Journal of Experimental Marine Biology and Ecology 451 (2014) 25–34

Contents lists available at ScienceDirect

Journal of Experimental Marine Biology and Ecology

journal homepage: www.elsevier.com/locate/jembe

Population trends of northern fur seals (*Callorhinus ursinus*) from a metapopulation perspective

Olivia A. Lee [a,*], Vladimir Burkanov [b], William H. Neill [a]

[a] Texas A&M University, Department of Wildlife and Fisheries Sciences, 2258 TAMU, College Station, TX 77843, USA
[b] National Marine Mammal Laboratory, Alaska Fisheries Science Center, 7600 Sand Point Way N.E., Seattle, WA 98115, USA

ARTICLE INFO

Article history:
Received 6 April 2013
Received in revised form 17 October 2013
Accepted 28 October 2013
Available online 5 December 2013

Keywords:
Colonization
Migration
Mortality rate
Northern fur seal
Population trend

ABSTRACT

A metapopulation model was created to explore source-sink population dynamics in northern fur seals (*Callorhinus ursinus*), for which the largest source population is declining, but smaller, newly established populations are either stable or growing. A declining source population could therefore slow down the growth of newly established populations. We also investigated changes in mortality and birth rates that could stabilize the declining population trend on the Pribilof Islands. The six main breeding populations—in the Pribilof Islands, Commander Islands, Kuril Islands, Robben Island, San Miguel Island, and Bogoslof Island—were modeled as individual age-structured populations, that were linked together using a migration model. The migration model component allowed movement of subadults among the six populations, with rules based on distances between populations, average travel speeds, habitat preferences, and El Nino events. The metapopulation model revealed the importance of immigration to newly established populations during the first 8 years of population growth. After the initial growth period, additional immigration had no noticeable effect on population growth in sink populations. The population trend on the Pribilof Islands was difficult to stabilize, and immigration from smaller populations could not slow the population decline. Consequently, conservation of the Pribilof Islands population likely requires a long recovery period following reductions in population-specific mortality rates for adult females, juveniles and pups.

1. Introduction

Northern fur seals (*Callorhinus ursinus*) are found throughout the North Pacific, with a southern limit at 40° N latitude. The two largest breeding populations occur in the Pribilof Islands (PI) and Commander Islands (CI), which currently make up approximately 50% and 20% of the total population, respectively (National Marine Mammal Laboratory, unpublished data). The remaining 30% of the population returns to breed in four main areas: Robben Island (RI), the Kuril Islands (KI), Bogoslof Island (BI) and San Miguel Island (SMI). Historically, commercial hunting of northern fur seals for their pelts severely depleted their numbers worldwide. Harvests began on the CI in the late 18th century and soon thereafter on the PI and RI. Increased demand for these pelts motivated the start of pelagic harvesting of seals—a particularly destructive practice in which both males and females were hunted.

The history of commercial hunting of northern fur seals is well documented (Atkinson, 1988; Gentry, 1998; Roppel, 1984; Roppel and Davey, 1965; Schaeffer et al., 1984) and shows a pattern that alternated between indiscriminant hunting, and implementation of conservation measures to restore declining stocks. Between 1950 and 1960 a management decision was made to allow culling of females as part of a herd reduction program in the PI. This management activity was implemented without a good understanding on northern fur seal population dynamics and subsequently, the culling of adult females was followed by a dramatic decline in fur seal populations in the PI. Commercial harvests ended in the 1970's and currently only subsistence harvests are permitted on the CI and PI. Subsistence harvests take less than 2000 animals per year (Angliss and Lodge, 2003) and are not thought to contribute significantly to the continued decrease of the PI population. However the PI population has continued to decline at 6% annually (National Marine Mammal Laboratory, unpublished data) despite the end of commercial harvesting.

Previous studies concentrated on causes of the population decline in the PI, and simulation models suggested that the decline was due to increased mortality possibly caused by entanglement in fishing gear or through greater competition with fishermen for prey resources (Trites and Larkin, 1989). Other suggested sources of mortality included increased predation (Springer et al., 2003), disease (Melin et al., 2005; Spraker and Lander, 2010), and environmental change effects on habitat (Ream et al., 1994; York, 1991). However, the previous simulation models omitted any potential for migration among the different breeding locations.

A metapopulation approach allows us to investigate how colonization of new rookeries may have affected the declining population in

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[*] Corresponding author at: 903 Koyukuk Dr, PO Box 747320, Fairbanks, AK 99775, USA. Tel.: +1 936 333 7239.
E-mail address: Olivia@gi.alaska.edu (O.A. Lee).

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http://dx.doi.org/10.1016/j.jembe.2013.10.029

the PI. Using a metapopulation approach, local populations of a species can be considered inhabitants of discrete habitat patches, and individuals may move between patches. This allows some locally unstable patches to become extinct, while new patches can become colonized (Hanski, 1998). In the 1950's previously unoccupied breeding territories in BI and SMI became colonized. Tracking studies on both adults and juveniles from the PI and CI show that individuals can range throughout the north Pacific and Bering Sea during a single 2 to 4 month migratory period (Belonovich, 2011; Loughlin et al., 1999; Ream et al., 2005) and therefore individuals are capable of dispersing to a new location within a year. The overlapping ranges of most of these breeding populations (Fig. 1), and the lack of genetic differentiation among the different breeding locations (Dickerson et al., 2008, 2010; Ream, 2002), suggest significant flux among the various northern fur seal populations. However, strong site fidelity had been observed in this species, particularly among adult females (Gentry, 1998). Therefore, migration presumably occurs mostly among juveniles that may have not yet established an affinity for a particular breeding location.

