BEHAVIORAL ECOLOGY AND CONSERVATION OF LARGE MAMMALS: HISTORICAL DISTRIBUTION, REINTRODUCTION AND THE EFFECTS OF FRAGMENTED HABITAT

A Dissertation

by

ORANIT GILAD

Submitted to the Office of Graduate Studies of
Texas A&M University
in partial fulfillment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

August 2006

Major Subject: Zoology

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Approved by:

Co-Chairs of Committee,	Rodney L. Honeycutt
	X. Ben Wu
Committee Members,	William E. Grant
	Michael Smotherman
Head of Department,	Vincent M. Cassone

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ABSTRACT

Behavioral Ecology and Conservation of Large Mammals: Historical Distribution, Reintroduction and the Effects of Fragmented Habitat. (August 2006)

Oranit Gilad, B.S., University of Houston

Co-Chairs of Advisory Committee: Dr. Rodney L. Honeycutt
Dr. X. Ben Wu

Conservation biologists have used reintroduction as a method to reestablish extirpated species in their native habitat. Three important aspects of a successful reintroduction effort include: (1) a habitat suitability study of the reintroduction area, including effects of migration corridors; (2) identification of possible predators of the reintroduced species; and (3) a post-reintroduction assessment including an evaluation of the species' population dynamics. In this study I examine the suitability of Guadalupe Mountains National Park (GUMO) as a reintroduction area for desert bighorn sheep. The study used landscape metrics to compare GUMO to a nearby mountain range that is currently supporting an estimated population of 400 bighorn sheep. This study identified migration corridors for bighorns throughout the region and evaluated mountain lion (a potential predator of bighorn sheep) numbers either residing in or passing through the park between the years 1997 to 2004.

Results on the studies in GUMO revealed 15,884 ha of suitable habitat for bighorn sheep and provided evidence of migration routes between GUMO and neighboring mountain ranges. In terms of potential predators, a minimum of 32 resident and/or transient mountain lions occurred in GUMO over a seven year period, and a

minimum of 15 cats used the park in 2002. Based on estimates of individual home range of males and females, GUMO should be able to support four to five individuals. The genetic data indicates a high number of transients or perhaps an unstable population of mountain lions that may be the result of intense hunting pressure of cats in Texas.

Finally, my study simulates parameters of the population dynamics of a different species, the Arabian oryx that was reintroduced as three separate populations to the Israeli Negev between 1998 and 2005. I simulated population growth and the effect of migration corridors on species persistence. Results suggest that migration corridors are essential for a self-sustaining viable metapopulation under current natality rates. In the event that natality rates increase (as was evident in a reintroduced population of Arabian oryx in Oman), metapopulation can reach viable size with only two of the release sites (open, flat terrain) connected by migration corridors.

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Jan Janecka taught me lab skills, provided priceless hours, knowledge and materials to help me through the mountain lion genetics work. Dr. John Patton and Dr. Jay Bradfield also provided advice and support through the difficult times of genetic work. Wesley Highfield and Feng Liu contributed technical GIS expertise, and Dr. Debbie Siegele and Dr. Kay Goldman from the Department of Biology gave endless support throughout my time at Texas A&M.

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CHAPTER I

INTRODUCTION

Many species have been suffering a drastic and continuous loss of habitat as a result of ongoing expansion of human activities (Stanley Price, 1989; Sarrazin and Barbault, 1996). This loss is especially detrimental to large mammals that require large home ranges to sustain a viable population (Wilcove et al., 1986). Many species have experienced severe range reductions as a result of habitat loss, and remaining populations of some species are experiencing added pressure from primarily anthropogenic sources (Griffith et al., 1989). Conservation biologists have used reintroduction and translocation as methods to reestablish extirpated species throughout portions of their native range (Griffith et al., 1989; Lubow, 1996; Hodder and Bullock, 1997). As indicated by the by the World Conservation Union (IUCN) in 1987, these efforts are aimed at enhancing the long-tern survival of a species in an ecosystem and maintain and/or restore natural biodiversity. Reintroduction, as a conservation approach, has been recommended in the majority of all recovery plans for endangered and threatened species in the United States (Tear et al., 1993) as well as in other regions of the world (Kleiman et al., 1994). Despite the large numbers of reintroduction plans, only a small number of all attempts at reintroduction in the US (reviewed by Tear et al., 1993) have been successful (Beck et al., 1994; Earnhardt, 1999), and very few are well documented. The scarce information regarding successful and/or failed reintroduction projects is due in part to the failure to document procedures, monitor released animals (Beck et al., 1994; Ostermann et al., 2001), reluctance to report

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This dissertation follows the style of Biological Conservation.

failures, and publication in obscure sources of literature (Scott and Carpenter, 1987; Griffith et al., 1989; Beck et al., 1994; Sarrazin and Barbault, 1996).

Several studies attempted to examine historical reintroductions and evaluate the causes for their success or failure (Griffith et al., 1989; Wolf et al., 1996; Wolf et al., 1998). Some of the findings of these studies indicated a correlation between a successful reintroduction and several key factors including the type of species reintroduced (higher success to native game species, especially herbivores), habitat quality (the higher quality of habitat, the more successful the reintroduction), the location of the habitat (historical range vs. peripheral or outside historical range), size of the initial reintroduced population (more animals released, higher chance of success), and habitat free of competitors. None of the evaluations included the effect of possible predators on the success of the reintroduction, although at least in the case of desert bighorn sheep, presence of mountain lion in the release area appeared to influence the persistence of introduced sheep (Hoban, 1990; Wehausen, 1996; Ross et al., 1997; Hayes et al., 2000; Rominger and Weisenberger, 2000; Logan and Sweanor, 2001). It is also possible that the correlation between a successful reintroduction and the presence of predators within the reintroduced area results from whether or not reintroduced animals were either wild-caught or captive bred (Hill and Robertson, 1988; Griffith et al., 1989; Marcstrom, 1990). In the case of the desert bighorn sheep, the main source of released animals to predator rich habitat were naïve animals (Vernon Bleich, California Department of Fish and Game, personal communication 2004), raised in a predator-free environment where behavioral attributes for predator recognition and avoidance failed to develop (Curio, 1993), alarm (Russock

and Hale, 1978; Thaler, 1987; Tulley and Huntingford, 1987; Dowell, 1990; Curio, 1993). In the translocation of black-faced impala (*Aepyceros melampus petersi*) to predator rich (cheetah) and predator free environments, Matson et al. (2004) found that the primary effect for a successful translocation was the initial size of the population being released followed by the presence of predators. This study showed that in the presence of cheetah (*Acinonyx jubatus*) the persistence of the black-faced impala decline was correlated with the initial size of the population that was translocated. Small, recently translocated population of impala had a lower survival rate in predator rich habitat while the larger populations survived. The impala released were obtained from predator-rich environment, and the populations did not require time to acquire recognition and escape techniques from the cheetah.

A high quality habitat is species-specific and must be evaluated in accordance to the biology of the species being reintroduced (Stanley Price, 1989). As in the case of the Arabian oryx, the abundance of water sources played a lesser role in selecting an area for reintroduction because the oryx lives independent of drinking water (Tear et al., 1997; Williams et al., 2001, Seddon and Ismail, 2002), while desert bighorn sheep, despite their adaptation to dry environmental conditions, spend most of their time in the proximity of water, especially during the summer (Smith and Flinders, 1992). Other factors contributing to habitat quality are availability and abundance of food, appropriate topography, distance from human development and other human disturbances as well as possible competitors (Griffith et al., 1989; Berner and Krausman, 1992). Habitat suitability studies prior to reintroduction are extremely important because the success of the reintroduction is directly

correlated to the quality of the habitat, and the source of the initial decline of the species must be identified and removed (Griffith et al., 1989).

Another problem associated with reintroduction of an endangered or threatened species is habitat alterations by humans that have created a network of fragmented patches of suitable habitat (Wilcove et al., 1986; Woodroffe and Ginsberg, 2000). Persistence of species in small patches can be aided with the establishment of migration corridors, where animals can migrate from one patch to another (Simberloff and Cox, 1987; Noss, 1987; McCullough, 1996; Hanski and Gilpin, 1997; Woodroffe, 2003). This migration will allow the species to extend its overall habitat as well as exchange individuals between subpopulations that will sustain a higher genetic diversity and prevent the long term effects of inbreeding depression and genetic drift (Woodroffe, 2003). An illustration of the importance of corridors is the study of juvenile cougar migration between the highly patchy habitat of the Santa Ana Mountains near Los Angeles in California. An average home range for an adult cougar is 100 km^2 but only 1,114 km^2 currently contains continuous suitable range connected to the rest of the land (and addition of 956 km^2) by highway underpasses and culverts (Diamond, 1993). A study by Beier (1993, 1995) found that each of the three corridors was used at least once and in several cases multiple times by dispersing juveniles. In addition, four of the dispersers explored stretches of habitat that overlapped with urban areas. Corridors would have enabled all of these juveniles to disperse.

With the increasing numbers of global reintroduction efforts, the need to identify criteria for pre- and post-reintroduction plans have emerged (Kleiman et al., 1994). Since

reintroduction is an expensive enterprise in funds, time and human involvement (Clark et al., 2002), it is important to take into consideration multiple factors that maximize the chances for a successful establishment of a self-sustaining population back to its historical range. Several factors were identified that contribute to the success of a reintroduction (Anderegg et al., 1983; Jungius, 1985; IUCN, 1987; Griffith et al., 1989; Stanley Price, 1989; Gilpin and Hanski, 1991; Tear and Forester, 1992; Tear et al., 1993; Kleiman et al., 1994; Saltz, 1998; Singer et al., 2000). These factors focused on: (1) historical and current status of the species through the evaluation of the causes for population decline, status of current populations, dynamics and trends associated with fluctuations in populations, and potential sources for the reintroduced population; (2) evaluation of habitat by assessing whether the causes for the population decline have been removed, assessing the ability of the habitat to support a self sustaining population (availability of water and food sources, proximity to human disturbances) and evaluating connectivity between populations especially for a migratory and dispersing species; (3) protection of the reintroduced population by identifying factors that might affect population persistence such as possible threat from hunters, interspecific competition (native and non-native species), and high predation risk; (4) studies of the social and political impact of the reintroduction; and (5) post-reintroduction monitoring by the evaluation of success of the release by comparing population status to the ultimate goal of the reintroduction, which is the persistence of a self sustaining population.

The research presented in this dissertation pertains to two major reintroduction programs, one involving bighorn sheep in Guadalupe Mountains National (GUMO) Park

in Texas and the other pertaining to the reintroduction of the Arabian oryx in Israel. There were three primary objectives as follows:

(1) A GIS-based habitat suitability study was prepared for the reintroduction of desert bighorn sheep (*Ovis canadensis*) to Guadalupe Mountains National Park (GUMO). This study considered the historical and current status and biology of the species as well as the conditions needed for a long-term persistence of the population. Migration corridors used to connect the GUMO population to other bighorn populations in the Trans-Pecos area were identified.

(2) The genetic structure of the mountain lion (*Puma concolor*) was evaluated along with an estimate of the spatial and temporal distribution of cats within within Guadalupe Mountains National Park and the relationship between the cat population in GUMO and other populations of cats in the region. These genetic studies were conducted using noninvasive genetic techniques.

(3) Subsequent to reintroduction, the effects of migration corridors and post-reintroduction changes in natality on the dynamics and viability of the reintroduced populations of Arabian oryx (*Oryx leucoryx*) in the Israeli Negev was investigated.

CHAPTER II

REINTRODUCING DESERT BIGHORN SHEEP TO GUADALUPE MOUNTAINS NATIONAL PARK: A SUITABILITY AND COMPARATIVE ANALYSIS

2.1. Introduction

The desert bighorn sheep (*Ovis canadensis*) is native to North America, and once inhabited Texas, New Mexico, Nevada, Arizona, California, Utah and northern Mexico. There were estimated 1,500 individuals of desert bighorn sheep (referred to as bighorn sheep) in West Texas in the 1800's (Gould, 1962; Cook, 1994), primarily distributed in the mountains along the drainage divide between the Pecos River and the Rio Grande, as well as in the Rio Grande canyons of the Big Bend region in the Trans-Pecos region of Texas (Monson and Summers, 1980). By 1905, an estimated 500 bighorn sheep remained, and their distribution was restricted to the main mountain ridges of the Trans-Pecos (Bailey, 1905). The last documented report of bighorn sheep in the Guadalupe Mountain range was made by Snow in 1938 (Davis and Taylor, 1939; Leftwich and Simpson, 1978), and at the time no more than 35 individual bighorn sheep were estimated to inhabit what is today Guadalupe Mountains National Park (Leftwich and Simpson, 1978). The main factors identified as the causes for the decline of bighorn sheep were disease transmission from domestic sheep and goats, unregulated hunting and loss of habitat (Leftwich and Simpson, 1978; Smith and Flinders, 1992).

Reintroductions of desert bighorn sheep in Texas were initiated by the Texas Parks and Wildlife Department approximately 25 years ago. To date, these restoration

efforts have resulted in four free ranging populations and one metapopulation estimated at 800 individuals distributed throughout west Texas. The largest of those populations, approximated at 600 individuals and classified as a metapopulation due to exchange of individuals between the mountain ranges, exists throughout the Sierra Diablo, Baylor and Beach Mountains (Brewer, 2003). Individual desert bighorn sheep have been observed to migrate to the nearby Delaware mountain range. Guadalupe Mountains National Park (GUMO), established in 1964, encompasses the southeastern part of the Guadalupe Mountain range and is a natural extension of the Delaware mountain range located in the Trans Pecos area of West Texas (Appendix A, Fig. 1). Reintroduction of a desert bighorn sheep population in GUMO is an important aspect in the restoration efforts to return desert bighorn sheep to its historic range. Management guidelines of the National Park Service state the importance of restoring native species to its historic habitat and support such actions (Singer et al., 2000; USDI, National Park Service, 2001).

Restoration of desert bighorn sheep is time consuming, labor intensive, very costly and bureaucratically challenging. Failed attempts have been reported in many of the early restorations attempts (Risenhoover et al., 1988) and were attributed to a probable lack of rigorous habitat assessment (Smith et al., 1988). As a result, many habitat evaluation models have been developed and used in efforts to ensure the best conditions possible for successful restoration (Berner and Krausman, 1992). The use of geographical information systems (GIS) has been suggested in the past few years as an important tool in evaluating bighorn habitat (McKinney et al., 2003), and the use of

spatial requirements has been identified as a possible approach to evaluate bighorn habitat (McCarty and Bailey, 1994; McKinney et al., 2003). Several indices have been identified as requirements for suitable habitat for desert bighorn sheep: escape terrain, visibility, water sources, appropriate forage, and proximity to human activity (reviewed by Krausman et al., 1999).

The overall objective of this study is to use criteria important to desert bighorn sheep for the assessment of Guadalupe Mountains National Park as a reintroduction site that will be used to sustain a viable population of sheep. Two independent approaches were taken in order to determine suitable bighorn sheep habitat. First, a GIS-based model based on recognized habitat criteria was used to assess the spatial distribution of habitat within the park. Second, a comparative study of landscape attributes between GUMO and the nearby Sierra Diablo (SD) mountain range, a region currently supporting a bighorn population of 400 individuals (Brewer, 2005), was initiated. Additionally, connectivity between proximal mountain ranges and GUMO was evaluated in an effort to identify potential avenues of exchange between various regions of suitable habitat

2.2. Methods

2.2.1. Study Area

Guadalupe Mountains National Park is located in West Texas, on the border of Texas and New Mexico, 110 miles east of El Paso, Texas. The park encompasses approximately 34971 ha and is the southeastern part of the Guadalupe Mountain Range that extends northeast into New Mexico (Appendix A, Fig. 1). The entire mountain

range is a division of the Sacramento Mountains, the southern branch of the Rocky Mountains. Topography is characterized by a rugged mountain range, deep, sheer-sided canyons, steep slopes, high ridges, and limited but dependable seeps and springs. The main plant communities in the park include creosote-tarbush desert scrub, desert grassland, yucca and juniper savannas, and montane forests of pinon pine and oak The species mostly consumed by desert bighorn sheep, including those that provide high nutritional value, comprise wild buckwheat (*Eriogonum* spp.), globemallow (*Sphaeralcea* spp.), sagebrush (*Artemisia* spp.), *Bouteloua* spp. prickly pear, sumac (*Rhus* spp.), honey mesquite (*Prosopis glandulosa*), ratany (*Krameria* spp.), cloak fern (*Notholeana* spp.), true mountain mahogany (*Cercocarpus montanus*), field ragweed (*Ambrosia confertifolia*), slender janusia (*Janusia gracilis*), sagebrush, dalea (*Dalea* spp.), filaree (*Erodium* spp.), Apache plume (*Fallugia paradoxa*), wild buckwheat, acacia (*Acacia* spp.), lupine (*Lupinus* spp.), Heath cliffrose (*Cowania ericifolia*), fleabane (*Erigeron* spp.), milkvetch (*Astragalus* spp.), and deervetch (*Lotus oroboides*) (DeYoung et al., 2000). Climate is characterized with hot summers, calm, mild autumns and cool to cold winters. Snow storms, freezing rain, or fog can occur in winter or early spring. Precipitation is mostly during the summer due to summer monsoons with an average annual rainfall of 19 inches at the lower elevations and 24 inches at the high country. Winter average temperatures range between 30°F and 53°F while summer temperature range from 63°F to 88°F.

2.2.2. Habitat Suitability Model for Desert Bighorn Sheep at Guadalupe Mountains National Park

Several important habitat variables were identified for evaluating desert bighorn sheep habitat suitability: escape terrain, water availability, appropriate vegetation (food source), open unrestricted terrain and distance from human activities (Smith et al., 1991; Singer et al., 2000). Exotic species were also identified as a factor to be considered.

Suitable escape terrain was determined primarily based on slope information derived from 30 meter resolution digital elevation models (DEM) from the National Elevation Dataset (NED) using ArcGIS 9.1 software (ESRI, 2005). Areas with 27°–85° slopes are considered optimal escape terrain because bighorn sheep have been observed to spend most of their time within this area. Areas within 300m of these slopes and areas within 500m of these slopes when escape terrain was located on both sides are defined as sub-optimal, but still suitable (Singer et al., 2000) because bighorn sheep were documented to utilize these areas but to lesser extent. Sources of perennial water within GUMO were identified using the GIS coverage of springs provided by the National Park Service (NPS). Based upon previous research (Smith and Flinders, 1992; Singer et al., 2000), two critical distances from water have been identified. During the lambing season (February - August), females and their young were found within 1000m from water sources (Smith et al., 1991) and this area was defined as suitable habitat for that part of the year. Outside the lambing season, areas within 3,200m of perennial water sources were defined as suitable for bighorn sheep with respect to water

availability. Therefore, areas that satisfy both of these criteria were considered suitable habitat and other areas are considered unsuitable (Appendix B, Table 1).

Woodland areas and areas associated with human disturbances were considered unsuitable for desert bighorn sheep (Appendix B, Table 1). The ability of bighorn sheep to see surrounding terrain is critical, and they will not inhabit areas that limit their sight (Risenhoover, 1981). Wooded areas are avoided by bighorn sheep as they restrict sheep visibility and are associated with high risks of predation. Wooded areas were identified through a spatial vegetation coverage provided by the NPS. Roads and hiking trails were also excluded as desert bighorn sheep tend to avoid areas with human presence (Smith et al., 1991). Roads and hiking trails were identified from Texas Department of Transportation (TxDOT) line coverage and digitized hiking trails provided by the NPS. One hundred and fifty meter buffers of both roads and hiking trails were generated and excluded from suitable habitat areas (Light, 1971).

