

Interactions between translocated and native queen conch *Strombus gigas*: evaluating a restoration strategy

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ABSTRACT: The proactive strategy for restoring Florida's depleted queen conch *Strombus gigas* population includes increasing the spawning stock by translocating reproductively deficient individuals into existing spawning aggregations where our previous research has shown that the translocated conch will develop normally. However, there may be unintended and potentially negative ecological ramifications if the translocated conch displace the native conch. To examine this issue, we translocated non-reproductive adult conch into 2 offshore spawning aggregations and used acoustic telemetry to track them relative to similarly tagged native conch. At one aggregation, the home-range sizes of native conch were significantly smaller than those of the translocated conch, which led to a significant reduction in the static interaction (i.e. home-range overlap) between the 2 groups of conch. However, the dynamic interaction (i.e. sociality coefficient) among the translocated conch was significantly higher. We hypothesize that these results were driven by reproduction: the translocations took place in July during the breeding season, and because the translocated conch were not yet in reproductive condition they moved into forage habitats, while the natives occupied the breeding habitats. At the other aggregation, there were no significant differences in the movements or interactions between native and translocated conch, a result probably due to the mosaic of habitats at this site, where breeding and forage areas are in close proximity. Our results indicate that displacement of natives did not occur at either site, and that translocating conch into spawning aggregations does not have adverse consequences relative to the interactions among conspecifics.

KEY WORDS: Queen conch · *Strombus gigas* · Restoration · Dynamic interaction · Static interaction · Translocation · Acoustic telemetry

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INTRODUCTION

Translocation of wild conspecifics between spatially discrete subpopulations can be used to restore a population whose numbers have been reduced by overharvest and/or habitat loss (Griffith et al. 1989). For example, translocations aimed at concentrating wild adults to increase reproductive output have previously been used in molluscan stock enhancement programs in an attempt to restore severely depleted populations of green abalone (Tegner 1992), hard clams (Arnold et al. 2002), and bay scallops (Peterson et al.

1996). However, concerns have been raised that some restoration efforts may have unintended negative consequences (Peterson et al. 1996, Caddy & Defeo 2003). For instance, the use of hatchery-reared fish for stock enhancement has recently come under fire because of potential negative ecological interactions (e.g. displacement of natives and loss of native genes) between hatchery and wild fish (see Weber & Fausch 2003 for a review). Nevertheless, applied studies addressing the efficacy of restoration efforts prior to implementation are rare (Caddy & Defeo 2003, Kellison et al. 2003).

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The queen conch *Strombus gigas* is a large marine gastropod whose populations support important fisheries in the Caribbean; however, the species has become so depleted that it is currently listed in the Convention on International Trade in Endangered Species of Wild Fauna and Flora (CITES) Appendix II. The queen conch once also supported commercial and recreational fisheries in south Florida. However, the ease of capture and the desirability of the shell and meat resulted in a severe depletion of the local population to the point that in 1985 a total harvest ban was instituted in state waters and in 1986 in federal waters. After the ban was established, less than 6000 adult conch remained in the Florida Keys (Glazer & Delgado 2003). Since then, ongoing surveys have shown a slow and very limited recovery with an estimated 25 500 adults in 2006 (Florida Fish and Wildlife Conservation Commission, FWC, unpubl. data).

Seeking a proactive restoration strategy, we settled on an approach that employs some unique characteristics of the Florida population. Queen conch that inhabit the nearshore waters of the Florida Keys are physiologically incapable of reproduction even when they have reached reproductively active sizes (Glazer & Quintero 1998, Delgado et al. 2004). In addition, these conch are isolated from offshore breeding aggregations by the poor conch habitat in Hawk Channel (Glazer & Berg 1994) (Fig. 1). However, conch translocated from nearshore habitats into offshore breeding aggregations become reproductively active within 6 mo (Delgado et al. 2004). Depensatory mechanisms have been hypothesized to be one of the main factors in the sluggish recovery of the conch population in the Keys. Intensive fishing may lead to depensation as densities are reduced, limiting the ability of conch to locate mates and increasing the chance of recruitment failure (Appeldoorn 1995). This seems to be the case in Florida, as the slow and incomplete recovery has been attributed to diminished recruitment due, in part, to small spawning aggregations (Stoner et al. 1997, Stoner & Ray-Culp 2000, Glazer & Delgado 2003). Therefore, based upon the readily available supply of nearshore conch and their ability to regain spawning capacity, we concluded that translocating conch into offshore breeding aggregations to enhance reproductive output could be an effective restoration strategy (Delgado et al. 2004).