1.1. Model objectives

The use of ecological modeling in this study is to provide a qualitative analysis of the population trends for each of the six main breeding populations of northern fur seals. The objectives of this study were to 1) use a metapopulation model to hindcast population trends for the six main populations of northern fur seal (PI, CI, KI, SMI, BI and RI); 2) model movements among the different populations to examine trends in immigration and emigration to identify effects on source and sink populations; and, 3) qualitatively model future population trends using various scenarios for predicted changes in mortality rates in order to identify strategies for conservation.

2. Methods

The model was created using a deterministic model created in STELLA 9.1.3 (ISEE Systems) with simulations set to occur with a time step of 1 month. The model started at month 0, which corresponded to December 1929, and ended at month 1008, which corresponded to December 2014. This time period allowed us to validate the model using data on population size collected from 1930 to 2012, and also allowed us to simulate future population trends under different scenarios of birth and mortality rates. The overall metapopulation model had two main parts: 1) site-specific variants of an age-structured population model that accommodated variation in birth and death rates in each of the six populations, 2) a migration component allowing the movement of a subsection of juveniles among populations.

2.1. Population model structure

The population model used an age-structured approach that assigned separate parameters by sex after the age of 2 years (Fig. 2). Females were expected to live up to 26 years and males up to 11 years (Gentry, 1998).

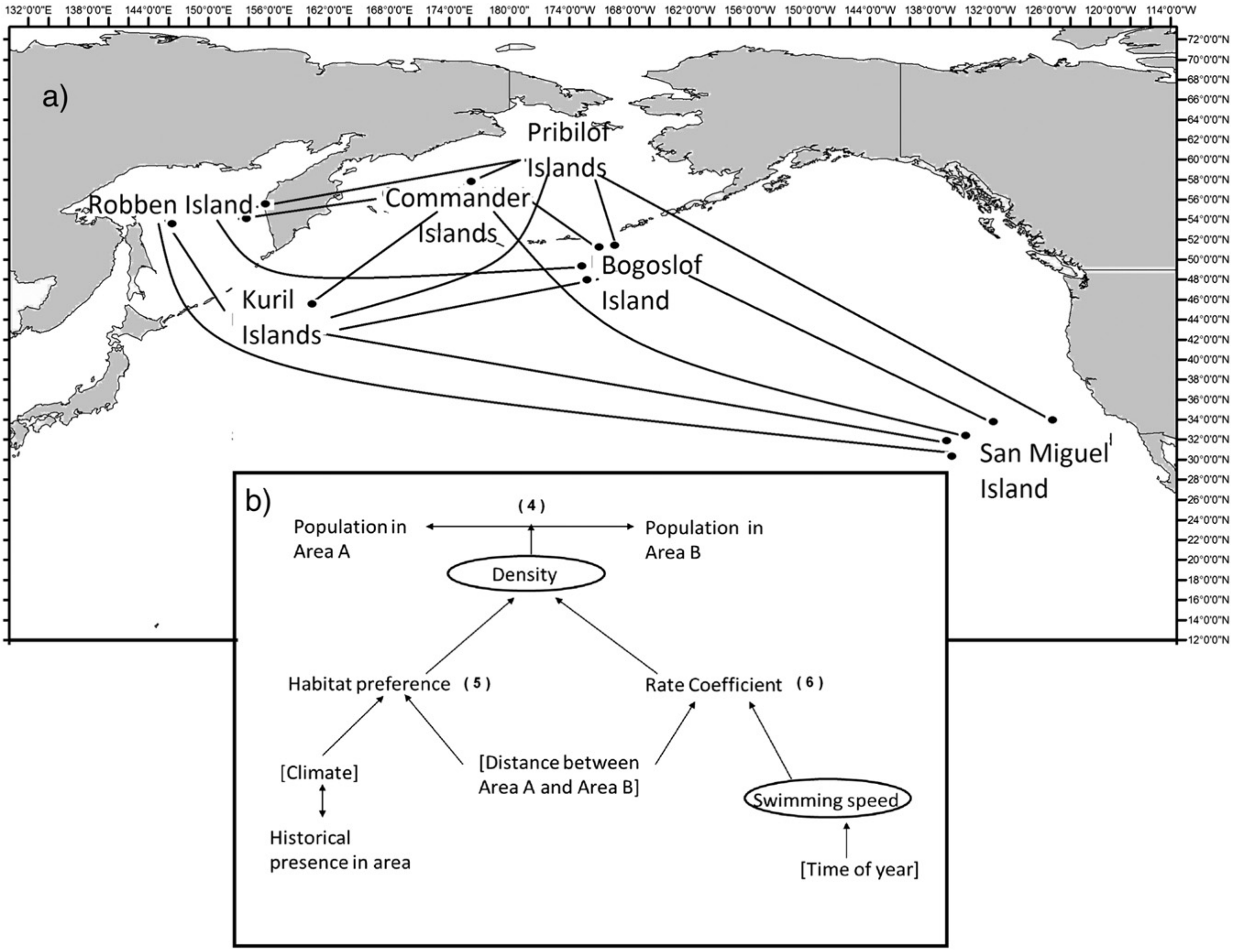

Fig. 1. Conceptual model showing (a) the location, and paired linkages for all six modeled populations with black circles indicating primarily sink populations, and (b) outline of the model parameters influencing migration between each paired population. Model equations used for different model processes are numbered (see text for details on numbered equations).