Suitable vegetation types, as mentioned in the study area description, are distributed throughout the suitable terrain in GUMO and supply appropriate food sources for the species; as a result, vegetation was not included in the habitat model. A small, unmonitored population of the exotic barbary sheep resides within park boundaries and travel feely within the park and the surrounded terrains. Due to lack of data regarding population size and distribution, as well as specific effects of this exotic species on the persistence of any reintroduced population of bighorn sheep, this factor has not been included as part of the park's suitability analysis.

2.2.3. Comparison between Guadalupe Mountains NP and Sierra Diablo in Their Landscape Characteristics

Evaluating landscape pattern in GUMO based on metrics of habitat patch and comparing these metrics to the Sierra Diablo (SD) mountain range allow one to evaluate the quality of habitat in GUMO relative to a habitat proven to be suitable for desert bighorn sheep. The SD mountain range serves as a good comparison to GUMO for several reasons: (1) It has an established populations of desert bighorn sheep (2) The landscapes are comparable in terms of general terrain, vegetation types, and climate (3) It is likely that the current population in SD will supplement the reintroduction of sheep into GUMO (Winkler, 1980 in Morrison, 1981).

Two separate scenarios of landscape metrics were calculated. One, landscape patterns of the optimal escape terrains (areas with 27°-85° slope) in GUMO and SD were compared based on patch metrics calculated using the Patch Analyst 3.0 extension within ArcView GIS 3.3 (ESRI, 1992). Two, landscape pattern of the all suitable escape terrain (optimal escape terrain buffered by 300m) was also calculated and compared through the use of patch metrics. Total landscape area, mean patch size, edge density and mean shape index were calculated and compared.

Due to a lack of comparable data for the SD regarding location of water sources, trails and exact locations of woodland areas, only habitat areas with suitable escape terrain were identified and used in the comparison. Many of the water sources at SD are artificially constructed by TPWD in the form of guzzlers and catchments that improve habitat and do not reflect natural habitat conditions; this form of habitat improvement

can be adapted by GUMO, making the two areas compatible in that regard. Both GUMO and SD experience light and infrequent human presence; and although GUMO is a National Park, the hiking trails usage is sporadic and consideration of hiking trails in this comparison is likely not essential. Furthermore, although desert bighorn sheep seem to avoid human presence and activities, it has been indicated that they will cross and use trail areas at night and other times where humans were not in the vicinity (Hamilton et al., 1982). According to Jansen (2005) desert bighorn sheep ignored heavy human activities (heavy traffic to and from a mine) in order to feed off palatable vegetation that grew adjacent to the roads leading to the mine. This behavior indicates that bighorn sheep adapt to different habitat conditions and alter their behavior accordingly. Due to the similarities in terrain and vegetation type it is inferred that type and presence of woodland areas are similar between GUMO and SD and were not taken into consideration in the comparison of the habitats.

2.2.4. Migration Corridors Identification

All areas of optimal escape terrain (27° – 85° slope) in the Trans-Pecos area, including historical range of desert bighorn sheep in West Texas, were identified. A travel distance by bighorn sheep of up to 7.5 km across flat terrain has been reported by Epps et al. (2005), and movement across 17.5km of open desert was documented by Cochran and Smith (1983). Furthermore, both ewes and rams were found in ranges not previously inhabited by a resident population (McQuivey, 1978). These reported travel distances document an attainable crossing distance for bighorn sheep between the Trans-Pecos mountain ranges. Based on this information, a conservative 5000m buffer

surrounding the optimal escape terrains and a larger 7500m buffer around the terrains were generated to evaluate habitat connectivity and corridors connecting major habitat areas.

2.3. Results

Guadalupe Mountain National Park was found to contain 7,273 ha of optimal escape terrain of slope 27-85° (Appendix B, Table 2). After buffering this area with a 300 meters buffer, an area of 20,736 was found suitable for desert bighorn sheep. Evaluating existing water sources within the park and applying a 3,200m buffer around them reduced the size of suitable habitat to 14,839 hectares. After excluding areas with continuous woody cover and areas within 150m of trails and roads, an area of 13,200 ha was identified as suitable to desert bighorn sheep in GUMO (Appendix A, Fig. 2). During the lambing season a buffer of only 1000m from water sources was calculated, resulting in 4,782 ha of suitable habitat for ewes and lambs.

Results of the landscape comparison of scenario one (optimal escape terrain comparison) showed that GUMO has greater amount of optimal escape terrain, is less fragmented with larger patches of suitable terrain and shorter distances between the patches than SD (Appendix B, Table 3). Density of The optimal escape terrain patches in GUMO was 54% lower in density, 48% greater in mean patch size, and 21.7% lower in edge density than in SD. The mean shape indices (MSI) of the habitat patches in GUMO and SD (1.48 and 1.46 respectively) were similar, indicating that the complexity of the patches is similar in the two areas since the smaller patch sizes in SD may reduce the MSI. Results of scenario 2 (optimal escape terrain buffered by 300m) showed a

continuous suitable habitat in both GUMO and SD with a 36.37% larger suitable habitat area in SD. This habitat size difference may indicate that a smaller population size may be supported in GUMO than in SD, but more detailed research is needed for such comparison in order to determine such population size. Based on a conservative estimate of 7km traveling distance by ewes, one migration corridor from SD to the Delaware and then GUMO was identified (Appendix A, Fig. 3).

2.4. Discussion

The amount of suitable habitat in GUMO was substantially greater than the minimum amount suitable habitat (1,500 - 1,700 ha) suggested by previous research to support a viable population of desert bighorn sheep (Smith et al., 1991; Smith and Flinders, 1992; McKinney et al., 2003) although the minimum size of a viable population is still controversial and estimated at 100 – 125 individuals (Berger, 1990, 1993, 1999; Smith et al., 1991; Krausman et al., 1992, 1993; Goodson, 1994; Wehausen, 1999, Singer et al., 2000). Both the amount and spatial pattern of the optimal escape terrains in GUMO also compared favorably to those in SD that was established as a good desert bighorn sheep habitat supporting a large and growing population of desert bighorn sheep, which suggests that GUMO is at least equally suitable to support a desert bighorn sheep population. Several factors should be considered when evaluating the results of my study and taken into consideration when evaluating GUMO as a possible habitat for a future population of desert bighorn sheep.

2.4.1. Human Presence

Within GUMO, current water sources correspond with trails used by visitors to the park and may or may not limit bighorn from using those areas during visitation hours. GUMO is not a highly visited park and except during the fall season (October-November) when the northwest trails of the park experience a larger number of visitors, most trails are used by individual hikers and can be easily avoided by animals (Fred Armstrong, resource manager, Guadalupe Mountain National Park, personal communication 2004). Conflicting reports are documented in regards to desert bighorn sheep behavior near trails. Complete avoidance of areas due to human activity has been reported in California (Krausman, 1993; Krausman and Etchberger, 1995) but opposing reports have documented avoidance of areas only when people where present and use of those terrains in the absence of activity (Hamilton et al., 1982). Other reports account for desert bighorn sheep complete indifference to hikers and have been observed to cross trails during high visitation hours with no visible signs of stress (Esther Rubin, bighorn sheep biologist, San Diego Zoological Society, personal communication 2005). Jansen et al. (2005) reported desert bighorn sheep feeding on the side of a heavily used mine road without regard to the heavy human activity. In this study I decided to calculate available habitat conservatively and buffer each trail with a 150m on each side (Smith and Flinders, 1992; Zeigenfuss et al., 2000). Available suitable habitat will increase by 1,826 ha outside lambing season and by 649 ha during lambing season if those buffers are removed.

2.4.2. Water Sources

Water development is an important aspect of desert bighorn sheep restoration efforts in Texas. Texas Parks and Wildlife Department constructs guzzlers and water catchments within suitable bighorn sheep habitat with distances of approximately 3 kilometers apart and 300 meters or less of escape terrain (Smith and Flinders, 1992; Foster et al., 2005). Within GUMO, water development can improve suitable habitat across the park since some of the perennial water sources that currently exist are located in areas of poor visibility (mostly springs within canyons). There is evidence that desert bighorn sheep populations increased in areas previously deficient of water through implementation of aggressive and effective water development programs (Bleich, 1983). The north-western area of the park lacks perennial water sources and construction of catchments would significantly increase suitable habitat. Suitable habitat within GUMO will increase by 38% if artificial water sources will be constructed.

2.4.3. Spatial Attributes of the Habitat

When evaluating suitable habitat for desert bighorn sheep, continuous terrain must be identified to ensure unobstructed movement. By identifying optimal terrain of 27-85° without establishing a 300m buffer, both GUMO and SD show certain degree of patchiness. My results indicate that under the first scenario (no buffer) in every landscape attribute evaluated, GUMO is superior to SD with respect to the amount and quality of terrain for the bighorn sheep. Habitat patch size has been identified as a critical factor in persistence of desert bighorn sheep population (Gross et al., 1997; Singer et al., 2001; McKinney et al., 2003) and GUMO has a larger mean patch size than

SD and a greater proportion of the landscape in suitable escape terrain. Under both scenarios, GUMO has lower edge density that SD which is an important indicator of more suitable quality habitat for desert bighorn sheep. Different species are affected by size and density of edge in various ways. Edge effect is influenced by the type of landscape the suitable habitat is bordering. Large forested areas adjacent to bighorn habitat are visually restrictive and may affect bighorn sheep ability to identify predators, maintain contact with group members (Zeigenfuss et al., 2000) and alert individual within the group to the presence of danger. Desert bighorn sheep are known to avoid areas of obstructed visibility. I interpret higher edge density as an increased association between suitable and unsuitable habitat and as a result, an increase in bighorn-predator interaction. As my results indicate, higher density of edges was found in SD than in GUMO. Under the second scenario, SD was calculated to include 36.37% more suitable habitat than GUMO. Since all other factors correlated with habitat suitability and patch metrics found GUMO compatible to SD, habitat size can be used to roughly estimate possible population size of bighorn sheep in GUMO. Based on an estimate of 400 sheep currently occupying SD, a rough estimate of 140 individuals could be sustained in GUMO if water development within the park will be compatible to that of SD.

2.4.4. Migration Corridors

The connectivity between GUMO and SD, as well as any other reintroduced populations in the region, is essential for dispersal and gene flow in order to maintain a healthy meta-population (Woodroffe, 2003). Ough and deVos (1984) identified migration corridors as areas where the “topography and associated vegetation type

provides a natural crossing between mountains which minimized the distance out of preferred habitat." They also found that the primary areas where bighorn crossed were those that directly connected mountain ranges associated with an existing desert bighorn sheep population. Continuous terrain and individual movements between ranges has been linked to increased persistence of species (Noss, 1987; Simberloff and Cox, 1987; McCullough, 1996; Hanski and Gilpin, 1997; Woodroffe, 2003), especially species that exchange individuals between populations and exist as a metapopulation. As a result, habitat fragmentation has been suggested as one of the primary causes of the current extinction crisis for animal species (Wilcox and Murphy, 1985). Annual travel of 5-7 mountain ranges was documented on indigenous desert bighorn sheep with distances traveled of 8 -18 km between those ranges (Geist, 1971; Demarchi and Mitchel, 1973; Thorne et al., 1979; Festa-Bianchet, 1986; Singer et al., 2000) and the importance of migration corridors for a species such as desert bighorn sheep that is observed to move within mountain ranges is recognized by most ecologists. The minimum population size can be relaxed if gene flow exists between subpopulations (Smith and Flinders, 1992) and the effect of inbreeding is avoided. Securing unobstructed migration corridors to and from GUMO, therefore, will ensure a higher probability of success for a reintroduced population.

Interpopulation movements of more than 50km have been observed (Geist, 1971; Schwartz et al., 1986) and bighorn sheep movement across open desert between ranges of up to 17.5km have been reported (Cochran and Smith, 1983). McQuivey (1978) documented both ewes and rams occupying ranges not known to previously sustain a

resident population with a mean distance to the closest ranges of 19.7km. Epps et al. (2005) identified recent colorizations of ranges not formerly inhabited by bighorn sheep by straight line crossing through unsuitable terrain of up to 7.5km and 20 km movement across unsuitable terrain characterized by wooded areas and high levels of human activity (Clinton Epps, University of California-Berkeley, CA, personal communication 2006). A salt plain of approximately 30 kilometers separates the Sierra Diablo and the Guadalupe Mountains and since movements of bighorn sheep exceeding this distance have been documented (Cochran and Smith, 1983) I decided to consider this distance as a possible migration distance and established a 7500m buffer around the optimal slopes to examine this scenario. Bighorn sheep are reported to cross between the Sierra Diablo's, Beach and Baylor mountains and the Eastern mountain ranges of the Delaware's (Morrison, 1981; Clay Brewer, bighorn sheep program director, TPWD, personal communication 2004); based on a more conservative crossing distance of 10km, my results indicate a continuous habitat between SD and the mountain range east to it, the Delaware. The Delaware extends north-northwest and provides not only suitable escape terrain for desert bighorn sheep, but also a direct connection between any subpopulation south of GUMO to the Guadalupe Mountain Range (Appendix A, Fig. 3). One consideration should be pointed out: The Delaware Mountain range, although suitable in terms of escape terrain, has power generated windmills along its mountain top. No research has been conducted regarding desert bighorn sheep behavior in the presence of windmills. Based on personal communication with Vernon Bleich (California Department of Fish and Game 2005), I believe that desert bighorn sheep may

get habituated to the windmills, especially since traffic leading to and from the windmills is infrequent and the windmills produce constant, monotonous sound. Regardless of the bighorn choice to permanently occupy the Delaware mountain range, it was considered as a possible migration corridor to and from the GUMO and SD. The Delaware mountain ranges are privately owned lands and the Texas Parks and Wildlife Department is continually working with the ranchers on improvement of the habitat for desert bighorn sheep (Clay Brewer, bighorn sheep program director, TPWD, personal communication 2005). These improvements do and should include removal of fences within and between the ranges to prevent unnecessary mortality of bighorn as they try to move from one area to another. These efforts should be extended to the Delaware/GUMO areas when reintroduction to GUMO takes effect and future research regarding bighorn sheep behavior in the presence of windmills is needed. This is extremely important in the face of future development of the Delaware and the plans to construct at least 100 more windmills in addition to the 112 mills already operating (Fred Armstrong, resource manager, Guadalupe Mountain National Park, personal communication 2006).

2.4.5. Exotic Species

A monitoring plan of the barbary sheep (aoudad, *Ammotragus lervia*) population within GUMO and adjacent areas should be considered. It is unclear to what extent aoudads affect bighorn persistence and to what extent can GUMO be successful in removing aoudads from their landscape. A viable population of aoudads resides in the Guadalupe Mountains of New Mexico (bordering GUMO on the north) and removing

the existing aoudad population from GUMO may create a void for the New Mexico aoudads to occupy these terrains. New Mexico manages aoudad as a game species and would not participate in the removal of those exotics.

2.5. Conclusion and Management Implications

Guadalupe Mountains National Park (GUMO) was historically inhabited by desert bighorn sheep. Reintroduction of desert bighorn sheep to GUMO will restore an important native species to an area from which it has been absent for seventy years. My study showed that GUMO has sufficient amount of suitable habitat for desert bighorn sheep and the amount and spatial attributes of the optimal escape terrains compared favorably to SD that currently supports a healthy population of desert bighorn sheep. Several management considerations must be discussed, however, before such a project is undertaken.

(1) Continuous assurance that ranchers in adjacent areas will not introduce domestic sheep or goats to their land, so that no nose-to-nose interaction between bighorn sheep and domestic sheep/goats will take place. Such interactions can result in a fast spread of diseases to the entire Trans-Pecos metapopulation and a local extinction of the species.

(2) Construction of artificial water sources such as guzzlers and catchments especially in the west and north-west terrain of the park should be considered. Suitable habitat can be increased from 9,817 ha to 15,884 ha, an increase of 38% of suitable bighorn habitat if artificial water sources are constructed. It has been observed that desert bighorn sheep will expand their home ranges and terrain usage if artificial

water sources will be constructed in water-deficient terrain (Campbell and Remington, 1979).

(3) Clearing of fences and other human-constructed structures that might inhibit safe movement of desert bighorn sheep to and from GUMO to other terrains needs to be addressed.

(4) Future monitoring of desert bighorn sheep and their behavior in the vicinity of windmills, windmill construction and windmill maintenance, should be undertaken as avoidance of such areas may have a negative influence towards migration.

(5) Monitoring of the mountain lion population within GUMO should be upheld since mountain lions have been identified as possible predators affecting the persistence of a naïve and small reintroduced population of desert bighorn sheep (Hoban, 1990; Wehausen, 1996; Ross et al., 1997; Hayes et al., 2000; Rominger and Weisenberger, 2000; Logan and Sweanor, 2001).

CHAPTER III

THE MOUNTAIN LION OF GUADALUPE MOUNTAINS NATIONAL PARK: GENETIC STRUCTURE, DISTRIBUTION, AND RELATIONSHIP TO OTHER POPULATIONS IN TEXAS

3.1. Introduction

One potential problem associated with the reintroduction of ungulates, such as desert bighorn sheep, is the risk of a small population not persisting long enough to increase in number (Berger, 1990). The mountain lion (*Felis concolor*), a native predator occurring throughout the southwestern and western portions of the United States as well as Florida, has been correlated to bighorn sheep kills in New Mexico, California and Texas. As such, the mountain lion is considered a potential threat to small, reintroduced populations of bighorn sheep (Hoban, 1990; Wehausen, 1996; Ross et al., 1997; Hayes et al., 2000; Rominger and Weisenberger, 2000; Logan and Sweanor, 2001), and in many cases extreme measures are being used to minimize the impact of such predation (New Mexico Department of Game and Fish, 1996-2002; U.S. Fish and Wildlife Service, 2000, 2003). These measures include the removal of all existing cats within the vicinity of the reintroduction area, removal of cats found in the vicinity of bighorn herds, and/or the removal of individual lions linked to bighorn kills (U.S Fish and Wildlife Service 2000, 2003; New Mexico Department of Game and Fish, 1996-2002).