An important first step in deciding whether to pursue a translocation strategy is to determine whether the

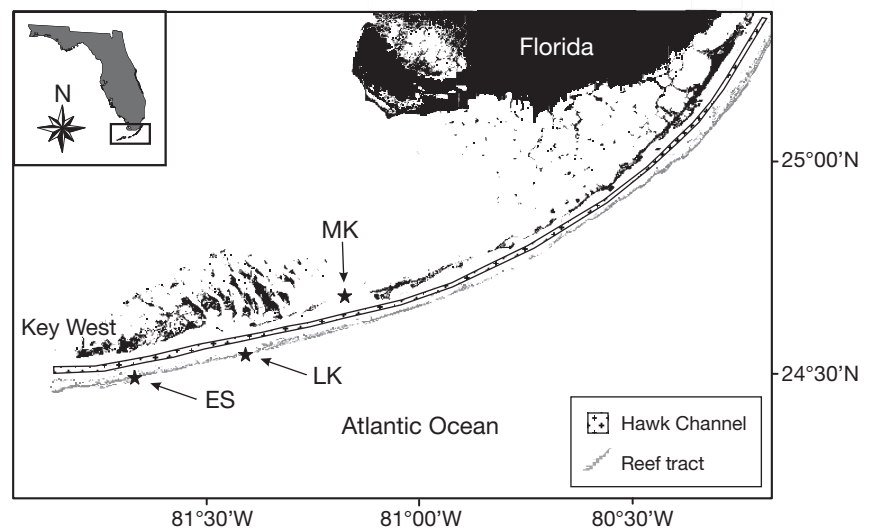


Fig. 1. Queen conch *Strombus gigas* translocation sites in the Florida Keys (ES: Eastern Sambo; LK: Looe Key). Nearshore conch were collected at Molasses Key (MK)

translocated conch will displace native conch or whether they will simply disperse after translocation as a result of intraspecific competition or, possibly, capture and handling stress. To examine this issue, we translocated nearshore conch into 2 offshore breeding aggregations and tracked a subset of translocated and native conch using acoustic telemetry to compare the long-term movements and interactions between the 2 groups.

MATERIALS AND METHODS

On July 16, 2001, we translocated adult queen conch from a non-spawning, nearshore aggregation located at Molasses Keys (MK) to 2 offshore sites, Eastern Sambo (ES) and Looe Key (LK) (Fig. 1). The habitat at MK was characterized as a hard-bottom community at a depth of 1 to 2 m. The habitat at both offshore sites consisted of back-reef rubble, sand plains, and seagrass *Thalassia testudinum* meadows at a depth of 2 to 4 m. ES was characterized by homogeneous expanses of rubble, sand, and seagrass, whereas LK consisted of a complex mosaic of rubble, sand, and seagrass habitats. The offshore sites were chosen because they contained resident, breeding aggregations that were typical of the Florida Keys (i.e. low abundance and small in areal extent). In addition, these aggregations were located within protected areas with the concomitant enhanced presence of law enforcement.

The number of conch needed for the translocations was based on the abundance of adult conch at the release sites. We estimated the abundance at ES and

LK to be 540 and 1060 adults, respectively, in 2000. We translocated 132 adults to ES and 255 adults to LK to increase the abundance at both sites by an arbitrary 25%. The translocated conch were released in the middle of the aggregations.

