THE POPULATION GENETIC
STRUCTURE OF PORTUNUS PELAGICUS
IN AUSTRALIAN WATERS

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DECLARATION

I declare that all sources are acknowledged and that this thesis is my own account of my research and contains as its main content work, which has not previously been submitted for a degree at any tertiary education institution. To the best of my knowledge and belief, the thesis contains no material previously written by another person except where due reference is made in the thesis itself.

__________________________
Ertuğ Sezmiş
To my dad (babam), mum (annem), sister (bibçirik), aunt (teyzecik) and grandma (annaneciğim).
TABLE OF CONTENTS

ABSTRACT ..................................................................................................................... I
ACKNOWLEDGEMENTS ............................................................................................... IV

CHAPTER 1. GENERAL INTRODUCTION ................................................................... 1
1.1 STUDY SPECIES: PORTUNUS PELAGICUS ..................................................... 2
1.2 APPROACH ........................................................................................................... 5
1.2.1 MOLECULAR METHODS ................................................................................. 5
1.2.1.1 Microsatellites ............................................................................................ 5
1.2.1.2 Mitochondrial DNA (mtDNA) ................................................................. 6
1.2.2 ANALYTICAL METHODS ............................................................................... 6
1.3 AIMS & THESIS RATIONALE ............................................................................ 7
1.4 RELATIONSHIP OF THIS STUDY TO OTHER PORTUNUS PELAGICUS RESEARCH... 9

CHAPTER 2. GENERAL METHODS ........................................................................ 11
2.1 SAMPLING DESIGN ........................................................................................... 11
2.2 DESCRIPTION OF STUDY SITES .................................................................... 16
2.2.1 WESTERN SEABOARD ................................................................................... 16
2.2.1.1 Geographe Bay ......................................................................................... 16
2.2.1.2 Peel-Harvey Estuary ................................................................................. 17
2.2.1.3 Cockburn Sound ...................................................................................... 18
2.2.1.4 Port Denison ............................................................................................. 20
2.2.1.5 Shark Bay ................................................................................................. 21
2.2.1.6 Exmouth Gulf ........................................................................................... 22
2.2.1.7 Broome ...................................................................................................... 23
2.2.2 NORTH COAST .............................................................................................. 25
2.2.2.1 Darwin .................................................................................................... 25
2.2.3 EASTERN SEABOARD ................................................................................... 25
2.2.3.1 Mackay .................................................................................................... 25
2.2.3.2 Hervey Bay .............................................................................................. 26
2.2.3.3 Moreton Bay ............................................................................................ 28
2.2.3.4 Wallis Lake ............................................................................................. 29
2.2.3.5 Port Stephens .......................................................................................... 30
2.2.4 SOUTH COAST ............................................................................................ 31
2.2.4.1 Gulf Saint Vincent ................................................................................... 31
2.2.4.2 Spencer Gulf ............................................................................................ 32
2.2.4.3 West Coast Region .................................................................................. 33
2.3 SAMPLE COLLECTION ....................................................................................... 34
2.4 MOLECULAR MARKERS ................................................................................... 35
2.4.1 MICROARRAYS .................................................................................................. 35
2.4.1.1 Characteristics of microarray markers ................................................... 35
2.4.1.2 DNA extractions ...................................................................................... 36
2.4.1.3 PCR amplifications ................................................................................ 36
2.4.1.4 Resolution and scoring of alleles .......................................................... 37
2.4.2 Mitochondrial DNA .................................................................37
2.4.2.1 Strategy for selection of appropriate mtDNA region ............37
2.4.2.1.1 Cytochrome Oxidase Subunit I (COI) .................................38
2.4.2.1.2 12S rRNA gene ...............................................................39
2.4.2.1.3 Cytochrome b gene (Cyt. b) ...............................................41
2.4.2.2 DNA extractions .................................................................43
2.4.2.3 PCR amplifications .............................................................43
2.4.2.4 Sequencing ..........................................................................44

CHAPTER 3. POPULATION GENETIC STRUCTURE OF PORTUNUS PELAGICUS IN AUSTRALIAN WATERS, AS INFERRED FROM MICROSATellite DNA EVIDENCE ........................................45
3.1 INTRODUCTION ........................................................................45
3.2 MATERIALS AND METHODS ..................................................48
3.2.1 SAMPLING REGIME ............................................................48
3.2.2 GENETIC ASSAYS ...............................................................49
3.2.3 DATA ANALYSES .................................................................49
3.2.3.1 Levels of polymorphism .....................................................49
3.2.3.2 Hardy-Weinberg equilibrium .............................................50
3.2.3.3 Measures of population differentiation ..............................50
3.2.3.3.1 Single-locus variation ......................................................50
3.2.3.3.2 Multi-locus variation ......................................................51
3.2.3.3.2.1 FST ...........................................................................51
3.2.3.3.2.2 Nei’s Genetic Distance ..............................................52
3.2.3.3.3 AMOVA .......................................................................52
3.2.3.4 Other considerations .......................................................53
3.3 RESULTS ..................................................................................53
3.3.1 LEVELS OF POLYMORPHISM ...........................................53
3.3.2 COMPARISON OF ‘REPLICATE’ SAMPLES ............................55
3.3.4 GENETIC VARIATION AMONG ASSEMBLAGES OF PORTUNUS PELAGICUS IN AUSTRALIA .........................................................65
3.3.4.1 Variation among geographic regions .................................65
3.3.4.2 Variation within geographic regions .................................71
3.3.4.2.1 Eastern seaboard .........................................................71
3.3.4.2.2 South coast .................................................................72
3.3.4.2.3 Western seaboard .........................................................75
3.4 DISCUSSION ..........................................................................78
3.4.1 METHODOLOGICAL CONSIDERATIONS ............................78
3.4.2 DO ASSEMBLAGES OF PORTUNUS PELAGICUS COMPRISE A RANDOMLY MATING GROUP OF INDIVIDUALS? .........................................................79
3.4.3 INTRINSIC DISPERSAL POTENTIAL ....................................81
3.4.4 GENETIC VARIATION AMONG ASSEMBLAGES OF PORTUNUS PELAGICUS IN AUSTRALIA .................................................................82
3.4.4.1 Variation among geographic regions .................................82
3.4.4.2 Variation within geographic regions .................................84
3.4.4.2.1 Eastern seaboard .........................................................84
3.4.4.2.2 South coast .................................................................86
3.4.4.2.3 Western seaboard .........................................................91
ABSTRACT