Mountain lions are ambush predators (Beier et al., 1995) that use cover (Seidensticker, 1976) to stalk white-tail deer and desert mule deer, their primary sources of prey (Logan and Sweanor, 2001; McKinney, 2003). Desert bighorn sheep are considered an alternative food source, and generally avoid dense cover, preferring instead open spaces with high visibility and a relief of 27 to 85 degrees (Etchberger et al., 1989, 1990, Singer et al., 2000). Consequently, mountain lions and bighorn sheep have low habitat overlap, thus implying that encounters between the two should be minimal in most circumstances. Several factors presumably contribute to an increased incidence of mountain lion kills of bighorn sheep. First, introduced sheep may lack appropriate predator avoidance, especially if they are either captive bred or raised in lion-free areas (Vernon Bleich, California Department of Fish and Game, personal communication 2004). Second, animals released in unfamiliar habitat are less likely to escape predators (Krausman et al., 1999). Third, a decrease in primary prey abundance such as mule deer can result in lions targeting other prey items (Leopold and Krausman, 1983; Rominger and Weisenberger, 2000; Logan and Sweanor, 2001). Fourth, in some cases individual lions may favor desert bighorn sheep as their source of prey (Hornocker, 1970; Hoban, 1990; Ross et al., 1997; Hayes et al., 2000; Logan and Sweanor, 2001). Factors 1-3 are frequently unavoidable. For instance, the source of bighorn sheep for reintroduction purposes is limited and in most cases animals released are selected from protected areas that are under predator control (Eric Rominger, bighorn sheep biologist, New Mexico Department of Game and Fish, personal communication 2004; Clay Brewer, bighorn sheep program director, TPWD, personal communication

2004). When animals are reintroduced to a new area, this area, by definition, will be unfamiliar, and predator-proofing the new area has proven unsuccessful at keeping mountain lions out of an area (Clay Brewer, bighorn sheep program director, TPWD, personal communication 2004). Local prey populations can experience decreases in number as a result of environmental stochasticity, such as long periods of drought that affect water and food abundance (Oregon Department of Fish and Wildlife 1993). Finally, individual lions that demonstrate bighorn sheep as a major prey item are of major concern for managers, and these individuals are often the target of predator control measures (U.S Fish and Wildlife Service, 2000, 2003).

The desert bighorn sheep (*Ovis canadensis)* is native to North America and has historically numbered up to an estimated 1500 individuals in the 1800's (Gould, 1962; Cook, 1994), inhabiting areas throughout west Texas. By 1960 there was no evidence of desert bighorn sheep north of New Mexico-Texas boundary in the Guadalupe Mountains (Buechner, 1960), and efforts to restore this native species to its historical range was initiated by Texas Parks and Wildlife Department (TPWD) in the past several years (Brewer, 2005). Guadalupe Mountains National Park (GUMO), encompassing the Guadalupe Mountain range in Texas, was established in 1964. Management guidelines of the National Park Service emphasize the importance of restoring native species to its historic habitat and support such actions as the reintroduction of a bighorn population to GUMO (USDI, National Park Service, 1988; Singer et al., 2000). In addition, the guidelines include protection to any other native species residing within the National Park's land allowing intervention to "manage individuals or populations of native

species only when such intervention will not cause unacceptable impacts to the populations of the species or to other components and processes of the ecosystems that support them" (USDI, 2001). The status of the mountain lion population within the Guadalupe Mountains and the surrounding area is unknown. Population size, distribution and trends have not been studied, and the effect of removing a top predator from its ecosystem has been linked to trophic cascades that influence other species in the food web. For instance, removal of a top predator will cause an increase in herbivore populations that will overgraze vegetative species which in itself influence the abundance, distribution and persistence of dependent species (Kay, 1990; Singer et al., 1994; National Research Council, 2002; Beschta, 2003). Current predator control trends outside GUMO include: (1) systematic removal of all cats entering The Sierra Diablo Management Area, a desert bighorn sheep reintroduction area belonging to TPWD located south of GUMO and (2) random (but continuous) capture and kill of mountain lions by local ranchers. The reported numbers of lions killed north of GUMO is 20 individuals per year based on permits issued (New Mexico Department of Game and Fish, 1996 – 2002). This number does not include either unreported killing of mountain lions or kills within the state of Texas where the species is listed as a non-protected, non-game species, thus allowing an open season on mountain lions (TPWD, 2005).

Guadalupe Mountains National Park's management requires data related to resident and transient mountain lions within park boundaries in order to estimate population density and movement before reintroduction of desert bighorn sheep is considered. This will allow park managers to estimate the feasibility of monitoring the

lion population within the park area and taking action if and when an offending lion is identified. The objectives of this study are to document the approximate number of lions using Guadalupe Mountains National Park as well as their movement patterns and distribution within the park. A survey for mountain activity was initiated over a seven year period (1997-2004) for the purpose of estimating these parameters. In addition, fecal samples from presumed mountain lions were collected and used in a noninvasive genetic study of mountain lion within the park for the purposes of comparing patterns of variation within the lion population in the park to other regions of Texas and estimating the number of genetically distinct individuals identified within the park.

3.2. Methods and Materials

3.2.1. Sampling Area and Specimen Preparation

Mountain lion scat (n = 98) was collected from transects along 74 km of trails within Guadalupe Mountains National Park from 1995 to 2004 (Appendix B, Table 4; Appendix A, Fig. 4). The park is located in west Texas on the border of Texas and New Mexico, 110 miles east of El Paso, Texas. The park encompasses approximately 350 km^2 and is the southeastern part of the Guadalupe Mountain Range that extends northeast into New Mexico. The entire mountain range is a division of the Sacramento Mountains, the southern branch of the Rocky Mountains. All samples of scat were packed in sealed plastic bags and stored at -20°C and were later transferred to a – 80°C freezer at Texas A&M University.

3.2.2. DNA Extraction

A QIAamp DNA Stool Mini Kit (GmbH, Hilden, Germany) was used to extract DNA from 98 scat samples. Initially, fecal material was removed from the external portions of the scat sample, and 200mg of this material was placed in a 2ml microcentrifuge tube containing 1.6ml of buffer ASL (Stool lysis buffer). The solution was incubated at 70°C for 5 minutes, vortexed until thoroughly homogenized and centrifuged at 13,400 rpm for 2 minutes. The supernatant (1.4ml) was transferred to a new 2 ml tube, and the pellet was discarded. One tablet of Inhibit X was added to each tube containing the supernatant (two at a time) and vortexed immediately for at least 1 minute or until homogenized. Samples were incubated at room temperature for at least 1 minute and then centrifuged at 13,400 rpm for 6 minutes. Immediately, the supernatant was transferred to 1.5ml tubes and centrifuged at 13,400 rpm for 6 minutes. After centrifugation, 600µl of the supernatant was pipetted into a new 2ml tube containing 25µl of Proteinase K. 600µl of Buffer AL was added to each tube separately, and the solution was vortexed immediately for 15 seconds or until homogenized. All processing samples were performed in groups of 12 to 14. Subsequent to processing each batch, samples were incubated at 70°C for 1 hour and centrifuged briefly to remove drops from lid. Then, 600µl of 100% ethanol was pipetted into each tube, vortexed and centrifuged briefly and 600µl of lysate was pitpetted into a spin column that was placed in a collection tube. Samples were centrifuged at 13,400 rpm for 2 minutes, and the flow-through was discarded. This step was repeated 3 times, and then 500µl of Buffer AW1 (wash buffer) was transferred to the spin column, which was centrifuged at 13,400 rpm

for six minutes, and the flow-through was discarded. Then, 500µl of Buffer AW2 (wash buffer) was transferred to the spin column, centrifuged at 13,400 rpm for six minutes, and the flow-through was discarded. Spin columns were transferred to new 1.5ml tubes and 200µl of buffer AE (elution buffer) was directly pipetted onto membrane, incubated at room temperature for 5 minutes and centrifuged at centrifuged at 13,400 rpm for 2 minutes to release the DNA from spin column, and the extracted DNA was kept frozen at 4°C until PCR amplification was performed. Extractions were performed twice for those samples that either did not provide positive DNA results or showed only small amount of PCR (polymerase chain reaction) product after the initial amplification of a mitochondrial DNA (mtDNA) fragment.

3.2.3. Mitochondrial DNA Sequencing

Scat samples were identified to species by amplifying an approximately 200bp region of the mitochondrial control region. Primers used for PCR amplification of the control region fragment were kindly provided by Melanie Culver (Arizona Cooperative Fish and Wildlife Research Unit, University of Arizona). Their sequences are as follows: 1) forward primer - PDL-1 5‘- CCC AAA GCT GAA GTT CTT TCT - 3’and 2) reverse primer PDL-6/PDL-6del 5‘ - TAT TCA TG(G/A) GGG AT(A/G) TGG/TAT TCA TGG GGA T(A/G)T GG - 3’. PCR reactions were performed in 20µl volumes containing 2µl of each 10µM primer, 2µl of 10X Hotmaster *Taq* buffer with 25 mM Mg^{2+}, 0.4µl of 10mM of each DNTP, 1.8µl of 10mg/ml BSA, 0.1µl of 5U/µl HotMaster *Taq* DNA Polymerase, 7.7µl of ddH_2O and 4µl of template DNA per reaction. PCR was performed at 94°C for 1 min, 48 cycles of 94°C for 15 sec, 52°C for 30 sec, 72°C for 1

min and a final step at 72°C for 2 min. All PCR reactions included a positive and a negative control. PCR products were electrophoresed and visualized on a 2% agarose gel containing 1X Tris-borate EDTA (TBE), and stained with ethidium bromide (0.5µg/ml). Samples with visible PCR products were cleaned by adding 2µl ExoSAP-IT (USB Corporation, Cleveland, OH) to 5µl PCR product and thrmocycled at 37°C for 15min and at 80°C for 5min. Fragments were sequenced with Big Dye termination following the supplier's protocol (Applied Biosystems, Foster City, California), 2µl HalfBD (Genetix, Boston, MA). Extra dye terminator was removed using Sephadax spin columns and dried in a spin-vac for 20 minutes. Fragments were sequenced in both directions on an ABI 3100 automated sequencer (Applied Biosystems, Foster City, California, USA) according to manufacture's instructions. All sequences were aligned and compared using Sequencher 4.2 (Gene Code Corporation, Ann Arbor, Michigan, USA). Samples identified as a species other than mountain lion were excluded from nuclear DNA genotyping.

3.2.4. Nuclear DNA Genotyping

The minimum number of microsatellite loci needed for individual identification of mountain lions in GUMO was determined by using allele frequency data from a reference group that included 7 tissue samples collected from mountain lions outside park boundary between 2001 and 2004 and provided by Jan Janecka, (Feline Research Program and Department of Wildlife and Fisheries, Texas A&M University). Six microsatellite loci characterized for the domestic cat (Menotti-Raymond and O'Brien 1995; Menotti-Raymond et al., 1999) and denoted as FCA23, FCA26, FCA35, FCA43,

FCA82, FCA96 were used to obtain a multilocus genotype for each samples that tested positive for mountain lion mtDNA. Each primer was used separately in a 20µl reaction containing 0.48µl of 10 µM of each forward and reverse primer, 2µl of 10X Hotmaster *Taq* Buffer with 25 mM Mg^{2+}, 0.4µl of 10mM of each DNTP, 1.6µl of 10mg/ml BSA, 0.15µl of 5U/µl HotMaster *Taq* DNA Polymerase, 8.89µl of ddH_2O and 0.3µl of template DNA per reaction. PCR reactions included an initial step of 94°C for 1 min, 48 cycles of 94°C for 15 sec, 54°C for 30 sec, 72°C for 45 sec and a final step at 72°C for 2 min. All PCR reactions included a positive and a negative control. Amplification products were electophoresed and visualized on a 1.5% agarose gel containing Tris-borate EDTA (TBE), and stained with ethidium bromide (0.5µg/ml). Samples with visible PCR product were diluted 1:20, and 1µl of diluted DNA product was mixed in a 10µl solution of 9.7µl formamide and 0.3µl size standard (GeneScan™-400HD [ROX]™, Applied Biosystems, Foster City, CA). Samples were genotyped using ABI 3200 (Applied Biosystems, Foster City, California, USA).

3.2.5. DNA Repair

Samples that failed to amplify for one or more microsatellite loci and 7 samples that tested positive for mtDNA but failed to amplify all microsatellite loci were treated with an experimental DNA repair kit, PreCR-A Repair Mix (New England BioLabs, Ipswich, MA). A 50µl reaction containing 38µl of ddH_2O, 5µl of 10X ThermoPol RX Buffer, 0.5µl of each 10mM DNTP, 0.5µl 100X NAD+, 1µl PreCR repair Mix-A and 5µl of template DNA was maintained at room temperature for 15 minutes; 5µl of the repaired DNA mix were added to a 5µl PCR reaction as described in section 2.3. PCR

products were visualized on a 1.5% agarose gel to determined if successful DNA repair had occurred, and samples testing positive for amplification were genotyped (as described in section 2.3).

3.2.6. Data Analysis

Multilocus microsatellite genotypes were used to identify individual mountain lions. The procedure used was as follows. (1) An individual was accepted as homozygous at a locus after repeating the genotyping twice. (2) Individuals were scored as heterozygous only after each allele is observed twice independently. To determine whether my results suffered from genotypic errors due to the non-invasive techniques of the sample collection (McKelvey and Schwartz, 2004), I estimated the minimum number of differences for all pairs of genotypes. Following Mowat and Paetkau (2002), this method will indicate whether samples were scored erroneously if a high percentage of genotypes differ from each other by a low number of loci. Results for the GUMO population were compared to 3 other west Texas populations of mountain lion (data kindly provided by Jan Janecka, Wildlife and Fisheries Department, TAMU) scored from blood and tissue samples, thus presumably reducing levels of potential allelic dropout.

Probabilities of identity or PI (Waits et al., 2001) for the six loci were computed using API-CALC 1.0 (Ayres & Overall, 2004). Estimates were derived from an adjacent population of mountain lions in Texas. Jan Janecka kindly provided allele frequencies for this mountain lion population and the six loci examined in this study. Probability of identity across these six loci was estimated as 1.21×10^{-4} for unrelated individuals.

Individuals identical for all six loci were interpreted as the same mountain lion. Measures of genetic variability at these 6 loci were calculated using GenAlEx version 5_1.1 (Peakall and Smouse, 2001). Deviation from Hardy-Weinberg equilibrium was tested using Chi-square test with pooling (Hartl and Clark, 1989) and the Markov Chain method (Guo and Thompson, 1992). Expected heterozygosity, H_e, was calculated for each locus and for the overall six loci and compared to both observed heterozygosity (H_o) within the population and between other Texas populations. Estimates of genotypic and genic differentiations between the Guadalupe population and the other populations of mountain lions in Texas were obtained by estimating F_{st} with GENEPOP 3.4 (Raymond and Rousset, 1995). F_{is} (inbreeding coefficient, the reduction in heterozygosity of an individual, due to non-random mating within the population) was also calculated and compared to the other Texas populations. GeneClass2 (Piry et al., 2004) was used for individual assignment of mountain lion genotypes to one of six populations in Texas. ArcGIS® 9.0 software (ESRI) was used to plot locations and usage of the park by mountain lions and surveyed areas suitable for desert bighorn sheep (see Appendix A, Fig. 5). A 30 meter resolution digital elevation model (DEM) from the National Elevation Dataset (NED) was used to plot the distribution map.

3.3. Results

3.3.1. Sequencing

DNA was isolated from 98 scat samples, and 54 samples (55%) provided a mtDNA amplification product. All mtDNA fragments were sequenced, and 44 (80%)

samples tested positive for mountain lion mtDNA. Only one mtDNA haplotype was found within the Guadalupe Mountains National Park population, and this haplotype was identical to haplotypes from a separate area in Terrell County, Texas (Jan Janecka, Wildlife and Fisheries Department, TAMU, personal communication 2006). The distribution of scat that tested positive for mountain lion mtDNA was plotted on the park's transects map and marked by KM number, the collection location on the park's transects (Appendix B, Table 4; Appendix A, Fig. 4).

3.3.2. Genotyping

Microsatellite analysis revealed 32 unique genotypes (73%) for all samples found to have mountain lion mtDNA, and this represents 33% of total DNA extractions (Appendix B, Table 5). Only two samples were identical for all loci (samples ID 4 and 14), thus indicating the same mountain lion. All loci were found to be polymorphic with a fixation index close to zero. The mean number of effective alleles per locus (N_a) was 3.286 (range: 5-9, S.E.= 0.619), and the number of private alleles (N_e), relative to other Texas populations, was 6.5 (range: 2.098 - 4.654, S.E. = 0.390). The expected (H_e) and observed (H_o) mean heterozygosity was 0.673 and 0.684, respectively (Appendix B, Table 6). Individuals comparisons revealed two loci (FCA26, FCA96) out of Hardy-Weinberg equilibrium, whereas across all loci the population was in equilibrium (P=0.343). In order to determine whether the two loci not in equilibrium were unique to the GUMO population, P values of the six loci in the other six mountain lions populations were examined. Three loci (FCA23, FCA26, FCA96) in 2 separate

populations were calculated to be out of HWE, although both populations were in equilibrium across all loci.

Pairwise estimates of genotypes observed at GUMO indicated differences as an average of 4.9 loci. Comparisons of other populations in west Texas reveal similar results with populations 1, 2, and 5 showing averages of 4.8, 4.36, and 3.57 differences, respectively (Appendix A, Fig. 6). These results indicate low levels of allelic dropout, and similarities to other populations in the region lend reliability to the data and may indicate low error rate.

Assignment tests of the GUMO mountain lions to the six different populations in Texas (Appendix B, Table 7; Appendix A, Fig. 5) assigned 11 individuals (n=32) to population 1 (34.4%, $\alpha = 0.001$), a population collected in the same county but outside the boundary of Guadalupe Mountains NP (Hudspeth County, Jan Janecka, Wildlife and Fisheries Department, TAMU, personal communication 2006). Two of the mountain lions were assigned to population 4 (Brewster County Area, 230-260 miles SE) and a two additional samples were also assigned to this population but had a higher probability to population 1. One of the samples assigned to population 1 was also assigned to Population 2 (Davis Mountains Area, ~120miles ESE), two of the samples were also assigned to Population 3 (Presidio County Area, ~250miles South of GUMO), and one sample was assigned to population 5 (Terrell County, 250 miles SE). All secondary and tertiary assignments had lower probabilities than assignments to either populations 1 or 4 (Appendix B, Table 4). None of the samples were assigned to population 6 (South Texas Area, 600-650 miles away from GUMO). Estimates of F_{ST} for the GUMO

population ranged from 0.103 (pop 1) – 0.199 (pop 6), suggesting population structure with some restrictions of gene flow between the GUMO population and the other populations in Texas. Like the other populations in west Texas, the least amount of gene flow was observed between GUMO and population 6 in South Texas. The uniqueness of the GUMO population may be the result of exchange between GUMO and mountain populations in New Mexico (Appendix B, Table 8).

3.4. Discussion

The mountain lion population in Guadalupe Mountains National Park shows evidence of high heterozygosity and shared alleles with other west Texas populations (defined by Jan Janecka, Wildlife and Fisheries Department, TAMU, personal communication 2006). Expected heterozygosity for the six other populations in Texas range between 0.357 and 0.745 (Jan Janecka, Wildlife and Fisheries Department, TAMU, personal communication 2006). In comparison to these six populations, GUMO averages about 15.15% higher levels of expected heterozygosity. In addition to similar expected heterozygosity and expected allele frequencies, both GUMO and the other populations in Texas showed similar patterns in terms of the minimal number of loci differing between pairs of genotypes found in a population (Appendix A, Fig. 6). There were no evidence genotypes in the GUMO population being skewed toward differences involving a single genotype. In addition with the other comparisons, these data provide little evidence of genotyping error (McKelvey and Schwartz, 2004). Probability of identity (PI), for the GUMO population was compared to the overall PI of the other Texas populations and was found to be similar to all five population in west Texas and

different from Population 6 in south Texas (Appendix A, Fig. 7). These results add another level of confidence in the accuracy of data analyzed for the GUMO mountain lion population.

Both assignment tests and estimates of F_{ST} suggest gene flow between the Guadalupe Mountains population and other populations in Texas, with some individual genotypes assigned to locations 230-260 miles away. Sweanor et al. (2000) indicated that dispersal distance for male lion is as high as 214 km for males and 78.5 km for females. The San Andres Mountains in New Mexico are protected lion habitat and sustain a population of lions approximately 160 miles from GUMO (Sweanor et al. 2000). Alleles not found in other Texas populations but found in the GUMO population may be the result of lions dispersing from New Mexico.