Acoustic telemetry and movement analyses. We used passive acoustic telemetry to compare the long-range movements of a subset of native and translocated conch at each offshore site. These conch were tagged with acoustic transmitters with a working life of approximately 1 yr (Sonotronics). Six native and 6 translocated conch were tagged *in situ* at ES; 5 native and 5 translocated conch were tagged *in situ* at LK. Acoustic transmitters were attached with Monel wire to the spire of each conch. Each transmitter emitted a unique frequency, which allowed a diver to track individual animals by using a VUR-96 hand-held receiver (Vemco). A Global Positioning System (GPS) receiver with Wide Area Augmentation System (WAAS) correction was used to determine the latitude and longitude of each conch's initial and subsequent positions. Conch were tracked on a bimonthly basis or, as weather permitted, from July 2001 through April 2002. Spatial data were analyzed in ArcView 3.3 (ESRI) using the Animal Movement Analysis Extension (AMAE) developed by Hooge et al. (2001). We calculated total distance traveled, movement rate, linearity, and home-range size for each animal. Because of the relatively small number of acoustically tagged conch (due to budgetary constraints), we used non-parametric statistical tests that would not be as influenced by outliers as would parametric tests. All statistical analyses were run on SPSS 11.0 (SPSS); results were considered significant if $p < 0.05$.

The total distance traveled (m) was defined as the sum of the linear distance between consecutive locations; movement rate (m d^{-1}) was calculated using the linear distance between consecutive locations and the number of days between consecutive sightings. Since conch do not move in straight lines, movement-rate calculations are undoubtedly underestimates; nevertheless, they allow relative comparisons to be made between native and translocated conch. We used the Mann-Whitney *U*-test to compare the total distance traveled and the movement rates of native and translocated conch at each site.

Linearity was defined as the distance between travel endpoints divided by the total distance traveled, and was used as a measure of migration. The closer this unitless value is to 1, the more likely a conch is simply migrating out of the area (i.e. moving in a straight line). Nomadic or highly migratory individuals do not exhibit site fidelity and so may lack fixed home ranges (White & Garrott 1990). Because

adult queen conch undergo seasonal migrations for reproduction (Stoner & Sandt 1992), an individual may appear to lack site fidelity if not tracked long enough through time; therefore, we used Spearman's ρ statistic to determine if the number of tracking days or the number of tracking points influenced linearity. We compared the linearity of native and translocated conch at each site using the Mann-Whitney *U*-test.

Home range was calculated using the probabilistic kernel model using the least-squares cross-validation within AMAE. This is one of the most robust techniques available for calculating home ranges (Powell 2000, Hooge et al. 2001). The 95% location probability contour for each conch was defined as the individual animal's home range (*sensu* Hooge et al. 2001). We compared the home-range size of native and translocated conch at each site using the Mann-Whitney *U*-test.

Static and dynamic interaction. Spatial data can also be used to describe how conspecifics move with respect to one another in order to better understand the behavioral and ecological interactions among individuals (White & Garrott 1990, Kenward 1992). There are 2 measures of animal association that can be used to explore the relationship between the movements of concurrently tracked individuals: static and dynamic interaction (Doncaster 1990, White & Garrott 1990, Kenward 1992).

The spatial overlap between the home ranges of a pair of animals is a static interaction (Doncaster 1990, White & Garrott 1990, Kenward 1992). We calculated the percentage of home-range overlap between all possible pairs of conch at each site using the GeoProcessing Wizard in ArcView 3.3. This yielded 3 types of static interaction: the interaction between (1) native–native pairs, (2) native–translocated pairs, and (3) translocated–translocated pairs. To determine if native and translocated conch were using the same areas, we compared the 3 types of static interaction at each site using the Kruskal-Wallis test.

