



Indirect detection of genetic dispersal (movement and breeding events) through pedigree analysis of dugong populations in southern Queensland, Australia



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ABSTRACT

Understanding the patterns of movement and breeding within and between wildlife populations is important for the assessment of conservation status of endangered species, the development of conservation management strategies and priorities, and the prediction of population behaviour based on future threats. Methods for determining long term gene flow and dispersal are well researched, but analysis of recent movement is more difficult, typically relying on real-time tracking of individuals using telemetry, or through identification of marked individuals at multiple locations. These methods are limited by the considerable sampling effort required over time periods sufficient to recapture individuals in multiple locations. In contrast, we can infer recent movement from a reconstructed pedigree based on genetic and ancillary biological data, by identifying parent-offspring relationships in which the parent and offspring may be found in different locations. Hence, this method can use a single sampling period to identify movement and possibly associated breeding events over the last one or two generations. This study demonstrates the utility of reconstructed pedigrees in inferring recent movements in a dugongs distributed across a number of spatially distinct foraging locations in southern Queensland, Australia. Dugongs, which are classified as vulnerable to extinction, have long lifespans and protracted breeding cycles and give birth to single offspring at irregular intervals, implying a complex pedigree without distinct generational structure or large sibling groups. A pedigree was constructed for 1002 different dugongs across four locations in southern Queensland: Moreton Bay ($n = 630$), the Great Sandy Straits ($n = 281$), Hervey Bay ($n = 59$) and Shoalwater Bay ($n = 27$) using *PR-genie* software. *PR-genie* is a pedigree reconstruction system designed specifically for complex multigenerational wildlife pedigrees based on genetic identity (microsatellite DNA) and including ancillary biological data (sex and body size-class). Movements of genetically tagged individuals between locations were detected as parent-offspring links found across locations. Approximately 30% of assigned parents had at least one offspring found in a different location, implying recent movement of the parent or offspring. Where multiple individuals in a family are present, parsimonious explanations of movement indicate that male dugongs move between populations more frequently than females. Markedly more movement between locations was found than has been previously possible to detect through repeated direct sampling of individuals or through telemetry.

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1. Introduction

The genetic analysis of populations, population structure and genetic dispersal is of significant interest in a wide variety of biological applications. In wildlife populations, genetic parameters

are crucial for conservation, as efficient management of any species requires at least a basic understanding of their population dynamics (Hampton et al., 2004). Patterns of genetic diversity within populations and genetic differentiation amongst populations are important for the assessment of the spatial extent of endangered species (Blouin et al., 2010) and development of appropriate conservation strategies (Excoffier and Heckel, 2006).

The F statistics developed independently by Wright (1949) and Malécot (1948) provide convenient measures of genetic

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differentiation among and within populations, and have long been used to infer demographic history, estimate movement rates and identify regions of the genome under selection (Holsinger and Weir, 2009). Population structure provides insight into the levels of dispersal and connectivity between wildlife populations, because populations that are genetically distinct have likely had little exchange or interbreeding, whilst populations with little structuring have had significant immigration/emigration and interbreeding. Coalescent methods are an alternative method of determining models for population structure and for the direct estimation of movement rates between populations, such as those implemented in the software Ima2 (Hey and Nielsen, 2007) or Migrate-n (Beerli and Palczewski, 2010). Assignment testing, i.e., the assignment of individuals to populations based on their genetic composition, can provide insight not only into the long-term differentiation between populations, but into movement on an individual level in the short term. Movement can be inferred, for example, where an individual found in one location is assigned genetically to a population found in a different location. A relevant method of assignment testing is via Bayesian clustering, which infers population structure without assuming predefined populations (Chen et al., 2007), with the program STRUCTURE (Pritchard et al., 2000) being the most influential system to implement these techniques (François and Durand, 2010).