Fifteen loci from 10 DNA samples failed to either amplify or provide a genotype. After treating the samples with PreCR-A Repair Mix, all 15 loci were scored successfully. Additionally, five samples that tested positive for mountain lion mtDNA but failed to amplify for any of the six microsatellites amplified and were successfully gentoyped for 28 of the total 30 loci (94% success). As a result, treatment of the degraded DNA with PreCR-A Repair Mix (Appendix B, Table 5) produced an overall 19.5% increase in successful amplification. Therefore, this method provides a marked improvement for noninvasive genetic studies that rely on scat, which yields DNA that is in low quantity, degraded, and prone to allelic dropout (Hedmark and Ellegren, 2005).

One conclusion that can be drawn from the genetic data is that the lion population in Guadalupe Mountains National Park is not confined to the park's

boundary. Based on allele frequencies, assignment tests, and F_{ST}, the park's population consists of individuals that disperse into and outside the boundaries. Although the number of scat samples was limited, the genotypic data suggest that at least 32 mountain lions have used the park over the past eight years. By pooling the additional seven individual samples collected in the vicinity of the park (Population 6, Jan Janecka, Wildlife and Fisheries Department, TAMU, personal communication 2006), as many as 39 distinct individuals may have been present in the park between 1997-2004. Only one animal's DNA was collected more than once. Over a three year period (2002-2004), 26 different mountain lions were either inside or near Guadalupe Mountains National Park, with a cat density per year of 8-9 individuals.

Logan et al. (1996) indicated that a male mountain lion's home range averages 187.1 km^2 and females average 73.5km^2. For desert bighorn sheep habitat, other studies have indicated an average of 3.3 lions per 100km^2 (Cunningham et al. 1995; Logan et al. 1996). Based on unpublished data (see Chapter II), GUMO contains approximately 80 - 98 km^2 of habitat suitable for desert bighorn sheep. Assuming that previously estimated home ranges of lions are similar for GUMO, the number of potential lions occupying this habitat should be three to four individuals, with approximately seven estimated for the entire park area of 350 km^2. Clearly, it is difficult to estimate lion density from the restricted data presented here. Nevertheless, 15 individuals were identified for 2002 alone, and given the area of the park relative to habitat suitable for lion and bighorn sheep (Appendix A, Fig. 5) an estimate of four to five resident cats is not excessive.

The low recapture rate and high number of potentially transient lions may be the result of a high frequency of turnover in lion populations in Texas. Lion hunting in west Texas is unregulated, and this may account for high levels of mortality in mountain lion. In his study of radio-collared lions in south Texas, Harveson (1997) estimated that the lifespan of mountain lions was approximately 2-3 years. With high levels of turnover, one would predict an increase in transients in GUMO area as well as in other areas of Texas. Studies have demonstrated that carnivore populations respond to heavy hunting pressures with an overall younger age structure (Smuts, 1978; Jedrzejewska et al., 1996) and removal of resident adults, especially those of males, may disrupt the social organization (Swenson et al., 1997; Lambert et al., 2006) resulting in higher immigration rate of juveniles or young adults (Lambert et al., 2006). Juvenile mountain lions have been correlated to higher livestock killings (Beier, 1991) as they tend to gravitate towards the easier kill since their hunting skills are not as developed (Ross, 1994). It is recommended that prior or simultaneously to the release of bighorn sheep into GUMO, more information on the lion population is required. First, a more thorough monitoring program needs to be established, and scat should be collected in a more systematic matter, with a minimum of 40 samples collected per year. Second, the density of primary prey needs to be determined. In addition, information on age and sex ratios needs to be gained by a combination of genetic sampling, radio telemetry, and remote imaging. These data should provide a better assessment of the number of resident cats and provide essential information regarding individual cats that might prove to prey on bighorn sheep. There is evidence that specific mountain lions may develop an affinity

for bighorn sheep, deviating from their main prey source, the mule deer (Hayes et al., 2000) but this behavior seems to be an individual, learned behavior and isolated to specific cats (Ross et al., 1997). Studies have indicated that bighorn sheep constitute only a small percentage of mountain lion diet (2%, Cunningham et al., 1999) and therefore mass removal of the cats from a reintroduction area is not an effective method for conservation. Mountain lions within GUMO should be collared and monitored in order to identify specific, offending cats, and removal should be specific for those mountain lions (U.S. Fish and Wildlife Service, 2000, 2003).

CHAPTER IV

SIMULATED DYNAMICS OF ARABIAN ORYX (*ORYX LEUCORYX*) IN THE ISRAELI NEGEV: EFFECTS OF MIGRATION CORRIDORS AND POST-REINTRODUCTION CHANGES IN NATALITY ON POPULATION VIABILITY

4.1. Introduction

The Arabian oryx (*Oryx leucoryx*) is endemic to the Arabian Peninsula and once roamed widely from the Sinai desert to the Euphrates River (Stewart, 1963). By the mid-19th century the species had vanished from the Sinai and Israeli Negev deserts (Griver, 1991); the last individual sighted near Israel was seen in Jordon in the 1930's (Clarke, 1978). The species was listed as critically endangered by the International Union for the Conservation of Nature (IUCN) in the 1960's (IUCN, 1969), with endangerment attributed to activities related to the oil industry, unregulated hunting, loss of habitat to domestic livestock, and the capture of animals for private collections (Stanley Price, 1989; Tear et al., 1997). During the early 1960's, a captive "world herd" was established in several zoos in the United States and Europe (London Zoo, Basles Zoo, and Phoenix Zoo) from the last individuals captured in the wild and a few individuals donated from private collections of Arabian leaders (Stanley Price, 1989). During the 1980's, a total of 40 animals from this captive herd were reintroduced at a site in Oman; the reintroduced population increased to approximately 400 animals over a 15-year period (Stanley Price, 1989), but then poaching during the late 1990's reduced the herd to only a few dozen individuals (Gorman, 1999).

A second reintroduction program currently is underway in Israel. In 1978, 7 animals from the same "world herd" were placed in a breeding facility in the Hai Bar Yotvata located in the Negev desert of southern Israel. This captive herd was the source for seven releases to the wild that have taken place at 3 sites: in 1997 and 1998 in Shahak Spring in the Arava Valley, in the eastern Negev (Site A); in 2000, 2001, and 2002 in Har-Hanegev, in the central-western Negev (Site B); and in 2003 and 2005 in Nachal Ketzev, in the southern Negev (Site C) (Appendix A, Fig. 8). Sites A and C have open, flat terrain whereas Site B has a more rugged terrain of canyons and low hills. Site A was monitored for approximately 3 years (until 2000) and the population was increasing, Sites B and C still (as of 2006) are being monitored; the population at Site B is decreasing, and it is still too early to determine the performance of the site C population although will be treated as increasing due to similarities in habitat conditions (David Saltz, Mitrani Center for Desert Ecology, Israel, personal communication 2004).

The greatest difficulty in projecting future trends for Arabian oryx populations in the Israeli Negev is related to uncertainties concerning (1) establishment of migration corridors among release sites and (2) post-reintroduction increases in natality rates. The Arabian oryx is a migratory species and the expectation is that animals will establish migration corridors among the release sites, however, individuals from the different sites have not yet encountered one another (David Saltz, Mitrani Center for Desert Ecology, Israel, personal communication 2004). The population at Site B apparently will not become self-sustaining without post-reintroduction increases in natality rates, similar to those observed in reintroduced Arabian oryx populations in Oman (Stanley Price, 1989;

Tear et al., 1997). Since oryx are adapted both physiologically and behaviorally to open, flat terrain (Tear and Stanley Price, 1991), there remains the possibility that even the wild-born animals will not acclimate well to the rugged terrain of Site B, and that corridors connecting Site B to Sites A and C may not be established.

In this research study, I first describe a model developed to aid in projecting future population trends for the Arabian oryx in the Israeli Negev. I then evaluate the potential usefulness of the model by examining its ability to simulate observed trends in population growth following reintroductions of Arabian oryx in Oman, and also its ability to simulate trends observed to date in the three populations that have been reintroduced in the Israeli Negev. Finally, I use the model to project future trends in the Israeli Negev populations under different assumptions regarding the establishment of migration corridors among the (currently isolated) populations, and regarding increases in natality rates after reintroduction.

4.2. Background Information

Arabian oryx populations consist of herds that adjust the size of their home ranges depending on availability of vegetation which is directly related to rainfall (Stanley Price, 1989; Van Heezik et al., 2003); individuals can satisfy their water requirements from vegetation, consume water infrequently, and can survive independent of drinking water (Tear et al., 1997; Williams et al., 2001, Seddon and Ismail, 2002). Herd home ranges may encompass several thousand square kilometers, and a herd might not return to a previously grazed area for several months (Stanley Price, 1988). Herds typically break into a variable number of smaller bands as herd size increases; the

activity ranges of bands within a herd overlap broadly (Maoz, 2003). Movement is age and gender specific, young staying within the shelter of the herd in a mother/calf pair, sub-adults or non-dominant males may leave the herd looking for territories and/or to establish new herds (Stanley Price, 1989; Tear and Ables, 1999).

Herds usually contain relatively equal numbers of males and females distributed roughly evenly across all age groups (Vie, 1996). The bands that typically form within a herd as the herd grows each consist of a dominant breeding male and several females and their young (Tear and Ables, 1999). Newly born calves spend their first 3 to 4 weeks apart from the band, watched by both the mother and the dominant male; no infanticide has been reported, and a new dominant male will show similar behavior to all young within its band regardless of paternity (Stanley Price, 1989). Solitary males often establish temporary territories, attracting females that move in and out of the bands of other males (Stewart, 1963; Dieckmann, 1980; Newby, 1985; Wacher, 1986; Stanley Price, 1989); bachelor herds are not common (Walther, 1978). Females are polyestrous and births are distributed throughout the year. Females can give birth at 9- to 12-month intervals after 20 months of age (Saltz, 1998), and individuals can live up to 17 years in the wild (Stanley Price, 1989).

4.3. Model Description

4.3.1. Overview of Model Structure

The model is formulated as a compartment model based on difference equations (Δt = 1 month), programmed in STELLA®7 (High Performance Systems, 2001), and

consists of 3 structurally identical sub-models representing the 3 reintroduced populations of oryx in the Israeli Negev (Appendix A, Fig. 9). Forms of the equations in each of the 3 sub-models are identical, but some parameters differ by habitat. For each sub-population:

$$N_{i,t+1} = N_{i,t} + (n_{i,t} - m_{i,t} - e_{i,t} - s_{i,t}) * \Delta t, \text{ for } i = 0 \quad (1)$$

$$N_{i,t+1} = N_{i,t} + (r_{i,t} + i_{i,t} + s_{i-1,t} - m_{i,t} - e_{i,t} - s_{i,t}) * \Delta t, \text{ for } i > 0 \quad (2)$$

where $N_{i,t}$ represents the number of individuals in age class i at the beginning of time t, $n_{i,t}$ represents the number of young born into the population (entering age class $i = 0$) during time t, $r_{i,t}$ represents the number of individuals in age class i introduced into the population as part of the reintroduction program during time t, and $m_{i,t}$, $e_{i,t}$, $i_{i,t}$, and $s_{i,t}$ represent the number of individuals dying, emigrating to another sub-population, immigrating from another sub-population, and surviving to age class $i + 1$ and remaining in the same sub-population, respectively, during time t. The identity of individual cohorts is maintained up to 204 months of age; Arabian oryx have been known to live up to 17 years (Stanley Price, 1989).

4.3.2. Natality

Natality is calculated as:

$$n_{i,t} = k1_j * k2_t * NR_t \quad (3)$$

where NR_t represents the number of females in the population that have attained reproductive maturity, $k1_j$ represents the natality rate per reproductive active female during the jth month after reintroduction (females born on site are assigned the maximum

reproductive rates; the values for j > 156 in Appendix B, Table 9a), and $k2_t$ represents a density-dependent reduction of natality per capita as availability of resources decreases.

$$k2_t = 1-(1/k3_t)*N_t \quad (4)$$

where N_t is the total population at time *t* and $k3_t$ is the carrying capacity of the site at time *t*, which depends on the availability of water, food, and shade within the site, all of which are directly correlation with rainfall (Field and Blankenship, 1973; Phillipson, 1975; Sinclair, 1975; Stanley Price, 1989; Spalton, 1999; Ostrowski et al., 2002; Van Heezik et al., 2003; Maoz, 2003). I assume a linear relationship between carrying capacity and annual rainfall:

$$k3_t = b_0 + b_1 * rf_t \quad (5)$$

where b_0 represents $k3_t$ during severe drought, b_1 represents the rate at which $k3_t$ increases with increasing annual rainfall, and rf_t represents annual rainfall (inches); rf_t, is a uniform random variant on the interval from zero to the maximum observed annual rainfall.

4.3.3. Mortality and Survivorship

The model represents three sources of mortality:

$$m_{i,t} = (k6_i + k7_i + k8_i) * N_{i,t} \quad (6)$$

where $k6_i$, $k7_i$, and $k8_i$ represent the proportions of individuals in age class *i* that die due to natural (non-human) causes, hunting (when animals cross the border and are not protected from hunting), and military activities (where animals die from exhaustion and/or starvation as a result entangling their legs in parachute strings attached to lanterns used by the Israeli air force). No predation of oryx has been recorded in Israel.

Survivorship from age class *i* to age class *i + 1* is calculated as:

$$s_{i,t} = N_{i,t} - m_{i,t} \quad (7)$$

4.3.4. Migration

The general structure of immigration and emigration rules was based on observed behavior of Arabian oryx (Stanley Price, 1989; Tear, 1992; Tear and Forester, 1992; Tear et al., 1997), specific parameter values were based on author's assumptions. Most migration occurs during winter, and animals less than 7 months of age do not migrate. If the population at a given site is below carrying capacity (k3), up to 5% of the population will migrate during winter (November through April) and up to 1% of the population will migrate during summer (May through October); much of this roaming is due to the roaming of bachelor males (Stanley price, 1989; Tear and Ables, 1999). If the population at a given site is above carrying capacity, in addition to this background roaming, up to 70% of the excess population at the site will migrate, provided that this number is smaller than the combined carrying capacities of the corridors leaving the site ($k3^{cor}$). Migration rules are represented in the model as:

$$e_{i,t}, = (N_{i,t} / \sum N_{i,t}) * (\sum N_{i,t} - k3_t) * ran(0.7,1) + (N_{i,t}) * ran(0, 0.05),$$

$$\text{for } i \geq 7 \text{ during winter, if } (\sum N_{i,t} > k3_t) \text{ and } (\sum N_{i,t} - k3_t) \leq k3_t^{cor} \quad (8a)$$

$$e_{i,t}, = (N_{i,t}) * ran(0, 0.05),$$

$$\text{for } i \geq 7 \text{ during winter, if } (\sum N_{i,t} \leq k3_t) \text{ or } (\sum N_{i,t} - k3_t) > k3_t^{cor} \quad (8b)$$

$$e_{i,t}, = (N_{i,t}) * ran(0, 0.01),$$

$$\text{for } i \geq 7 \text{ during summer, if } (\sum N_{i,t} \leq k3_t) \text{ or } (\sum N_{i,t} - k3_t) > k3_t^{cor} \quad (8c)$$

where ran(a, b) represents a uniform random variate on the interval a to b. I assume that no mortality occurs while moving among sites, and that emigrants originating from one site arrive as immigrants at the destination site one month later.

$$i_{i+1,t+1}, = e_{i,t} \quad (9)$$

4.4. Model Evaluation

To evaluate the potential usefulness of the model, I examined its ability to simulate observed trends in population growth following the reintroductions of oryx in Oman, and also its ability to simulate trends observed to date in the three, currently isolated, populations that have been reintroduced in the Israeli Negev.

4.4.1. Simulated and Observed Population Growth in Oman

I simulated population growth in Oman during the 14-year period from 1982 through 1996, when the population crashed as a result of poaching; 10 animals, 11, 11, and 8 animals were released during 1982, 1984, 1988, and 1989, respectively (Stanley Price, 1989). I parameterized the model (Appendix B, Table 9) based on data collected during the first four years after reintroduction, including age at sexual maturity, natality rates (*k1*), and natural mortality rates (*k6*) (Stanley Price, 1989), but recalibrated natality rates as a function of time since reintroduction based on observed increases in natality rates after 1986 (Tear et al., 1997). Hunting mortality (*k7*) and mortality due to military activities (*k8*) were zero, and since only one site was defined, there was no migration between sites. I ran 10 replicate stochastic (Monte Carlo) simulations in which annual rainfall (*rf*) was represented as a uniform random variant on the interval from zero to

0.29 inches, which was the average observed monthly rainfall for the reintroduction area (Yalooni, Oman) (International Center for Agricultural Research in the Dry Areas, 2003); I simulated rainfall-related changes in carrying capacity (*k3*) as $k3_t = 33 + 2586 * rf_t$. Simulated population trends paralleled observed trends reasonably well; mean simulated population sizes differed from those observed by +13% 60 months after the initial reintroduction and by -19% 144 months after reintroduction, and underestimated the final available field estimate 168 months after reintroduction by 9%, or approximately 2 standard deviations of the mean (Appendix B, Table 10). These differences are within the range of uncertainty associated with the field estimates (Stanley Price, 1989; Tear et al., 1997), and I chose not to recalibrate model parameters.

4.4.2. Simulated and Observed Population Growth in the Israeli Negev

I simulated population growth in the Israeli Negev during the 8-year period from 1997 through 2005; 21 and 11 animals were released at Site A in 1997 and 1998, 18, 14, and 12 animals were released at Site B in 2000, 2001, and 2002, and 18 and 10 animals were release at Site C in 2003 and 2005, respectively (David Saltz, Mitrani Center for Desert Ecology, Israel, personal communication 2004). I parameterized the model (Appendix B, Table 9) based on data collected from each of the three reintroduced populations, including age at sexual maturity, natality rates (*k1*), and natural mortality rates (*k6*), (David Saltz, Mitrani Center for Desert Ecology, Israel, personal communication 2004). I assumed that only animals aged 7 months and older were vulnerable to hunting mortality (*k7*) and mortality due to military activities (*k8*); younger animals seldom venture out from the security of familiar habitat. There was no

migration. I ran 10 replicate stochastic (Monte Carlo) simulations in which annual rainfall (*rf*) was represented as a uniform random variant on the interval from zero to 0.29 inches, which was the average observed monthly rainfall for the reintroduction area (Israeli Negev) (Central Bureau of Statistics, 1996-1999); I simulated changes in carrying capacity (*k3*) as described in Section 4.4.1. Simulated population trends at all 3 sites corresponded reasonably well with available field observations; mean (±1 SD) simulated total population size (114 ± 1.57) was 14% larger than the last field estimate 96 months after the initial reintroduction (100, David Saltz, Mitrani Center for Desert Ecology, Israel, personal communication 2004). Mean (±1 SD) simulated population trends at Sites A (47 ± 1.10, and increasing), B (43 ± 0.46, and decreasing), and C (24 ± 0.11, and increasing) all were consistent with field observations.