Although static interactions can show a large amount of overlap in home ranges, it is possible that the animals avoided being in the same location at the same time (Doncaster 1990, Kenward 1992). This shortcoming can be overcome by examining dynamic interactions, which measure the degree of attraction, repulsion, or indifference between a pair of individuals (Brown et al. 2000). In other words, dynamic interaction can ascertain whether the simultaneous movements of a pair of acoustically tagged conch were correlated (*sensu* Doncaster 1990, White & Garrott 1990). We used the randomization test detailed by Kenward (1992) and Kenward et al. (1993) to investigate the dynamic interaction between all possible

pairs of acoustically tagged conch at each site. First, temporally coinciding locations were used to compute the observed mean distance (D_o) between a pair of conch. Then, an expected mean distance (D_e) between the 2 conch was calculated based on the randomization of all their possible locations. Finally, a sociality coefficient (S_c) was obtained for the 2 conch using the following formula from Kenward et al. (1993):

$$S_c = (D_e - D_o)/(D_e + D_o)$$

Values of S_c approaching 1.0 indicate that the 2 conch were closer to one another than expected (i.e. attraction); values approaching -1.0 indicate that the pair were further away than expected and were actively avoiding one another (i.e. repulsion); values close to zero indicate indifference (sensu Brown et al. 2000). These calculations provided the dynamic interactions between (1) native–native pairs, (2) native–translocated pairs, and (3) translocated–translocated pairs. The 3 types of dynamic interaction at each site were compared using the Kruskal-Wallis test.

RESULTS

Total distance traveled and movement rate

For those conch tagged with acoustic transmitters, total distance traveled varied from a minimum of 66.1 to a maximum of 519.7 m, with an overall mean of 212 m. Movement rate ranged from 0.31 to 3.06 $m\ d^{-1}$, with an overall mean of 1.23 $m\ d^{-1}$. There was no statistically significant difference in total distance traveled between native and translocated conch at ES (Fig. 2A; $U = 14.0$, $p = 0.522$) or at LK (Fig. 2A; $U = 4.0$, $p = 0.076$). Similarly, there was no statistically significant difference in the movement rates of native and translocated conch at ES (Fig. 2B; $U = 11.0$, $p = 0.262$) or at LK (Fig. 2B; $U = 11.0$, $p = 0.754$).

Linearity

Conch were tracked an average of 187 d, from a minimum of 41 to a maximum of 246 d. Neither the number of tracking days ($\rho = -0.067$, $n = 22$, $p = 0.766$)