This thesis describes the results of an investigation into the population genetic structure of the blue swimmer crab, *Portunus pelagicus*, in Australian waters. *P. pelagicus* is an Indo-West Pacific species, with adults and juveniles that inhabit sheltered benthic coastal environments and a planktonic phase (of modest duration) in its life cycle.

The investigation was done by examining the patterns of variation at six microsatellite loci and in a 342 bp portion of the cytochrome oxidase subunit I (COI) gene in the mitochondrial DNA in samples of *Portunus pelagicus* from a total of 16 different assemblages/waterbodies. Overall, the samples were collected from throughout the geographical range of this species in Australian waters, *i.e.* from the western seaboard, from the eastern seaboard, from Darwin on the north coast and from South Australia on the south coast. The samples sizes ranged from 4 to 57 individuals, depending on the sample and the genetic assay. The population genetic structure of *P. pelagicus* was analysed from both a traditional population structure perspective and from a phylogeographical and historical demography perspective.

The traditional assessment of the population genetic structure of *Portunus pelagicus* indicates that this species exhibits a significant amount of genetic heterogeneity in Australian waters (*e.g.* $F_{ST}$ for microsatellite data = 0.098; $\theta_{ST}$ for COI data = 0.375 and $\Phi_{ST}$ for COI data = 0.492). This assessment also indicates that *P. pelagicus* exhibits varying degrees of genetic heterogeneity within and between geographical regions in Australian waters, as follows. (1) The genetic compositions of the samples from the
different coastlines (i.e. north, south, east and west) invariably showed statistically significant differences for at least two microsatellite loci, although the differences between the samples from the eastern seaboard, Darwin and those from the western seaboard to the north of Port Denison were not as great as those within the western seaboard samples or within South Australian samples. (2) The genetic compositions of the samples from the assemblages on the eastern seaboard of Australia, which ranged from Mackay (21°06′S) to Port Stephens (32°40′S), were essentially homogeneous. (3) The samples from the assemblages on the western seaboard of Australia, which ranged from Broome (17°58′S) to Geographe Bay (33°35′S), exhibited significant levels of genetic heterogeneity. Furthermore, those from south of Port Denison formed a highly distinctive (but not invariant) group compared to those from elsewhere. (4) The samples from South Australia were also highly genetically distinctive compared to those from elsewhere, although they also showed significant heterogeneity amongst themselves. The above findings were more or less suggested by both the microsatellite and COI markers, although the former generally provided a higher resolution picture of the population structure of *P. pelagicus* than did the latter.

The main findings of the investigation into the phylogeography and recent demographic history of *Portunus pelagicus* in Australian waters were as follows. (1) A phylogeny constructed from COI sequence variation was shallow, with the lineages showing varied geographical distributions. (2) The results of a nested clade analysis of this variation indicate that range expansion has been a predominant influence on the historical demography of *P. pelagicus* in Australian waters. (3) The samples from the assemblages on the western seaboard to the south of Port Denison contained low levels of genetic diversity, a sub-set of the diversity present in the samples from lower latitude sites on the western seaboard, and microsatellite-based evidence of having coming from
assemblages that have undergone a bottleneck (or founder effect) followed by an expansion in size. (4) The samples from the assemblages in South Australia contained low levels of genetic diversity, phylogenetic affinities with samples from the eastern seaboard, and microsatellite-based evidence of having coming from assemblages that have undergone a bottleneck (or founder effect) followed by an expansion in size.

The two major interpretations to stem from the results of this investigation are as follows. (1) Overall, *Portunus pelagicus* has undergone a recent (in an evolutionary sense) range expansion, from a single source, within Australian waters. At a finer-scale, this species appears to have colonised south-western Australia from a lower latitude site(s) on the western seaboard and probably colonised South Australia from the southern margins of its range on the eastern seaboard. Regardless, there has been limited penetrance of genetic variation into temperate waters on the western seaboard and into South Australia, presumably due one or more of the barriers to gene flow listed below. (2) *P. pelagicus* experiences significant restrictions to gene flow within its present-day geographical range in Australian waters due to (i) geographic distance *per se*; (ii) discontinuities in the distribution of the sheltered coastal environments; (iii) hydrological barriers to dispersal and (iv) possibly low temperatures in the temperature margins of the range.
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