4.5. Projecting future trends for the Israeli Negev Populations

The greatest difficulty in projecting future trends for the Israeli Negev populations is related to uncertainties concerning (1) establishment of migration corridors among release sites and (2) post-reintroduction increases in natality rates. I simulated six possible scenarios involving all combinations of three assumptions regarding migration: (1) no migration, (2) migration among all three sites, and (3) migration between sites A and C only; and two assumptions regarding natality rates: (1) no adjustment to natality after reintroduction and (2) increased natality after reintroduction. For each scenario, I ran 10 replicate stochastic (Monte Carlo) simulations with carrying capacities of the sites depending on randomly generated

rainfall, as described in Section 4.4.2, and monitored population dynamics at each site as well as dynamics of the meta-population.

Simulation results indicate that without migration the population at Site B is not sustainable and the populations at Sites A and C stabilize well below the minimum viable population size (MVPS, 100 animals, Saltz, 1998) if natality rates do not increase after reintroduction (Appendix B, Table 11; Appendix A, Fig. 10a). If post-reintroduction natality rates increase, all populations are self-sustaining, but all stabilize below MVPS (Appendix B, Table 11; Appendix A, Fig. 10b). With migration among all sites, even without increases in natality rates, the meta-population stabilizes above MVPS, with animals approximately equally distributed among the three sites (Appendix B, Table 11; Appendix A, Fig. 10c). However, with post-reintroduction increases in natality rates, the meta-population stabilizes at a size approximately two-and-a-half times larger, again with animals approximately equally distributed among the three sites (Appendix B, Table 11; Appendix A, Fig. 10d). With migration between Sites A and C only, without increases in natality rates, the meta-population stabilizes below MVPS, and the isolated population at Site B is not sustainable (Appendix B, Table 11; Appendix A, Fig. 10e); numbers of animals at the three sites stabilize at essentially the same levels as in the scenario without migration. If post-reintroduction natality rates increase, the meta-population stabilizes at a size approximately three times larger, well above MVPS, with slightly more than two-thirds of the animals approximately equally divided between Sites A and C, and slightly less than one-third of the animals at Site B (Appendix B, Table 11; Appendix A, Fig. 10f).

Three important trends immerge from these simulations: (1) no individual site supports a viable population under any of the scenarios, (2) if there are no post-reintroduction increases in natality rates, the area supports a viable metapopulation only with establishment of migration corridors among all sites, and (3) if there are post-reintroduction increases in natality rates, the area also supports a viable metapopulation with establishment of migration corridors only between Sites A and C. Sensitivity analysis indicated these trends are robust to changes of up to ± 50% in my estimates of model parameters (Appendix B, Table 9), except for reduction of natality rates (*k1*): even with establishment of migration corridors among all sites, the area will not support a viable metapopulation if estimates of natality rates are reduced by > 20%. Sensitivity analysis consisted of changing the value of each of the parameters, one at a time, by ± 50% of its baseline value and re-running the complete set of scenarios. I feel that it is unlikely that I have over- or underestimated any of the parameters by more than 50%.

4.6. Discussion

Projecting future trends in the Israeli Negev populations of Arabian oryx remains problematic in view of uncertainty regarding establishment of migration corridors among the (currently isolated) populations, and regarding (to date unobserved) post-reintroduction increases in natality rates. The expectation that animals will establish migration corridors is based on observations in Oman (Tear and Forester, 1992) and Saudi Arabia (Strauss, 2002) that herds showed lower home range fidelity and that migratory movements increased as population sizes increased, and the observation that distances between sites in the Israeli Negev are within the potential range of movements

of herds (David Saltz, Mitrani Center for Desert Ecology, Israel, personal communication 2004). The expectation of post-reintroduction increases in natality rates is based on increases observed in reintroduced Arabian oryx populations in Oman (Stanley Price, 1989), and the fact that reproductive success commonly is different for animals released into the wild compared to wild-born individuals (O'Bryan and McCullough, 1985; Chivers, 1991; Saltz and Rubenstein, 1995; Tear and Ables, 1999).

Uncertainty arising from lack of knowledge about key ecological processes ("parametric" uncertainty) and from inherently unpredictable and uncontrollable environmental and/or socio-economic factors ("background noise") is an almost universal feature of natural resource management; the long-recognized challenge, of course, is to manage wisely in the face of such uncertainty (Holling, 1978; Walters 1986). Within the context of metapopulation dynamics, uncertainty associated with the relative importance of on-site reproduction versus migration among sites often is a critical issue (Scott and Carpenter, 1987; Hanski, 1994, 1999; Walters, 2001; Reed and Levine, 2005).

In the present case, the role of Site B in maintaining population viability is particularly enigmatic. Model projections suggest that if there are no post-reintroduction increases in natality rates, the population at Site B is essential to metapopulation viability, even though it acts as a "sink", that is, is not self-sustaining and decreases the stable population sizes at the other two sites. If there are post-reintroduction increases in natality rates, the population at Site B is not essential to metapopulation viability,

although it does increase metapopulation size by roughly one-third, and, since it is self-sustaining, provides a buffer against catastrophic losses at the other two sites.

Model projections also suggest the aspects of uncertainty regarding natality and migration most critical to management might be reduced substantially by continued field monitoring of Sites A and C over the next 5 or 6 years. If natality rates increase as observed in Oman, the metapopulation should reach viable size within 5 or 6 years with the establishment of migration corridors between Sites A and C; mean time to reach 100 individuals was 68.5 (±1.08) months with establishment of migration corridors among all sites and 68.8 (±2.04) months with establishment of migration corridors among Sites A and C only (Appendix B, Table 11). Without increases in natality, it will take almost 4 decades (442.2 ±46.11 months) for the metapopulation, consisting of populations at all 3 sites, to reach viable size, and the population at Site B will become extinct within the same time frame if it remains unconnected to the other 2 sites (Appendix B, Table 11). Thus model projections suggest that management of Site B should remain a critical management issue over the next several years, either until increases in natality rates and the establishment of a migration corridor between at least Sites A and C have been confirmed, or until the decision is made to abandon Site B in favor of the establishment of an alternative release site.

CHAPTER V

SUMMARY AND CONCLUSION

Wildlife conservation has become a multi-faceted field, influenced by economic and social factors, where science plays only one role in decision making (Schaller, 1992). Conservation biologists can no longer work in a vacuum where scientific principals are the only driving force behind identification, design and implementation of a conservation project (Machlis 1992). Multiple sources influence a success or failure of a conservation initiative, sources such as government agencies, land owners, commercial agencies and the level of involvement of the local population (Schneider, 1992; Wondolleck et al., 1994).

During the process of evaluating courses of action in conservation, an approach has emerged to evaluate the entire ecosystem instead of targeting a single species (Minta and Kareiva, 1994). This approach not only evaluated the biological system itself, but also identified outside sources that may influence the success of a conservation initiative. The ecosystem approach that incorporated landscape ecology with conservation biology, better equipped scientists to analyze habitat factors that contribute to a successful project (such as reintroduction), as well as evaluate the underlying processing that sustain species within a system (Minta and Kareiva, 1994). Habitat suitability studies have emerged as a prerequisite to any reintroduction effort in order to minimize risks of failure (Griffith et al., 1989). Knowledge of the system of concern allows conservation biologists and other interest groups to make educated decisions regarding favorable locations for a species, size of habitat needed, resources availability, possible predators as well as exotic species within the reintroduction area. Habitat suitability studies also determine whether any alterations

are required to the landscape in order to support a viable population of a reintroduced species. Supplemental water sources may be required if natural water sources are unavailable due to proximity to human activities, over-exploitation or contamination. Another factor that can be determined through a comprehensive system evaluation is whether the habitat is large enough to sustain a viable, self-sustaining population or whether migration corridors are required to connect small sub-populations and allow gene flow, prevent inbreeding and accumulation of deleterious genetic effects that may threat population persistence (Allendorf and Leary, 1986; Frankham, 1995) and may eventually lead to local extinction (Caro, 1998). Habitat evaluation also includes any additional influences such as private land owners bordering the reintroduction area as well as hunters and other interest groups that may support or inhibit such a project.

In chapter II, I used GIS modeling and landscape analysis to evaluate whether Guadalupe Mountains National Park (GUMO) includes suitable habitat for the reintroduction of desert bighorn sheep. Despite the fact that GUMO has once sustained a population of bighorn sheep, human settlement has altered the landscape and introduced factors that may or may not prevent such reintroduction. Based on identified parameters required for bighorn sheep, I concluded that GUMO has adequate habitat to sustain a population of bighorn sheep although some consideration to added artificial water sources, clearing migration corridors and evaluating the impact of the exotic species of aoudads in the park must be undertaken. Bighorn sheep reintroduction has so far proved successful in the region, as Texas Parks and Wildlife Department continuously release, monitor and augment bighorn sheep populations south of GUMO (Brewer, 2005). These populations

and subpopulations will provide a source of gene flow to a reintroduced population of bighorn sheep in GUMO and increase probability of a successful reintroduction to the park.

Successful conservation projects are often a result of a productive collaboration between many agencies and interests groups (Wondolleck et al., 1994). Hunters might be willing to invest in conservation efforts if the species of interest is a game species but stakeholders may try to either prevent policy that protects species that are considered harmful to agriculture, such as wolves (Kellert, 1987), brown bears (Mattson, 1990; Craighead et al., 1995) and mountain lions that may prey on livestock (Lambert et al., 2006), or oppose policy that contradict cultural, social or commercial interests (such as whales that are hunted for both cultural and commercial reasons (Kellert, 1991). Conservation biologists must incorporate knowledge of the socio-political trends within their area of interest in order to make educated decisions regarding a conservation of habitat or species. Many projects fail due to misunderstanding, underestimating or a total ignorance of the local community's attitude towards a particular species or conservation plan (Yaffee, 1994). To a great extent, conservation projects are funded and run by government agencies such as the Fish and Wildlife Service and the National Marine Fisheries Service. These government agencies may be under pressure from interest groups to be selective of the species they protect, which may leave some species without adequate protection while policy supporting commercial or sport harvesting is in effect (Wilson, 1980); this is the case of the mountain lion. For example, studies have indicated that despite a popular belief that mountain lion population is increasing in the Pacific

Northwest, research indicates that population densities and survival rates are low and population numbers are declining (Lambert et al., 2006). Mountain lions are only one species of large carnivores that suffers from growing human encroachment. Increase in carnivore-human interactions due to habitat loss causes a false sense that carnivore numbers are growing (Spencer et al., 2001; Dickson and Beier, 2002) and many local governments choose to react with increased and unregulated hunting practices without a reliable monitoring system to evaluate repercussions of such acts (Lambert et al. 2006). As I indicated in chapter III, it is possible that a high turnover rate of mountain lions inn Guadalupe Mountains National Park is an indication of high number of transient cats moving north from Texas and south from New Mexico. Population size, dynamics and the effect these cats have on a reintroduced population of bighorn sheep or livestock is currently unknown although policy in Texas classifies mountain lions as unprotected, non-game animal that can be killed freely (TPWD, 2005).

Any conservation project must be assessed continuously and projects such as reintroduction of a species must be evaluated post-release to determine whether criteria for success have been attained (Stanley Price, 1991). In chapter IV I used simulation to predict population dynamic of three reintroduced populations of Arabian oryx in the Israeli Negev. This simulation demonstrated the importance of migration corridors for the persistence of the species and will allow managers to make decisions regarding such movement corridors as the populations increase in size. Griffith et al. (1989) defined a successful reintroduction as the establishment of a self sustainable population but in order to evaluate such goal, a long period of time is required, and for many species exceeds the

life-span of a conservation project (Kleiman et al., 1991). One suggested practice has been to include an educational component to every conservation effort in order to try and solicit public support for conservation projects as it has been demonstrated that long-term success in conservation projects has been correlated to the local public and government support (Kleiman et al., 1991). Education will also allow conservation biologist to be aware of the local attitudes towards the habitat, the species and their interactions and as a result be able to communicate ideas and information that may influence the long-term success of a project (Clark and Reading, 1994).

In a world where expanding human population increases its encroachment on wildlife habitat, increases its demand for natural resources and where funds are scarce, new effective ways must be employed to halt and reverse biodiversity erosion (Mace, 2000). Conservation biologist must be more than scientists; they must interact, communicate, educate and influence diverse groups that may affect the success of a conservation project.

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APPENDIX A

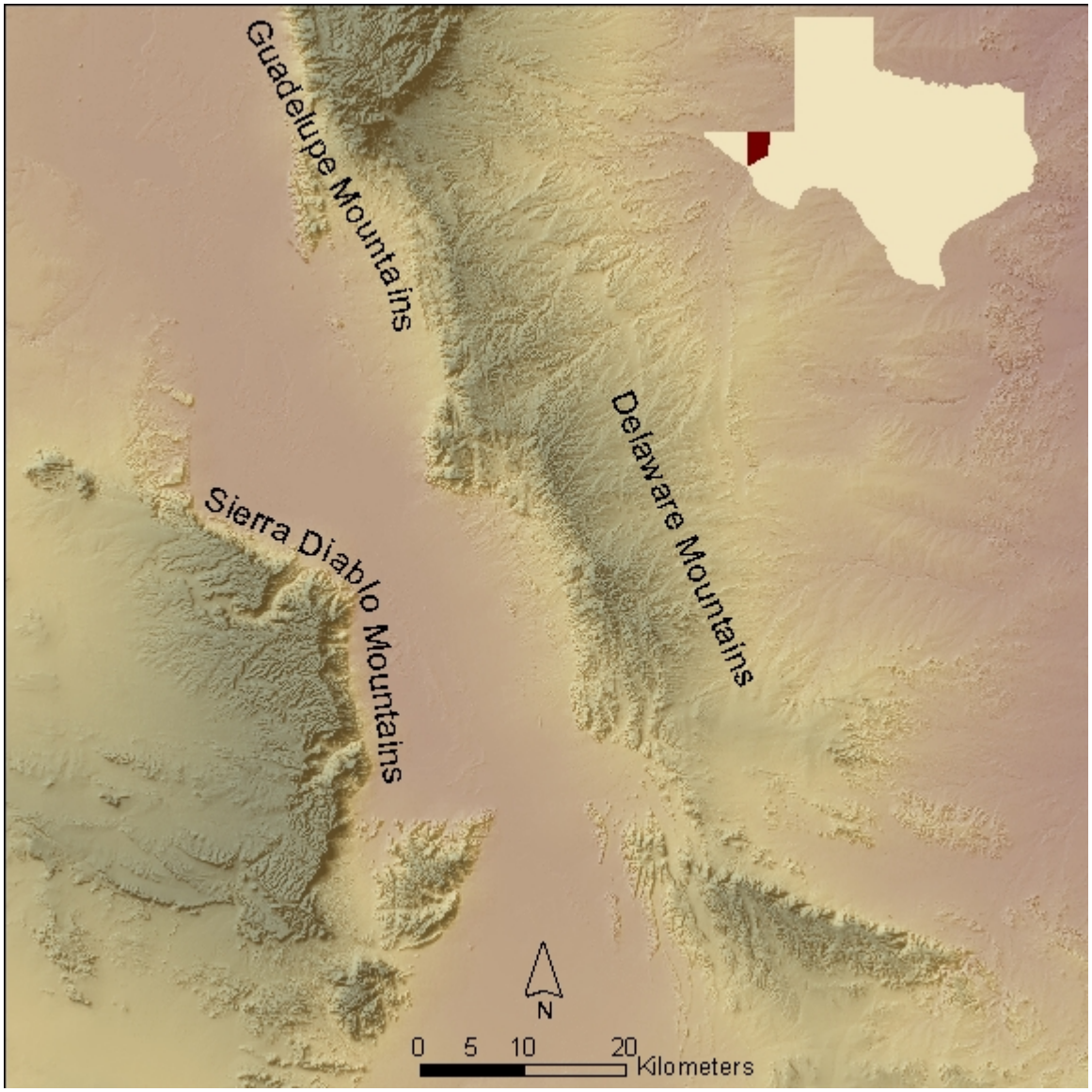


Figure 1: Study Area.