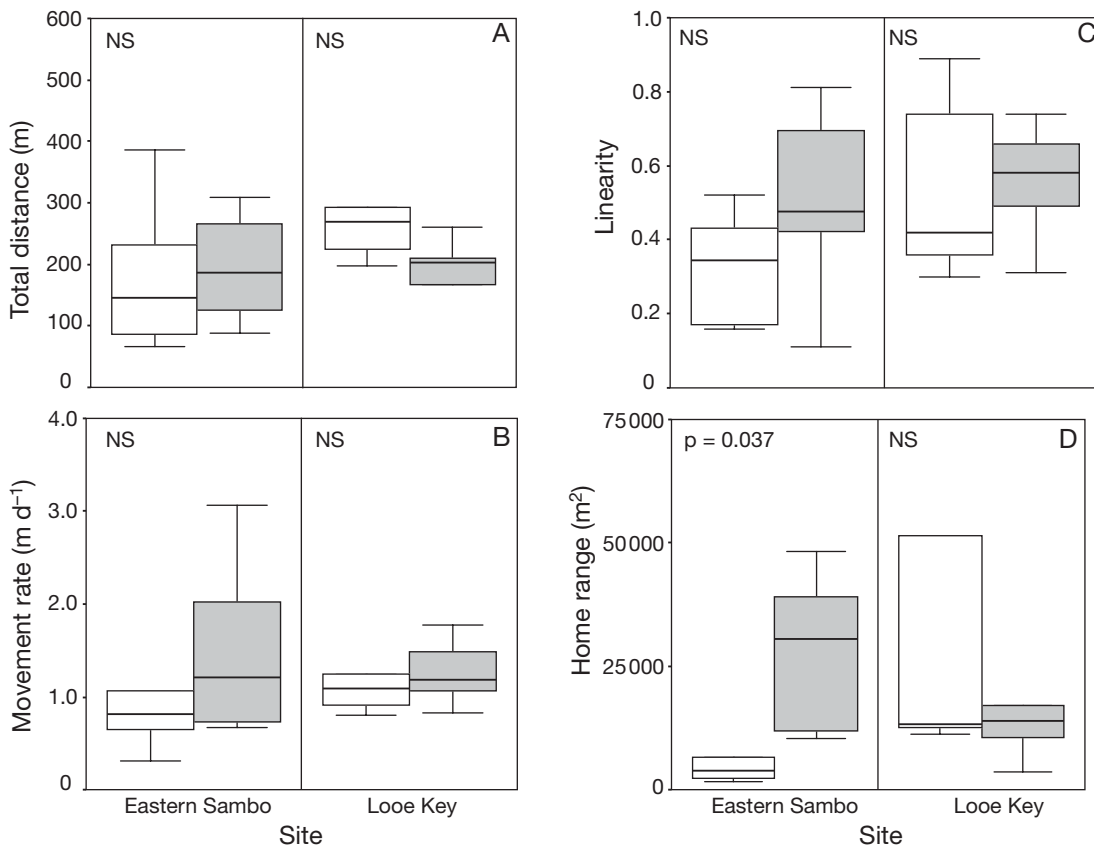


Fig. 2. *Strombus gigas*. (A) Total distance traveled, (B) movement rate, (C) linearity, and (D) home-range size of native and translocated queen conch tagged with acoustic transmitters, by site. White boxes: native; grey boxes: translocated. Boxes represent the interquartile ranges; the horizontal line bisecting the box represents the median; whiskers extend to the highest and lowest values excluding outliers. The one significant p-value from the Mann-Whitney U -test is given; NS: not significant

nor the number of tracking points ($\rho = -0.181$, $n = 22$, $p = 0.420$) influenced linearity. Linearity ranged from 0.11 to 0.89, with a mean of 0.48. There was no statistically significant difference in the linearity of native and translocated conch at ES (Fig. 2C; $U = 10.0$, $p = 0.200$) or at LK (Fig. 2C; $U = 11.5$, $p = 0.834$).

Home range

Home ranges varied from a minimum of 1676 to a maximum of 189867 m²; the mean home-range size was 27705 m². At ES, native conch had significantly smaller home ranges (Figs. 2D & 3A; $U = 5.0$, $p = 0.037$) than translocated conch. In contrast, at LK there was no statistically significant difference in home-range size (Figs. 2D & 3B; $U = 11.0$, $p = 0.754$) between native and translocated conch.

Static interaction

The overlap in home ranges between pairs of conch at ES (Fig. 3A) varied from a low of 3.5% to as much as 61.0%, with an average of 23.1% (Fig. 4A). There was a statistically significant difference in the home-range overlap among native–native pairs, native–translocated pairs, and translocated–translocated pairs at ES (Fig. 4A; $\chi^2 = 9.82$, $df = 2$, $p = 0.007$). The overlap of native–translocated pairs was lower than the overlap of native–native pairs and translocated–translocated pairs (Fig. 4A).

Home-range overlap at LK (Fig. 3B) varied from 2.0 to 40.9%, with an average of 17.9% (Fig. 4A). There was no significant difference in the home-range overlap among native–native pairs, native–translocated pairs, and translocated–translocated pairs at LK (Fig. 4A; $\chi^2 = 0.230$, $df = 2$, $p = 0.891$). The home-range overlap of the 3 interaction types was very similar, hovering between 15 and 20% (Fig. 4A).

Dynamic interaction

The sociality (S_c) between conch pairs at ES varied from -0.08 to 0.60 , with a mean of 0.15 (Fig. 4B). There was a statistically significant difference in the sociality among native–native pairs, native–translocated pairs, and translocated–translocated pairs at ES (Fig. 4B; $\chi^2 = 18.4$, $df = 2$, $p < 0.001$). There was a higher degree of sociality between translocated–translocated pairs than between native–native pairs and native–translocated pairs (Fig. 4B).