Whilst long-term population structure parameters are valuable and assignment testing provides some insight into movements (e.g., Nater et al., 2012), information on recent movements and effects on population structure of wildlife is critical for population management. Such data are used to address significant questions in conservation such as determining immediate causes of fluctuations and particularly declines in population size, and hence distinguishing movement events from mortality events, particularly in relation to anthropogenic or natural disturbance. Typically, short term movement patterns have been understood through direct observation, such as the tracking of individuals using telemetry (e.g., Maxwell et al., 2011), or through identification of individual animals in multiple locations, either by natural discriminatory marks or physical or genetic tags, e.g., Wells et al. (2008). While they can be effective in many situations depending on the question being asked, these methods come at considerable expense, require significant sampling effort over the duration of a study to recapture or re-observe individuals in multiple locations (particularly difficult for cryptic species), can be disrupted by loss or changes in discriminatory markings such as scar patterns, and can only detect those movements that occur during the study. In contrast, the use of genetic methods to detect contemporary movements, i.e., movements occurring within the lifetimes of extant individuals, can overcome some of these challenges, in particular the necessity of observing the same individual in multiple locations, and the limitation to movements that occur within the duration of the study. The use of genetic assignment testing, however, requires sufficiently genetically distinct populations, and may not provide significant insight into the timing of movement events nor indicate if these were accompanied by subsequent breeding and hence gene flow into the new location. Recently, assignment of parent-offspring relationships between individuals has been used to infer contemporary dispersal in wildlife, with Waser and Hadfield (2011) finding similar rates of dispersal though recapture and parentage analysis methods informed by spatial data for banner-tailed kangaroo rats (*Dipodomys spectabilis*). Here, we suggest that constructing a pedigree based primarily on genetic data will provide insight into contemporary movements and breeding events, by identifying individuals observed in different locations to their parents, siblings or offspring. We demonstrate this technique by considering the dugong (*Dugong dugon*) populations of southern Queensland, Australia.

The dugong is a large marine mammal inhabiting tropical and subtropical regions of the western Pacific and Indian oceans, its range covering the territories of over 37 countries (Marsh, 2002). Dugong are classified by the IUCN as vulnerable to extinction (Marsh, 2008), and aerial surveys over the past few decades indicate that significant population declines have occurred throughout their range and that many populations are currently under threat (Marsh et al., 2001a; Marsh and Lawler, 2001c; Sobotzick et al., 2012). Their long lifespans, protracted breeding cycles, and specialised seagrass diets make dugongs vulnerable to human impact, particularly where their habitats are close to large population centres (Marsh, 2002). In particular, dugong populations along the urban coast of southern Queensland, Australia, are found close to developed population centres featuring significant industrial and coastal activity. Modelling of long term trends in dugong bycatch in a government shark control program have indicated that significant declines in dugong populations may have occurred along the entire southern Queensland coast, to approximately 3% of 1960 population levels (Marsh et al., 2001a, 2005). Within south-east Queensland, the majority of dugongs are found in two spatially distinct foraging areas (300 km apart): in Moreton Bay (MB) and the Hervey Bay-Great Sandy Straits (HB-GSS) region, each of which includes designated sanctuary areas. Aerial surveys conducted over the past two decades have indicated short-term fluctuations in the HB-GSS region; a population of 2206 ± 420 in 1988 (Lee Long et al., 1993) declined to 807 ± 151 in 1994 (Marsh et al., 1996) after flood-associated loss of seagrass in 1992 (Preen and Marsh, 1995), and was then documented as 1654 ± 248 in 1999 (Marsh and Lawler, 2001b), 2547 ± 410 in 2005 (Marsh et al., 2006), and 2116 ± 108 in 2011 (Sobotzick et al., 2012), i.e., population estimates varied between 36% and 115% of the 1988 estimate. In MB, population estimates have ranged from 442 ± 69 in 1988 (Preen, 1992), 968 ± 44 in 1995 (Lanyon et al., 2003), 454 ± 41 in 2005 (Marsh et al., 2006) to 883 ± 63 in 2011 (Sobotzick et al., 2012), i.e., population estimates varying up to 219% of the 1988 estimate. However, because survey methodology in MB has not been consistent, population trends are doubtful, likely reflecting changes in survey technique rather than actual changes in population (Marsh, 2002; Lanyon et al., 2003). All estimates are 95% confidence intervals.

In order to appropriately manage threats to the south-east Queensland dugong populations, it is important to understand population connectedness and determine if population fluctuations in the region have been due to local mortality and/or large-scale movements between locations. Telemetry-based studies have previously indicated that dugongs are capable of large-scale movements of up to a maximum observed journey of 560 km by one individual, with a further 14 of 70 tagged individuals making movements of over 100 km (Sheppard et al., 2006). On a larger scale, gene-flow based studies on dugongs suggest significant dispersal between populations Australia-wide, and indicate that population-genetic structure exists on large geographic scales (Blair et al., 2013). Comparisons between population structure suggested by mitochondrial DNA and nuclear DNA indicated that gene-flow has been primarily male-mediated (McDonald, 2006). More recently, population genetic analysis has indicated low but significant population differentiation within southern Queensland (e.g., $F_{ST} = 0.021$ between MB and GSS), and a Bayesian clustering analysis (via STRUCTURE) suggested two clusters, primarily distinguishing MB dugongs from those in the more northern populations (Seddon et al., 2014).

When large-scale movement is likely to be occurring, insight into the extent of movements between foraging areas is required, particularly to determine if these are routine or occur only in response to major disturbances or environmental stressors. In 1992, the combination of a cyclone and flooding events caused sig-

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