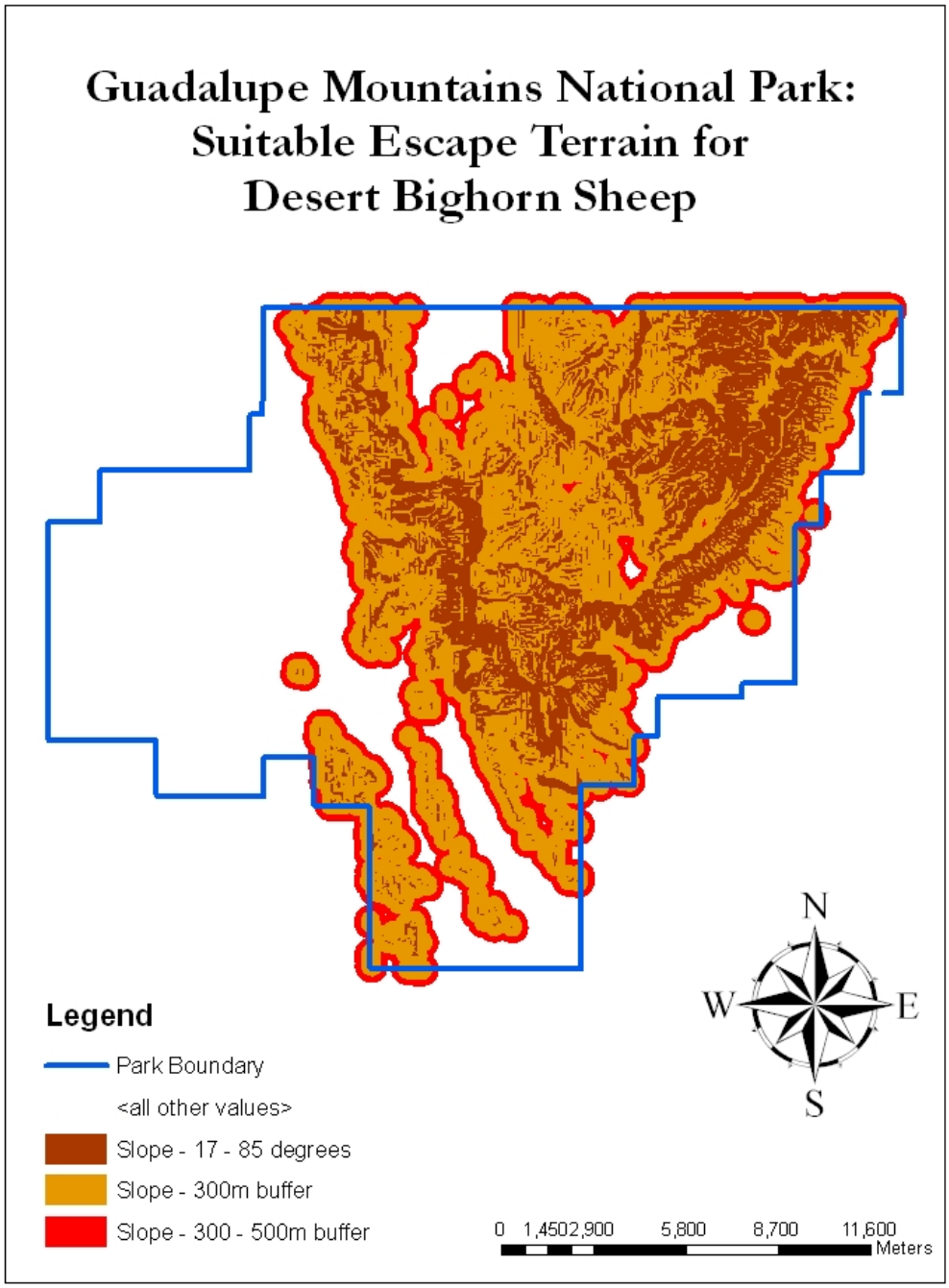
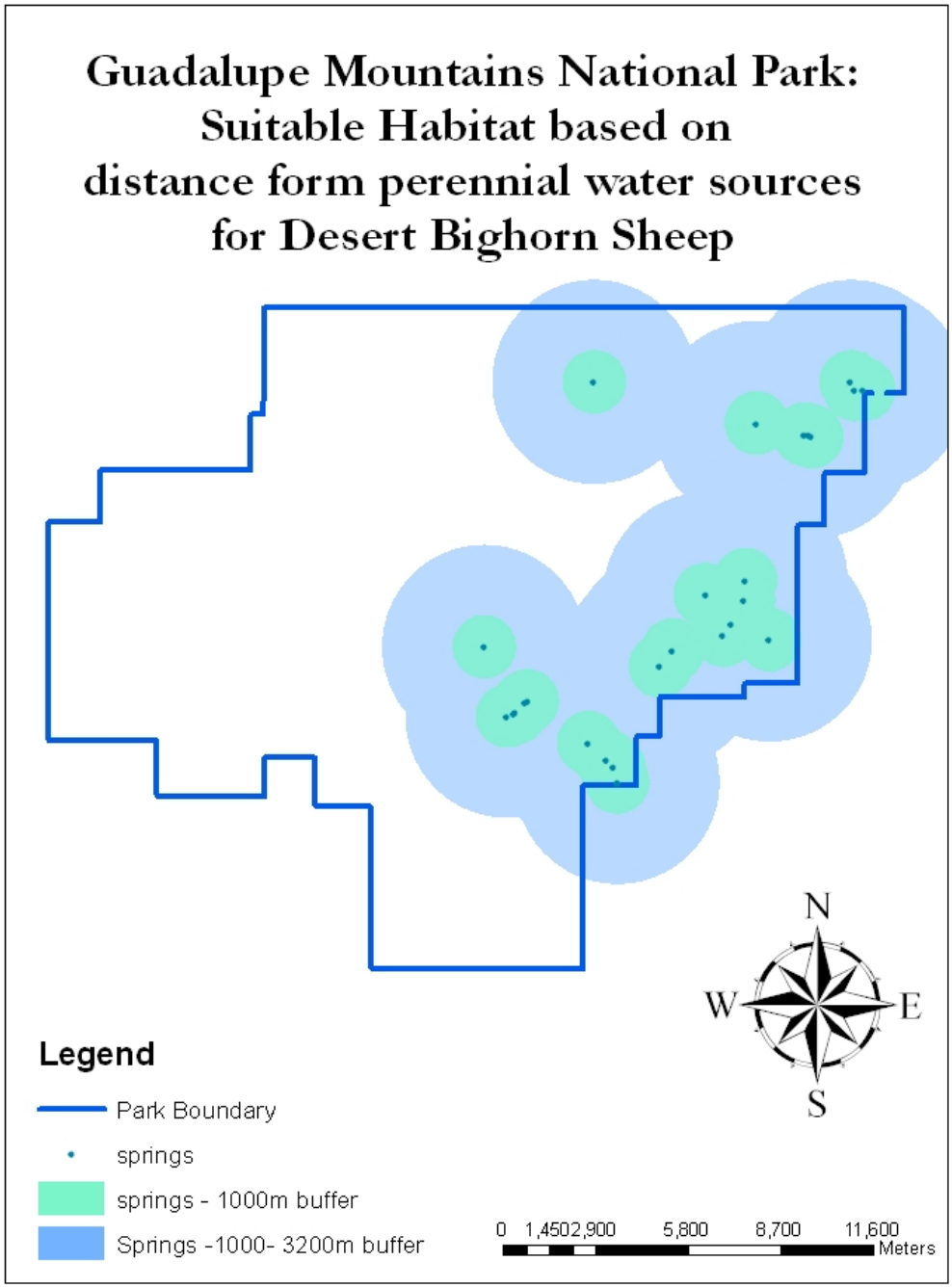


Figure 2: Habitat Suitability Maps for Guadalupe Mountains National Park.



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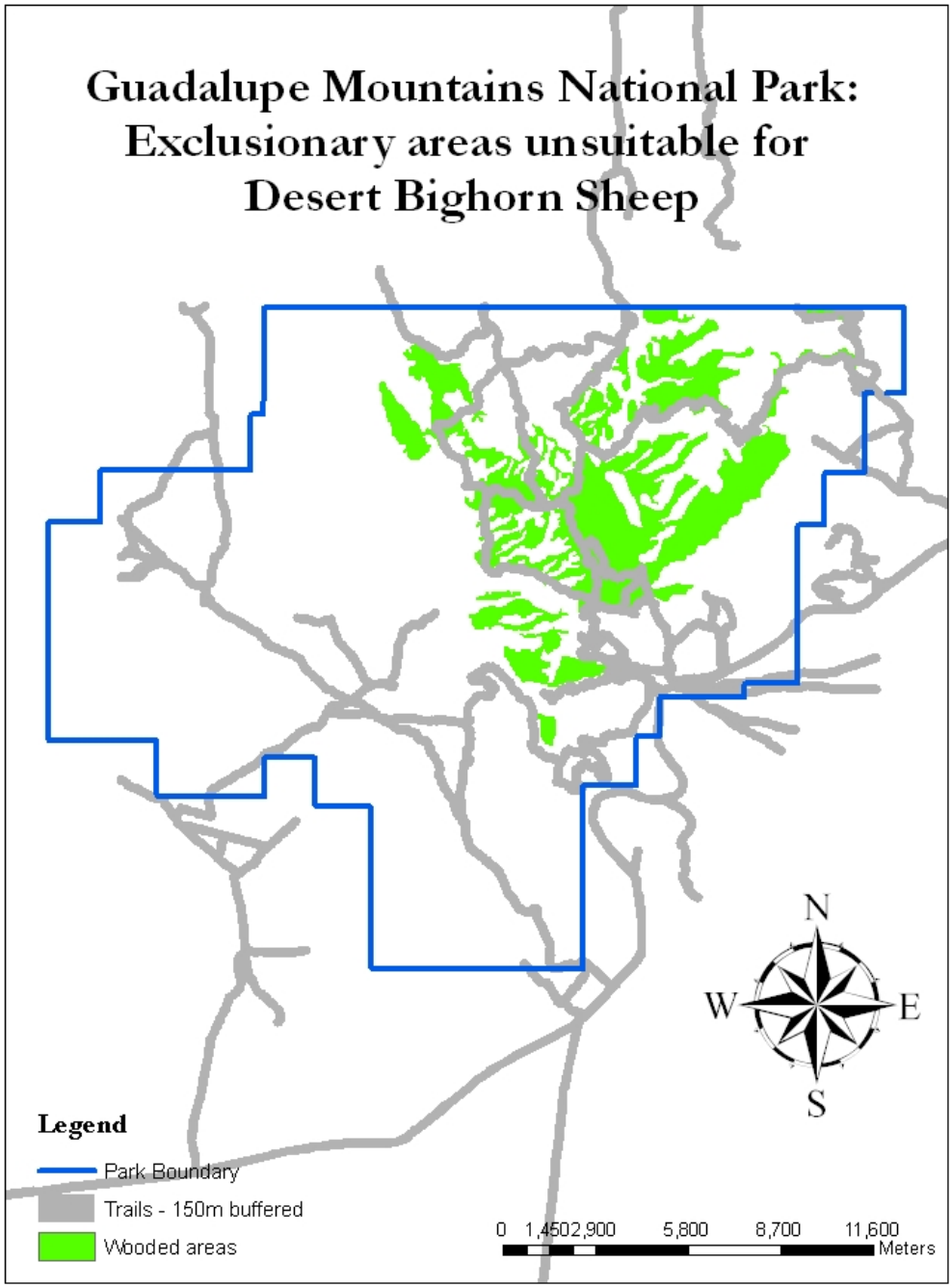

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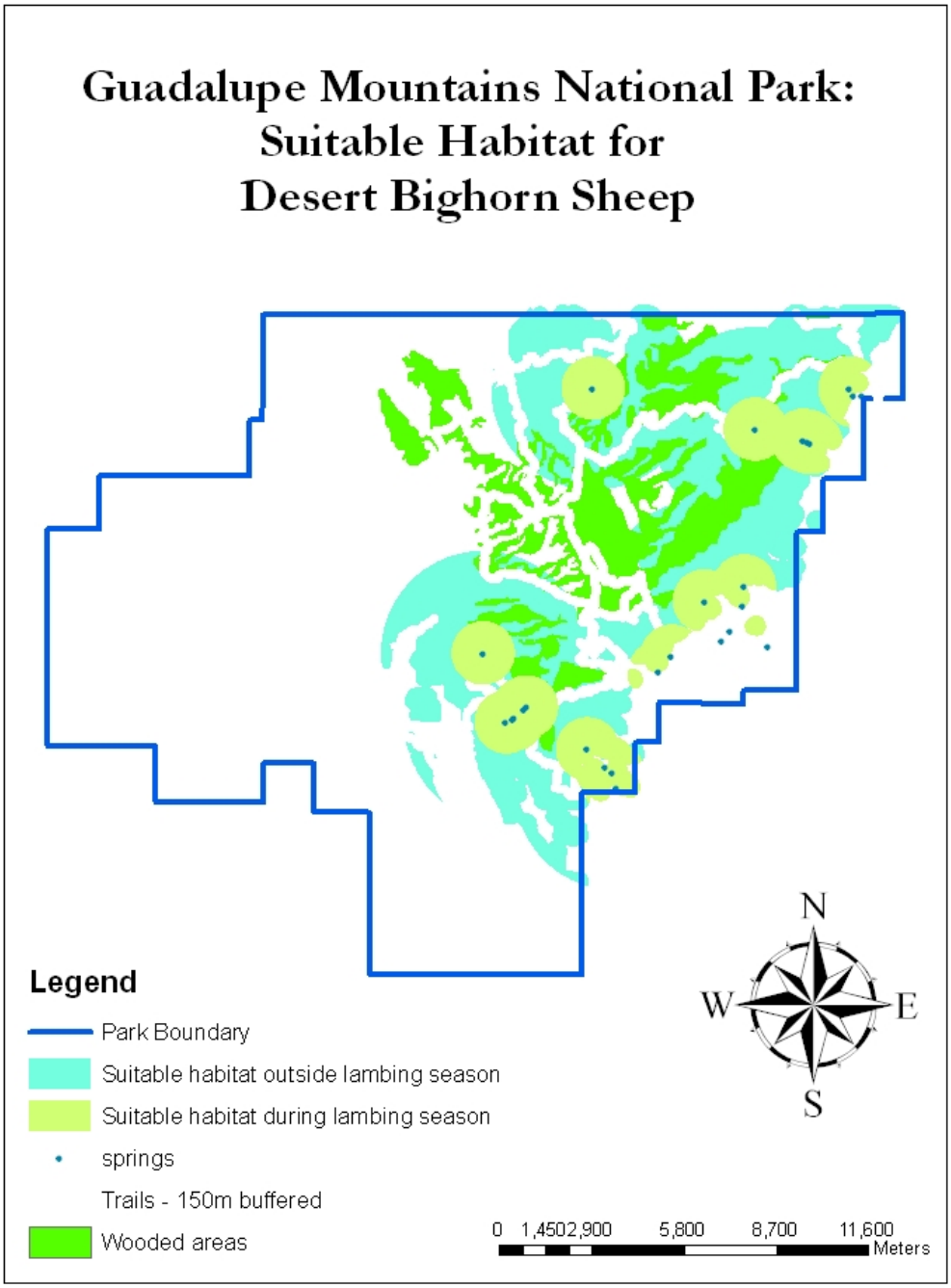

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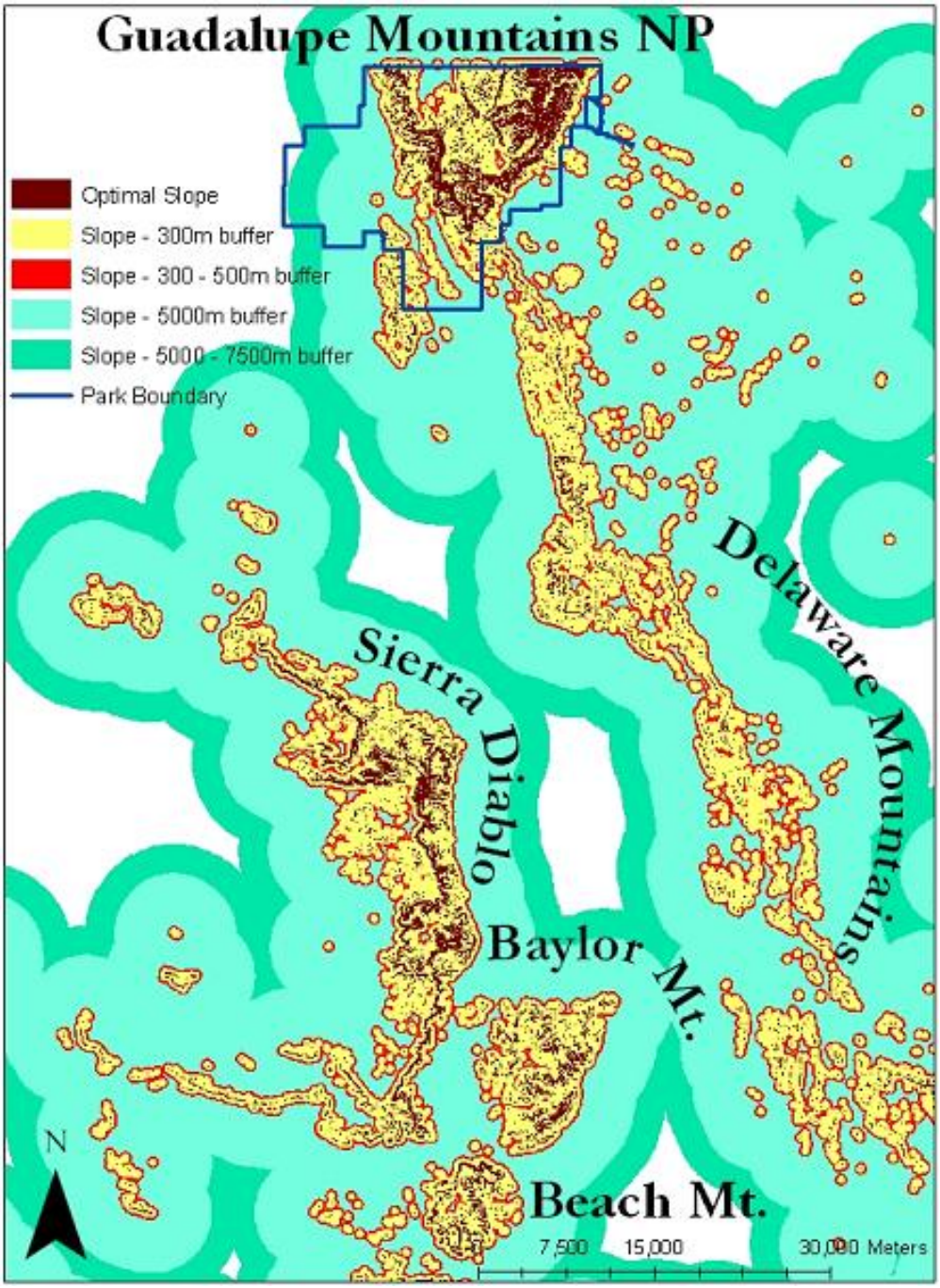


Figure 3: Migration Corridors.

Migration corridors are defined for a 10km and 15km migration distance.

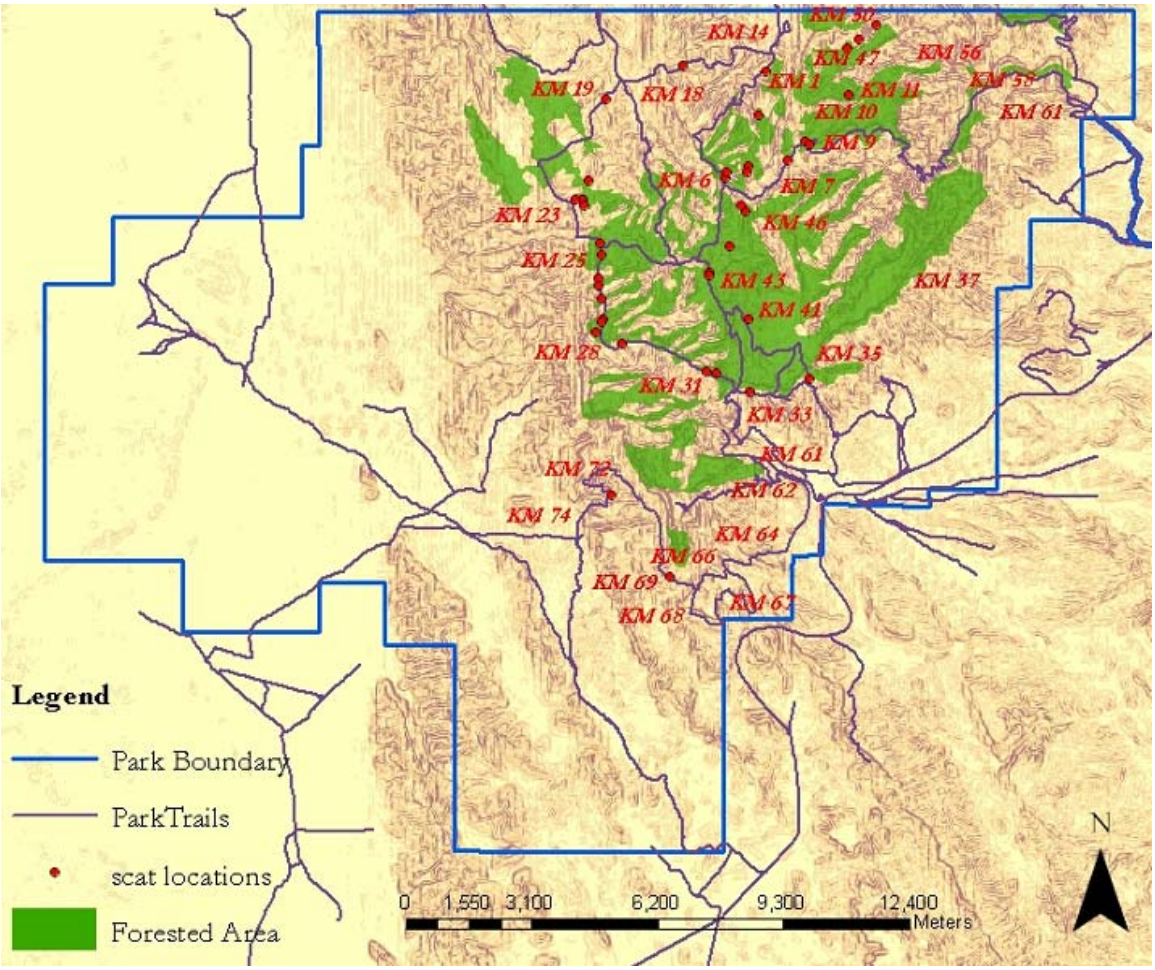


Figure 4: Scat Collection Locations in Guadalupe Mountains National Park.