The S_c between conch pairs at LK ranged from -0.15 to 0.68 , with a mean of 0.22 (Fig. 4B). There was no sig-

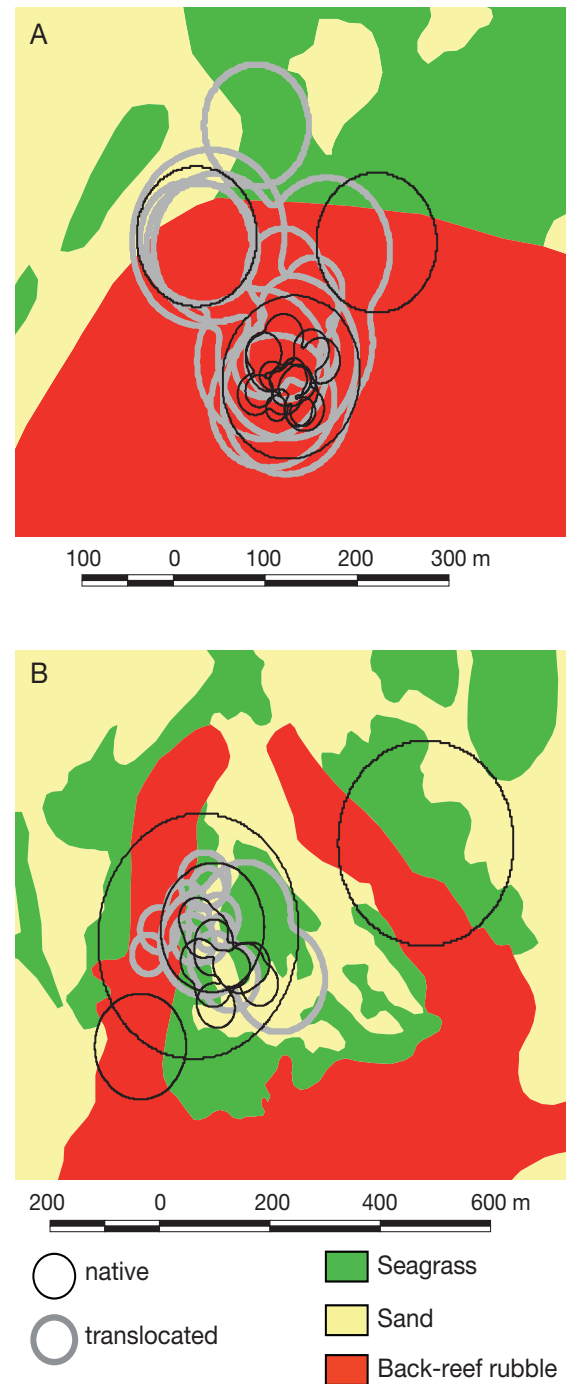


Fig. 3. *Strombus gigas*. Individual home ranges of native and translocated queen conch tagged with acoustic transmitters in relation to habitat at (A) Eastern Sambo and (B) Looe Key

nificant difference in sociality among native–native pairs, native–translocated pairs, and translocated–translocated pairs (Fig. 4B; $\chi^2 = 0.687$, $df = 2$, $p = 0.709$). The value of S_c was approximately 0.20 for all 3 interaction types (Fig. 4B).

