 1986), most Australian phyllosomas that enter

the Tasman Sea will be carried in this north-easterly flow and will, therefore, fail to contribute to New Zealand stocks. Water in the East Auckland and East Cape Currents, the flows along the east coast of northern New Zealand where most puerulus settlement of *J. verreauxi* in New Zealand has been found to occur (Booth 1986), has its origins south of this north-easterly flow (Heath 1980). Booth et al. (1990) found that *J. edwardsii* phyllosomas were widespread in the central and southern Tasman Sea. The movement of only the more southerly waters of the Tasman Sea from Australia towards New Zealand may explain why the genetic difference found in this study between Australian and New Zealand stocks of *J. verreauxi* was not found between analogous samples of *J. edwardsii* (Ovenden et al. 1992), despite the similar life histories of both species.

Furthermore, phyllosomas may not simply be at the mercy of ocean currents but instead may regulate their distribution with vertical migratory behaviour (Phillips & McWilliam 1986). Such behaviour may enable phyllosomas to use surface and sub-surface currents flowing in different directions or at different speeds to remain in, or return to, the adult habitat (e.g., *Panulirus cygnus*: Phillips 1981). This strategy, combined with the presence of slow-moving, long-lived eddies and other recirculations in the East Australian current (Hamon 1965; Cresswell 1976), may ensure that most Australian *J. verreauxi* phyllosomas remain, for the duration of their development, near the Australian coast. The absence of *Jasus* larvae offshore in the north Tasman Sea (Booth et al. 1990) supports this local recruitment strategy. Such recruitment mechanisms do not invoke widespread dispersal of *J. verreauxi* phyllosomas into the South Pacific Ocean before recruitment back to the benthic stock, as proposed by Pollock (1990). Additional evidence against the widespread dispersal hypothesis was provided by a recent study (Booth & Grimes 1991) which found that *Jasus* rock lobster phyllosomas in southern waters occurred in greatest abundance in the general vicinity of adult habitat.

The behaviour of juvenile and adult *J. verreauxi* also affects the distribution of phyllosomas. Booth (1979, 1984, 1986) found the major breeding area for New Zealand *J. verreauxi* was near Cape Reinga, at the extreme north of the North Island. Tagging showed that juveniles moved northwards to this area from the east coast of the North Island. This movement, which is against the prevailing current, appears to ensure larval recruitment back to the east coast and reduces larval wastage to the east and south of New Zealand. This strong contranatal migration in *J. verreauxi*

suggests that most phyllosomas originate from local hatching (Booth 1986), with little recruitment from Australian stocks.

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REFERENCES

- Avisé, J. C.; Arnold, J.; Ball, R. M.; Bermingham, E.; Lamb, T.; Neigel, J. E.; Reeb, C. A.; Saunders, N. C. 1987: Intraspecific phylogeography: the mitochondrial DNA bridge between population genetics and systematics. *Annual review of ecology and systematics* 18: 489–522.
- Booth, J. D. 1979: North Cape—a 'nursery area' for the packhorse rock lobster, *Jasus verreauxi* (Decapoda: Palinuridae). *New Zealand journal of marine and freshwater research* 13: 521–528.
- 1984: Movements of packhorse rock lobsters (*Jasus verreauxi*) tagged along the eastern coast of the North Island, New Zealand. *New Zealand journal of marine and freshwater research* 18: 275–281.
- 1986: Recruitment of packhorse rock lobster *Jasus verreauxi* in New Zealand. *Canadian journal of fisheries and aquatic sciences* 43: 2212–2220.
- Booth, J. D.; Grimes, P. 1991: Tangaroa's first research. *New Zealand professional fisherman* 5(8): 61–62.
- Booth, J. D.; Street, R. J.; Smith, P. J. 1990: Systematic status of the rock lobsters *Jasus edwardsii* from New Zealand and *J. novaehollandiae* from Australia. *New Zealand journal of marine and freshwater research* 24: 239–249.
- Brasher, D. J.; Ovenden, J. R.; White, R. W. G. in press: Mitochondrial DNA variation and phylogenetic relationships of *Jasus* spp. (Decapoda: Palinuridae). *Journal of zoology, London*.
- Cresswell, G. R. 1976: A drifting buoy tracked by satellite in the Tasman Sea. *Australian journal of marine and freshwater research* 27: 251–262.
- Hamilton, L. J. 1990: Temperature inversions at intermediate depths in the Antarctic Intermediate Waters of the south-western Pacific. *Australian journal of marine and freshwater research* 41: 325–351.
- Hamon, B. V. 1965: The East Australian Current, 1960–1964. *Deep-sea research* 12: 899–921.
- Heath, R. A. 1980: Eastwards oceanic flow past northern New Zealand. *New Zealand journal of marine and freshwater research* 14: 169–182.
- Kensler, C. B. 1967: The distribution of spiny lobsters in New Zealand waters (Crustacea: Decapoda: Palinuridae). *New Zealand journal of marine and freshwater research* 1: 412–420.

- Lansman, R. A.; Avise, J. C.; Huettel, M. D. 1983: Critical experimental test of the possibility of 'paternal leakage' of mitochondrial DNA. *Proceedings of the National Academy of U.S.A.* 80: 1969–1971.
- Nei, M. 1987: Molecular evolutionary genetics. New York, Columbia University Press. 293 p.
- Nei, M.; Tajima, F. 1983: Maximum likelihood estimation of the number of nucleotide substitutions from restriction sites data. *Genetics, Austin, Texas* 105: 207–217.
- Ovenden, J. R. 1990: Mitochondrial DNA and marine stock assessment: a review. *Australian journal of marine and freshwater research* 41: 835–853.
- Ovenden, J. R.; Brasher, D. J.; White, R. W. G. 1992: Mitochondrial DNA analysis of the red rock lobster (*Jasus edwardsii*) supports an apparent absence of population subdivision throughout Australasia. *Marine biology* 112: 319–326.
- Palumbi, S. R.; Wilson, A. C. 1990: Mitochondrial DNA diversity in the sea urchins. *Evolution* 44: 403–415.
- Phillips, B. F. 1981: The circulation of the southeastern Indian Ocean and the planktonic life of the western rock lobster. *Oceanography and marine biology, an annual review* 19: 11–39.
- Phillips, B. F.; McWilliam, P. S. 1986: The pelagic phase of spiny lobster development. *Canadian journal of fisheries and aquatic sciences* 43: 2153–2163.
- Pollock, D. E. 1990: Palaeoceanography and speciation in the spiny lobster genus *Jasus*. *Bulletin of marine science* 46: 387–405.
- Silas, E. G. 1967: On the taxonomy, biology and fishery of the spiny lobster *Jasus lalandei frontalis* (H. Milne-Edwards) from St. Paul and New Amsterdam Islands in the southern Indian Ocean, with an annotated bibliography on species of the genus *Jasus* Parker. In: Proceedings of the Symposium on Crustacea, Marine Biological Association of India, Part IV, pp. 1466–1520.
- Stanton, B. R. 1973: Circulation along the eastern boundary of the Tasman Sea. In: Fraser, R. comp. Oceanography of the South Pacific 1972. New Zealand National Commission for UNESCO, Wellington, pp. 141–147.
- Takahata, N.; Palumbi, S. R. 1985: Extranuclear differentiation and gene flow in the finite island model. *Genetics, Austin, Texas* 109: 441–457.
- Williamson, D. I. 1967: Some recent advances and outstanding problems in the study of larval crustacea. In: Proceedings of the Symposium on Crustacea, Marine Biological Society of India. Part II, pp. 815–823.