Figure 5: Populations of Mountain Lions in Texas.

Guadalupe Mountains National Park (GUMO) mountain lion population location and the six different populations of mountain lions it was compared to. (Jan Janecka, Wildlife and Fisheries Department, TAMU, personal communication 2006). Original map: ESRI (2005).

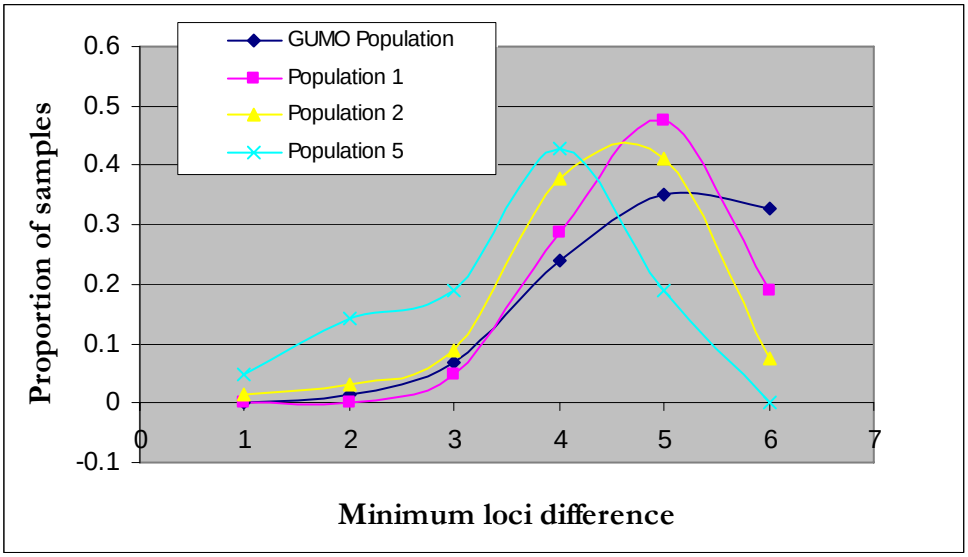


Figure 6: Minimum Loci Difference.

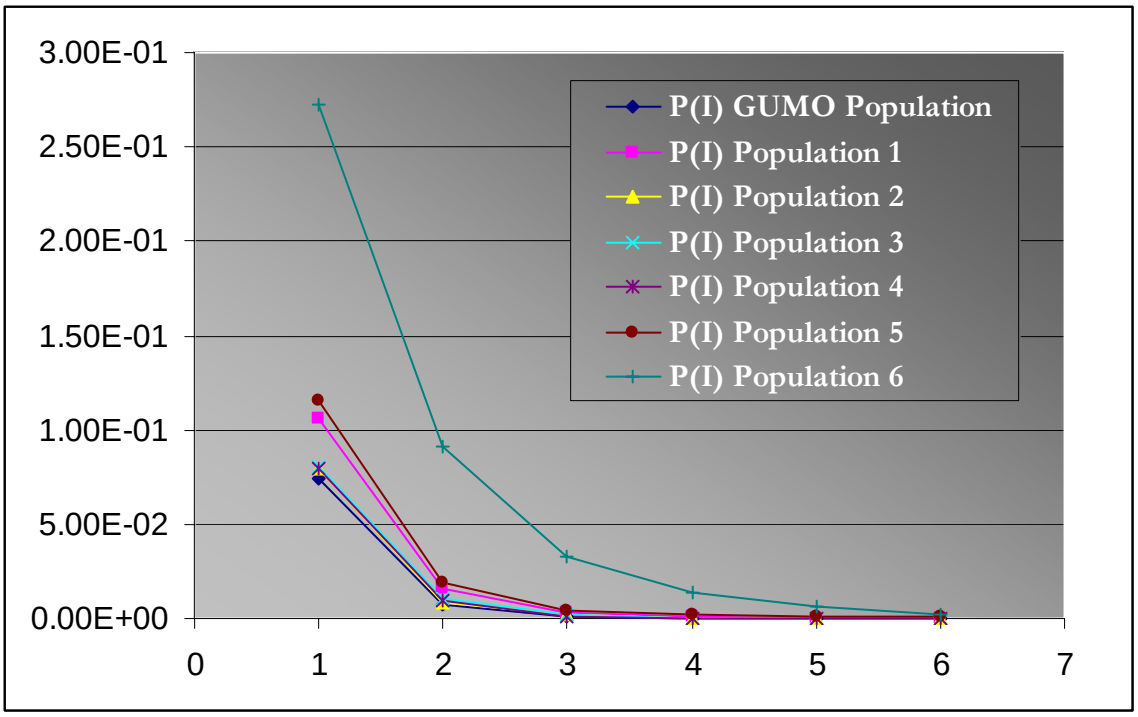


Figure 7: Probability of Identity P(I) Calculated for all Alleles in Each Mountain Lion Population in Texas.

The GUMO population shows high similarity to all 5 west Texas populations and a distinct separation form the south Texas population (Population 6).

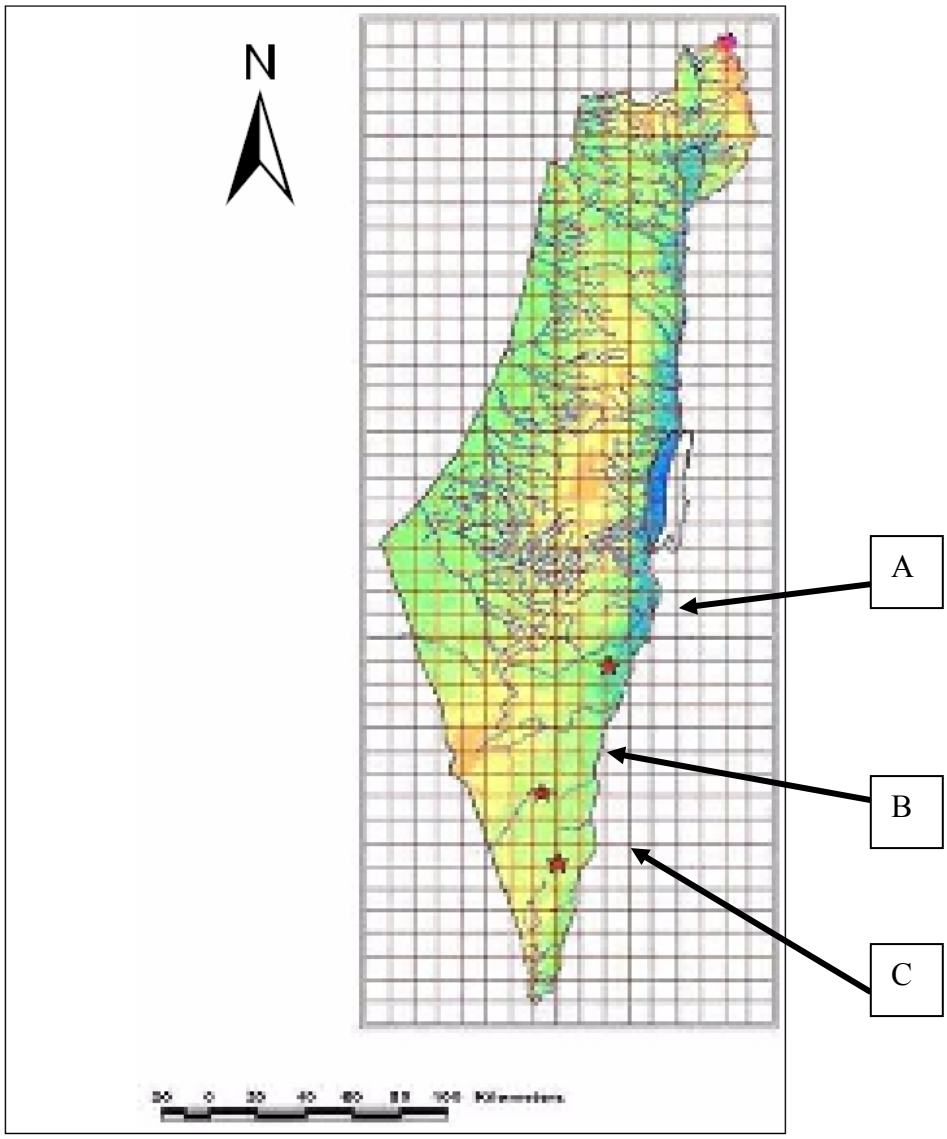


Figure 8: Reintroduction Sites of Arabian Oryx in Israel.

The map indicates the three sites at which Arabian oryx (*Oryx leucoryx*) have been reintroduced into the Israeli Negev; Shahak Spring in the Northern Arava Valley (A), Har Ha-Negev (B), and Nachal Ketzev (C). (Map provided by David Saltz, Mitrani Center for Desert Ecology, Israel, personal communication 2004)

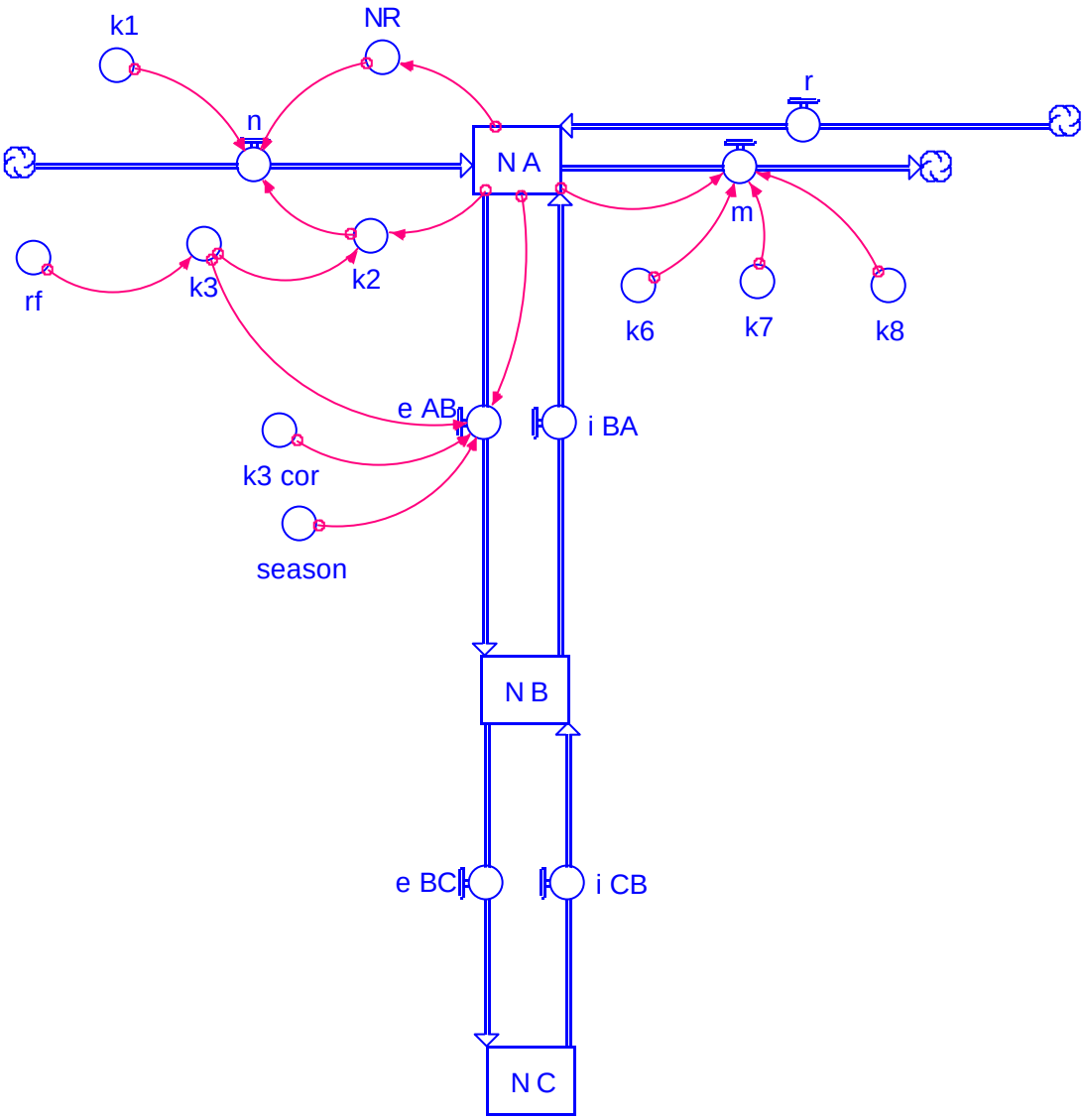
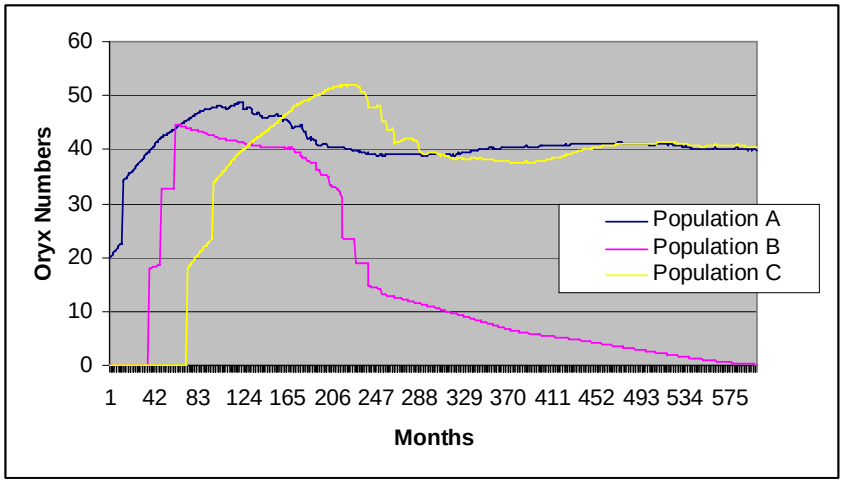


Figure 9: Conceptual Model of Arabian Oryx Metapopulation Dynamics.

Components are defined in the text.

A. No Migration, No Natality Adjustment



B. No Migration, Natality Increased

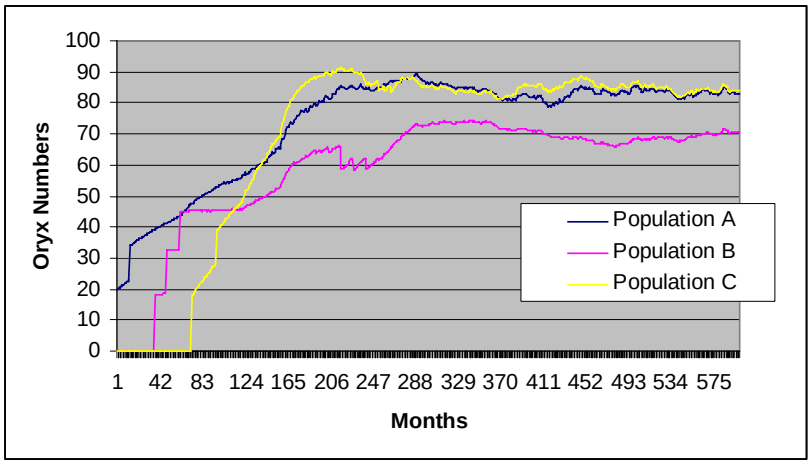
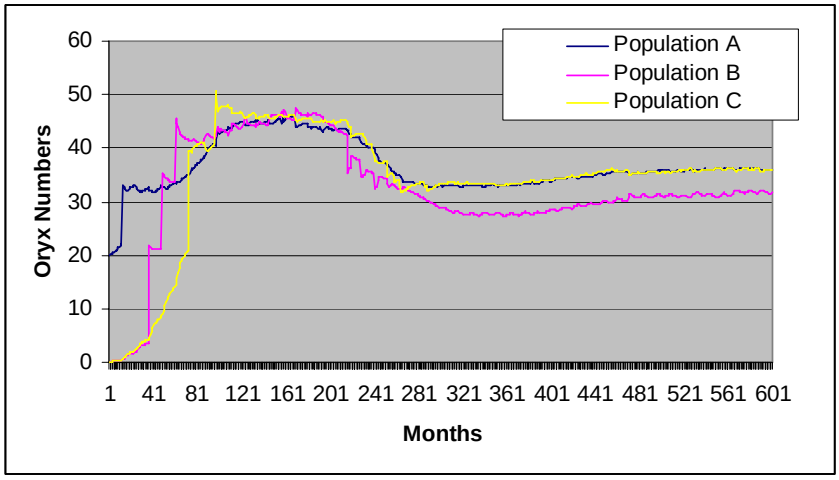


Figure 10: Simulations of Metapopulation Dynamics of Arabian Oryx under Different Scenarios.

Mean (n = 10) simulated sizes of the Arabian oryx (*Oryx leucoryx*) populations in the Israeli Negev during the 50 years (600 months) after reintroduction in 1997 under each of six possible scenarios. Scenarios represent all combinations of three assumptions regarding migration: (1) no migration, (2) migration among all three sites, and (3) migration between sites A and C only; and two assumptions regarding natality rates: (1) no adjustment to natality after reintroduction and (2) increased natality after reintroduction.

C. Migration among All Sites, No Natality Adjustment



D. Migration among All Sites, Natality Increased

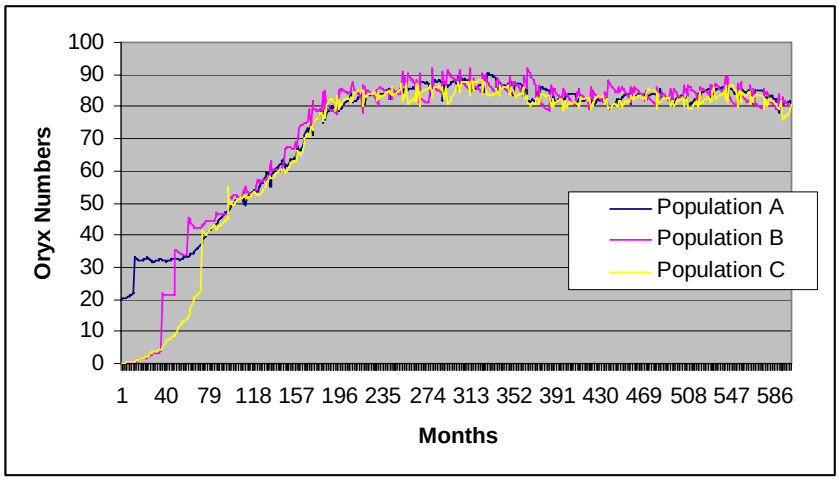
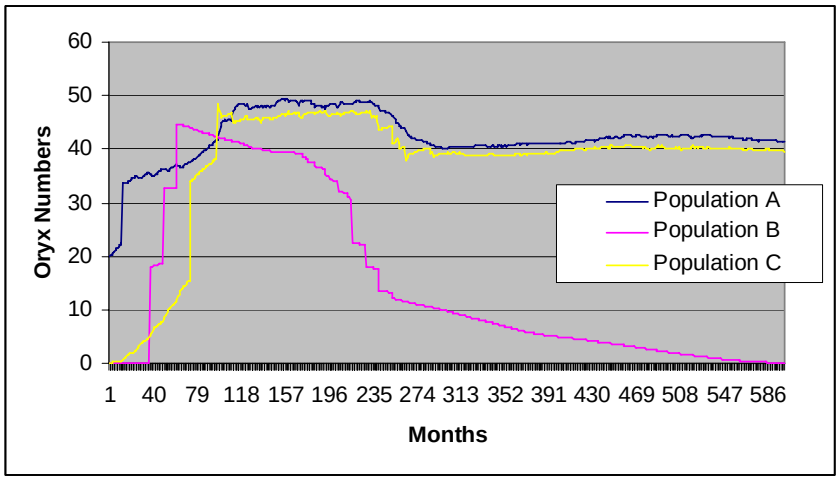


Figure 10: Continued.