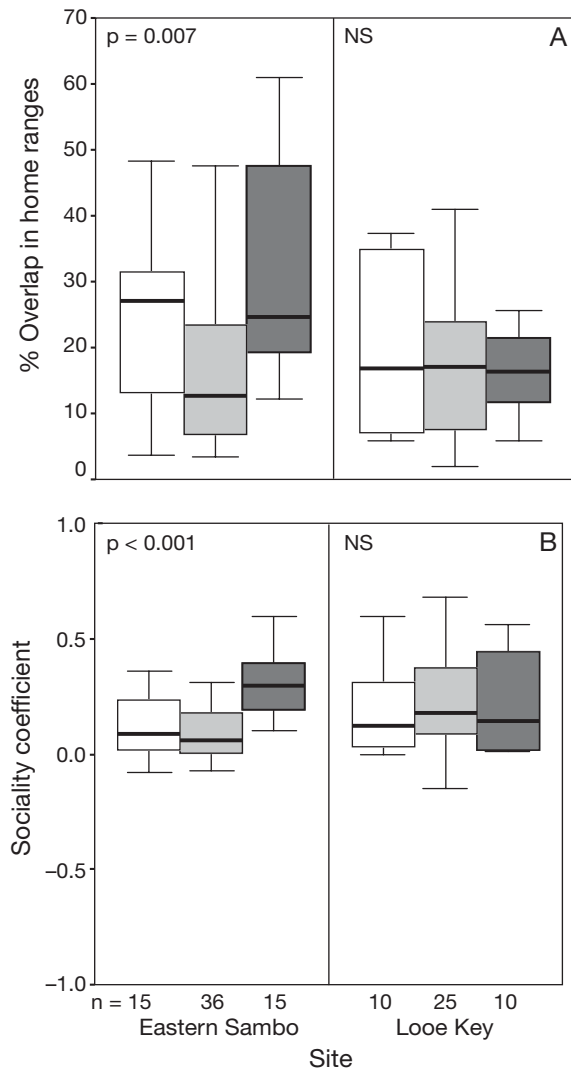


Fig. 4. *Strombus gigas*. (A) Static interaction (home-range overlap) and (B) dynamic interaction (sociality coefficient) between pairs of queen conch tagged with acoustic transmitters, by site. White boxes: native–native pairs; light grey boxes: native–translocated pairs; dark grey boxes: translocated–translocated pairs. Boxes represent the interquartile ranges; the horizontal line bisecting the box represents the median; whiskers extend to the highest and lowest values excluding outliers. p-values from the Kruskal-Wallis test are given where significant; NS: not significant

DISCUSSION

Effective restoration of depleted populations requires innovative strategies that are designed to develop self-sustaining populations. Depensatory mechanisms (e.g. total reproductive output is a positive function of the number of spawners; Appeldoorn 1995) have been hypothesized as a contributing factor in the slow recovery of the queen conch population in Florida (Stoner et al. 1997, Stoner & Ray-Culp 2000, Glazer &

Delgado 2003). Consequently, our strategy is to translocate nearshore conch into offshore spawning aggregations to increase the number of spawners in order to boost total reproductive output. However, for this to be effective, the translocated conch should not displace the native animals and must remain with the aggregation. Therefore, assessing the spatial distribution and interactions between translocated and native conch is critical in evaluating the efficacy of this management strategy.

At LK, there were no significant differences in the movement parameters, linearity, home-range size, or interactions between acoustically tagged native and translocated conch (Figs. 2 & 4). The results from the static interaction analyses (i.e. home-range overlap) indicate that both groups of conch were cohabiting the same areas (Fig. 3B). Furthermore, the sociality coefficient (i.e. dynamic interaction) between the native and translocated conch was positive, as one would expect from a species that forms aggregations (Fig. 4B). In addition, one of the acoustically tracked translocated conch was observed spawning 9 mo after being moved offshore.

At ES, the total distance traveled, movement rate, and linearity between native and translocated conch were not significantly different (Fig. 2A–C). However, in contrast to LK, translocated conch at ES had significantly larger home ranges than natives (Fig. 2D). Furthermore, the static interaction between native and translocated conch was significantly reduced compared to the interactions between native–native pairs and translocated–translocated pairs (Fig. 4A). Curiously, the sociality coefficients for native–native pairs and native–translocated pairs were quite similar, but the sociality between translocated–translocated pairs was significantly higher (Fig. 4B). We hypothesize that this increased sociality among translocated conch and their larger home ranges was related to habitat and the reproductive condition of the translocated conch.