E. Migration between Sites A and C only, No Natality Adjustment.



F. Migration between Sites A and C only, Natality Increase.

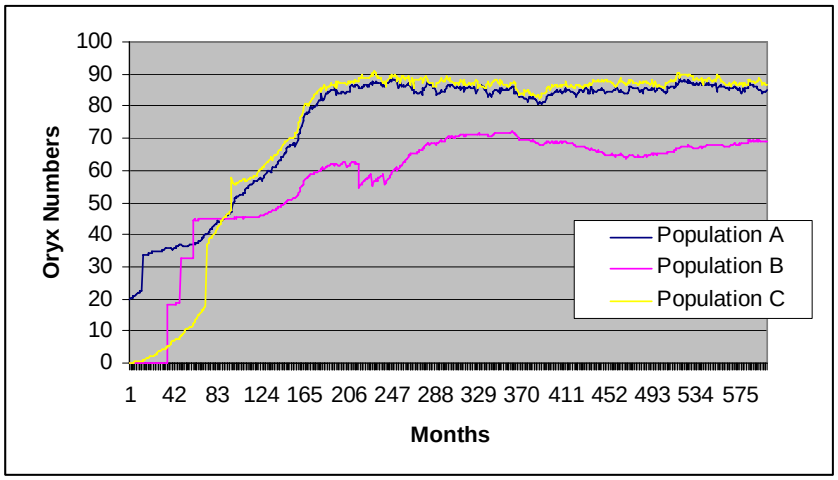


Figure 10: Continued.

APPENDIX B

Table 1:Habitat Suitability Model for Desert Bighorn Sheep in Guadalupe Mountains National Park.

<table>
<tr><th>Woodland and disturbance</th><th>Escape terrain</th><th>Proximity to perennial water</th><th>Habitat suitability</th></tr>
<tr><td rowspan="2">Non-wooded areas

AND

>150 m from roads or trails</td><td>27°-85° slopes plus 300 m buffer

OR

300m-500m from 27°-85° slopes if connected to two suitable escape terrains</td><td>≤1000 m of perennial water during lambing season (females and young)

OR

≤3200 m from perennial water for non-lambing season</td><td>Suitable</td></tr>
<tr><td colspan="2">>300 m (or 500 m, see above) from 27°-85° slopes

OR

>1000 m in lambing season and >3200 m in non-lambing season from perennial water</td><td rowspan="2">Unsuitable</td></tr>
<tr><td colspan="3">Wooded OR <=150 m of roads or trails</td></tr>
</table>

Table 2: Areas (Hectares) of Suitable Habitat for Desert Bighorn Sheep.

Areas are described for Guadalupe Mountains National Park and follow exclusionary criteria.

Criteria	*Area*	*Area Less Wooded Areas*	*Area less woodland areas and buffered trails*
Optimal slopes (27° - 85°)	7,273.41	7,134.02	5,614.92
Optimal slopes with 300m buffer	20,736.36	15,884.03	13,200
Optimal slopes with 300m buffer within 1000m Water	5985.59	5431.75	4,782.39
Optimal slopes with 300m buffer, within 3200m Water	12,968.66	9817.47	7,991.34

Table 3: Landscape Pattern Comparison.

Landscape patterns are compared between Guadalupe Mountains National Park (GUMO) and Sierra Diablo Mountain (SD).

Landscape metric	GUMO		SD		% difference	
	Optimal Slopes (27 - 85°)	Optimal slopes plus 300m buffer	Optimal Slopes (27 - 85°)	Optimal slopes plus 300m buffer	Optimal Slopes (27 - 85°)	Optimal slopes plus 300m buffer
Total Land Area (ha)	7,273	20,736	6,997	32,572	3.8% larger	36.37% smaller
Number of patches (NumP)	1,228	1	2,258	1	45.6% less patchy	Equal
Patch Density (NumP/ha)	0.16	N/A	0.32	N/A	50% less dense	N/A
Mean patch size (ha)	5.92	20,736	3.10	32,572	47.6% larger patches	36.37% smaller
Mean nearest neighbor distance (m)	67.86	N/A	77.95	N/A	12.94% smaller	N/A
Edge density (m/ha)	0.018	0.00087	0.023	0.00146	22% lower	40.41% lower
Mean shape index	1.48	3.521	1.46	7.429	1.35% more complex	52.6% less complex

Table 4: Scat Collected by Year and Location.

Refer to Appendix A, Fig. 4.

Year	*Sample ID*	*Transect Name*	*Location Collected*	*Year*	*Sample ID*	*Transect Name*	*Location Collected*
1997	16	Middle McKittrick	KM 49	2002	24	Dog Canyon	KM 4
	26	Upper S. McKittrick	KM 43		27	Dog Canyon	KM 4
	37	Middle McKittrick	KM 51		30	Bush Mt.	KM 25.5
	53	Upper S. McKittrick	KM 44		31	Middle McKittrick	KM 48
	90	Upper S. McKittrick	KM 46		33	Frijole Ridge	KM 35.3
1998	1	Upper S. McKittrick	KM 45		35	Cox	KM 21.8
	22	Middle McKittrick	KM 50-51		36	Dog Canyon	KM 4
	51	Middle McKittrick	KM 49-50		42	Upper S. McKittrick	KM 46
	72	Dog Canyon	KM 10		44	Cox	KM 23.4
1999	28	Middle McKittrick	KM 49		49	Upper S. McKittrick	KM 43
	29	Dog Canyon	KM 3		50	Dog Canyon	KM 9
	34	Dog Canyon	KM 11		52	Frijole Ridge	KM 32
	38	Frijole Ridge	KM 32		56	Frijole Ridge	KM 33.6
	40	Dog Canyon	KM 11		57	Bush Mt.	KM 26.8
	41	W. Dog Canyon	KM 19		59	Dog Canyon	KM 8
	45	Bush Mt.	KM 25		64	Upper S. McKittrick	KM 38.3
	46	Dog Canyon	KM 11		66	Dog Canyon	KM 10
	55	Dog Canyon	KM 5		67	Dog Canyon	KM 49
	70	Dog Canyon	KM 5		68	Dog Canyon	KM 6
2000	8	Cox	KM 21		84	Dog Canyon	KM 11
	12	Cox	KM 22.6		85	Frijole Ridge	KM 31
	14	Upper S. McKittrick	KM 41		87	Upper S. McKittrick	KM 39.5
	20	Dog Canyon	KM 8		91	Middle McKittrick	KM 47
	25	Dog Canyon	KM 1		96	Dog Canyon	KM 7
	39	Dog Canyon	KM 9		98	Dog Canyon	KM 6
	48	Dog Canyon	KM 12	2003	43	Upper S. McKittrick	KM 42.5
	58	Bush Mt.	KM 26		60	Dog Canyon	KM 2.5
	63	Dog Canyon	KM 9		61	Upper S. McKittrick	KM 39
2001	2	Frijole Ridge	KM 33		62	Frijole Ridge	KM 31
	4	Frijole Ridge	KM 31		71	Cox	KM 23.7
	18	Frijole Ridge	KM 35		73	Upper S. McKittrick	KM 38
	32	Middle McKittrick	KM 49		74	W. Dog Canyon	KM 16.8
	47	Frijole Ridge	KM 32		75	Dog Canyon	KM 10
	54	Dog Canyon	KM 10		81		Frijole Ranch
	69	Dog Canyon	KM 9		82	Frijole Ridge	KM 32
	88	Middle McKittrick	KM 49		89	Frijole Ridge	KM 33
2002	3	Bush Mt.	KM 26.8		92	Dog Canyon	KM 9
	5	W. Dog Canyon	KM 17.5		93	Bush Mt.	KM 26.9
	6	Bush Mt.	KM 27.1		95	El Capitan	KM 69.2
	7	Bush Mt.	KM 25.1	2004	65	El Capitan	KM 69.2

Table 4: Continued.

Year	*Sample ID*	*Transect Name*	*Location Collected*	*Year*	*Sample ID*	*Transect Name*	*Location Collected*
2002	9	Bush Mt.	KM 25.5		76	El Capitan	KM 69.4
	10	Bush Mt.	KM 28.5		77	W. Dog Canyon	KM 17
	11	Cox	KM 22.6		78	Bush Mt.	KM 25
	13	Dog Canyon	KM 12		79	Bush Mt.	KM 26
	15	Bush Mt.	KM 30.8		80	Dog Canyon	KM 5.8
	17	Bush Mt.	KM 24.5		83	Bush Mt.	KM 26
	19	Bush Mt.	KM 25.5		86	Shumard Canyon	KM 72.8
	21	Bush Mt.	KM 22.6		94	Bush Mt.	KM 28.5
	23	Dog Canyon	KM 11		97	Bush Mt.	KM 27

Table 5: List of Samples That Successfully Genotyped for the Presence of Six Loci.

Loci designated with x genotyped after a single PCR reaction; loci designated with an R had to be treated with PreCR-A DNA Repair Mix before positively genotyped; loci designated with failed to amplify after being treated by PreCR-A DNA Repair Mix. Samples 11, 15, 58, 74 and 94 tested negative for mtDNA before repair.

Tube number	*Sample ID*	*FCA_23*	*FCA_26*	*FCA_35*	*FCA_43*	*FCA_82*	*FCA_96*
1	4	x	x	x	x	x	x
2	6	R	x	x	x	x	x
3	7	x	x	x	x	x	x
4	11	R	R	R	R	R	R
5	12	x	x	R	x	x	x
6	13	x	x	x	x	x	x
7	14	x	x	x	x	x	x
8	15	R	R	R	R	R	R
9	17	x	x	R	x	x	x
10	19	x	x	x	x	x	x
11	20	0	x	x	x	x	x
12	21	R	x	x	x	x	x
13	22	x	x	x	x	x	x
14	25	x	x	x	x	x	x
15	26	R	x	x	x	x	x
16	29	x	x	x	x	x	x
17	35	R	x	x	x	x	x
18	39	x	x	x	x	x	x
19	45	x	x	x	x	x	x
20	49	x	x	x	x	x	x
21	50	x	x	x	x	x	x
22	53	x	x	R	x	R	x
23	58	R	R	R	R	R	0
24	60	x	x	x	x	x	x
25	64	R	x	x	x	R	x
26	65	x	x	x	x	x	x
27	68	x	x	x	x	R	R
28	70	x	x	R	x	R	R
29	74	R	R	R	R	R	R
30	85	x	x	x	x	x	x
31	94	R	R	R	R	R	R
32	98	x	x	x	x	x	x

Table 6: Genotypic Variations Calculated for Six Microsatellites.

Genotypic variations calculated for six microsatellites among 32 unique genotypes of mountain lions extracted from scat collected at Guadalupe Mountains National Park. Locus name, size (in nucleotides), number of alleles, number of effective alleles, expected heterozygosity, observed heterozygosity, Expected and observed heterozygosity after including 7 additional samples collected outside park boundary (Jan Janecka, Wildlife and Fisheries Department, TAMU, personal communication 2006), Chi-square for Hardy-Weinberg equilibrium, inbreeding coefficient.

Locus	*Size*	N_a	*Ne*	H_e	H_o	H_e *After Pooling*	H_o *After Pooling*	*P*	P (Pop. 1)	F_{is}
FCA 23	132-144	5	3.230	0.690	0.742	0.720	0.684	0.578	0.415	-0.075
FCA 26	118-134	7	2.098	0.523	0.469	0.497	0.410	0.000[a]	0.070	0.104
FCA 35	120-150	6	2.456	0.593	0.563	0.692	0.564	0.784	0.772	0.051
FCA 43	112-120	7	4.047	0.753	0.875	0.770	0.846	0.243	0.814	-0.162
FCA 82	233-247	5	3.230	0.690	0.813	0.694	0.821	0.450	0.765	-0.177
FCA 96	177-203	9	4.654	0.785	0.742	0.822	0.632	0.001[b]	0.562	0.178
Population		6.5	3.286	0.673	0.684	0.699	0.660	0.343	0.566	-0.014

[a] $P<0.001$, [b] $P<0.01$

Table 7: Individual Assignment.

Individual assignment was performed on each of the Guadalupe Mountains National park mountain lions to each of the six mountain lions populations in Texas.

Assigned sample	*Probability Population 1*	*Probability Population 2*	*Probability Population 3*	*Probability Population 4*	*Probability Population 5*	*Probability Population 6*
13	**0.007**	*0.000*	*0.000*	***0.001***	*0.000*	*0.000*
19	**0.003**	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*
20	**0.048**	*0.000*	***0.001***	*0.000*	***0.004***	*0.000*
22	**0.007**	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*
29	**0.007**	*0.000*	*0.000*	***0.001***	*0.000*	*0.000*
35	**0.005**	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*
39	**0.011**	*0.000*	*0.000*	*0.002*	*0.000*	*0.000*
45	**0.012**	*0.000*	*0.000*	*0.001*	*0.000*	*0.000*
64	**0.002**	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*
68	***0.005***	***0.001***	***0.010***	**0.013**	*0.000*	*0.000*
83	***0.024***	***0.016***	***0.002***	**0.048**	***0.004***	*0.000*
74	**0.005**	*0.000*	*0.000*	*0.000*	*0.000*	*0.000*

Table 8: Pairwise Population F_{ST} (via Frequency) Values.

Pop1	Pop2	Pop3	Pop4	Pop5	Pop6	GUMO	
0.000							Pop1
0.044	0.000						Pop2
0.044	0.027	0.000					Pop3
0.031	0.014	0.013	0.000				Pop4
0.080	0.045	0.029	0.040	0.000			Pop5
0.105	0.086	0.083	0.083	0.167	0.000		Pop6
0.103	0.135	0.120	0.121	0.168	0.199	0.000	GUMO

Table 9: Parameter Values for Metapopulation Dynamics Simulations.

Parameter values used to simulate reintroductions of Arabian oryx (*Oryx leucoryx*) in Oman and in each of the three sites in Israel (Appendix A, Fig. 8), including (a) natality rates ($k1_j$, females born per female per month) as a function of months (j) since reintroduction, and (b) age-specific mortality rates ($k6_i$, $k7_i$, and $k8_i$, proportions of individuals aged i that die per year due to natural causes, due to hunting, and due to military activities, respectively). Data for Oman are from Stanley Price (1989) and Tear et al. (1997), and data for Israel are from David Saltz, (Mitrani Center for Desert Ecology, Israel, personal communication 2004); see text for details.

A. Natality rates[1]

Months since reintroduction (j)	$k1_j$ (Oman)	$k1_j$ (Israel- Sites A and C)	$k1_j$ - adjusted (Israel- Sites A and C)	$k1_j$ (Israel- Site B)	$k1_j$ - adjusted (Israel- Site B)
0 - 60	0.059	0.071	0.071	0.021	0.021
61 - 120	0.1012	0.071	0.1218	0.021	0.036
121 - 144	0.185	0.071	0.223	0.021	0.066
145 - 156	0.21	0.071	0.253	0.021	0.075
>156	0.5	0.071	0.602	0.021	0.178

1. Age at sexual maturity is 24 months

B. Mortality rates

Age in months (i)	$k6_i$ (Oman)	$k6_i$ – Sites A & C (Israel)	$k6_i$ – Sites B (Israel)	$k7_i$ All sites (Israel)	$k8_i$ Sites A and C (Israel)	$k8_i$ Site B (Israel)
0 - 1	0.1883	0.1478	0.08637	For i >=7 ran(a, b)[3]	0.00275	0.001875
2 - 6	0.024	0.0188	0.011007		0.00275	0.001875
7 - 36	0.0715	0.056	0.03279		0.00275	0.001875
37 - 120	0.119	0.0934	0.05457		0.00275	0.001875
120 – 204[2]	0.0240	0.0188	0.011007		0.00275	0.001875

2. Longevity is 17 years (204 months)
3. ran(a, b) is a uniform random variate on the interval a to b

Table 10: Simulated and Observed Arabian Oryx Population in Oman.

Mean (±1SD, n = 10) simulated and observed sizes of Arabian oryx (*Oryx leucoryx*) populations the indicated number of months after initial reintroduction in Oman. Ten, 10, 11, 11, and 8 animals were introduced 1982, 1984, 1988, and 1989, respectively (Stanley Price 1989).

Months After Initial Reintroduction in 1982	Observed Population Size	Mean (±1SD) Simulated Population Size	Difference (Simulated / Observed)
60	31	35 (0.06)	1.13
96	100	91 (0.65)	0.91
120	134	128 (1.60)	0.96
132	181	173 (4.05)	0.96
144	263	213 (3.40)	0.81
156	284	259 (5.76)	0.91
168	400	363 (17.32)	0.91

Table 11: Simulated Meta/population(s) Sizes of Arabian Oryx in Israel.

Mean (±1SD, n = 10) simulated sizes (number of individuals) of the Arabian oryx (*Oryx leucoryx*) populations in the Israeli Negev 50 years (600 months) after reintroduction in 1997 under each of six possible scenarios. Scenarios represent all combinations of three assumptions regarding migration: (1) no migration, (2) migration among all three sites, and (3) migration between sites A and C only; and two assumptions regarding natality rates: (1) no adjustment to natality after reintroduction and (2) increased natality after reintroduction.

Scenarios		*No Natality Adjustment*	*Natality Increased after Reintroduction*
	Site	Population Size	Population Size
No Migration	A	40(1.79)	83 (4.09)
	B	0[4]	71 (2.44)
	C	40 (1.69)	84 (3.24)
Migration among all sites	A	36 (1.55)	80 (7.63)
	B	32 (2.46)	80 (6.78)
	C	36 (1.84)	81 (8.36)
	Meta pop.	104 (4.90)[1]	241 (15.85)[2]
Migration between sites A and C only	A	41 (1.18)	85 (4.17)
	B	0[5]	69 (2.92)
	C	40 (1.27)	87 (3.21)
	Meta pop.	81 (2.27)	172 (9.50)[3]

1. Time to reach viable population size (100 individuals, Saltz, 1998) was 442.2 (±46.11) months
2. Time to reach viable population size was 68.5 (±1.08) months
3. Time to reach viable population size was 68.8 (±2.04) months
4. Time to extinction was 555.2 (±18.58) months
5. Time to extinction was 537.8 (±20.06) months

VITA

Name: Oranit Gilad

Address: Department of Biology, Texas A&M University, 3258 TAMU,
College Station, TX 77843-3258, College Station, TX 77843

E-Mail Address: ogilad@tamu.edu

Education: B.S., Biology, University of Houston, 1998
Graduate work, Marine Biology, University of Haifa Israel, 2001
Ph.D., Texas A&M University, 2006

Research and professional experience:

Establishing a privately owned reserve at Finca Alto San Juan, Costa Rica. (2003 –).

Habitat suitability study for the reintroduction of desert bighorn sheep (*Ovis canadensis*) to Guadalupe Mountains National Park. (2004 - 2006).

Kin discrimination in Giant Pandas (*Ailuropoda melanoleuca*). (2004-2005).

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