Adult queen conch undergo seasonal migrations between forage and breeding habitats (Stoner & Sandt 1992). In general, conch feed in seagrass beds and move to back-reef rubble and sand habitats for reproduction during summer months (Stoner & Sandt 1992, Glazer & Kidney 2004). The nearshore conch used for the translocations were physiologically incapable of reproduction (Glazer & Quintero 1998, Delgado et al. 2004). Since the translocations took place in July during the breeding season and the translocated conch were not yet in breeding condition, they moved into forage habitats, while the natives remained in the breeding habitat (Fig. 3). This may explain the significantly larger home ranges of the translocated animals, the reduced static interaction between native and translocated conch, and why there was a higher

degree of sociality (i.e. dynamic interaction) among the translocated conch as they moved off together to forage in the adjacent seagrass beds. Ideally, the translocations should have occurred in January, in which case the translocated conch would have become reproductively active at the same time as their native counterparts (the July translocation date was due to logistical constraints).

Habitat heterogeneity has an effect on animal behavior and dispersal (Revilla et al. 2004). At LK, where the mosaic of habitats is more complex than at ES, the breeding and forage areas were in close proximity (Fig. 3), and so there were no significant differences in the movements or interactions between acoustically tagged native and translocated conch. At ES, the translocated conch had to move farther away from the translocation site to the forage habitat (Fig. 3), thus causing the significant differences in home-range size, home-range overlap, and sociality.

In this vein, a cautious approach must be taken when artificially increasing abundance to augment reproductive output, as most failed translocations and stock enhancement attempts are due to inadequately evaluating the availability of suitable habitat (Griffith et al. 1989, Caddy & Defeo 2003). A lack of available habitat may lead to negative interactions (i.e. repulsion) between conspecifics and eventual displacement of either the native or translocated animals. However, it seems unlikely that there was a paucity of useable habitat, as queen conch aggregations can effectively utilize and expand into less favorable habitats (Glazer & Kidney 2004). The dynamic interactions between native and translocated individuals at both sites were positive, indicating attraction (Fig. 4B) and that the aggregations remained cohesive. If the sites had been saturated, the conch would have moved away from each other to avoid intraspecific competition, and the dynamic interactions would have been negative, indicating repulsion. Nevertheless, our results reinforce the position that care should be taken, and translocations tailored to the specific situation at the release site to ensure success.

Translocations can provide an inexpensive, genetically sound alternative to the popular scheme of hatchery production. Outplanting hatchery-reared juvenile conch for stock enhancement purposes is costly due to high mortality after release (Glazer & Delgado 2003). Translocating naturally recruiting, nearshore adults to offshore areas is undoubtedly more cost effective. Furthermore, the genetic identity of the native population should be maintained. Translocating wild conch is preferable to releasing hatchery conch, as animals grown in a hatchery are often deficient in rare alleles because of the relatively few founders from which the cohort is derived (*sensu* Allendorf & Ryman 1987).

Wild conch have no such deficiencies. Larvae that settle nearshore presumably originated either within the spawning aggregations offshore or, at the very least, from the same sources that provide recruits to the offshore region. Thus, it is unlikely that nearshore conch are genetically dissimilar to those offshore (Campton et al. 1992) or that hybridization between translocated and native conch will reduce the fitness of the population through outbreeding depression (i.e. poorly adapted hybrids).

The present study has shown that translocations have the potential to be an effective management tool in queen conch restoration efforts. Translocated conch did not displace the natives and cohabitated the same areas as native conch at both sites. In addition, the aggregations remained cohesive, as suggested by the positive dynamic interactions between acoustically tracked individuals. Thus, moving conch from nearshore larval sinks to offshore larval sources may be the key to expediting the recovery of the queen conch population in the Florida Keys. Further research (e.g. larval retention and viability studies) and monitoring will determine the ultimate success of this restoration strategy.

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