Determining Ranging Patterns and Association Preferences of Bottlenose Dolphin Communities in Southeast Florida

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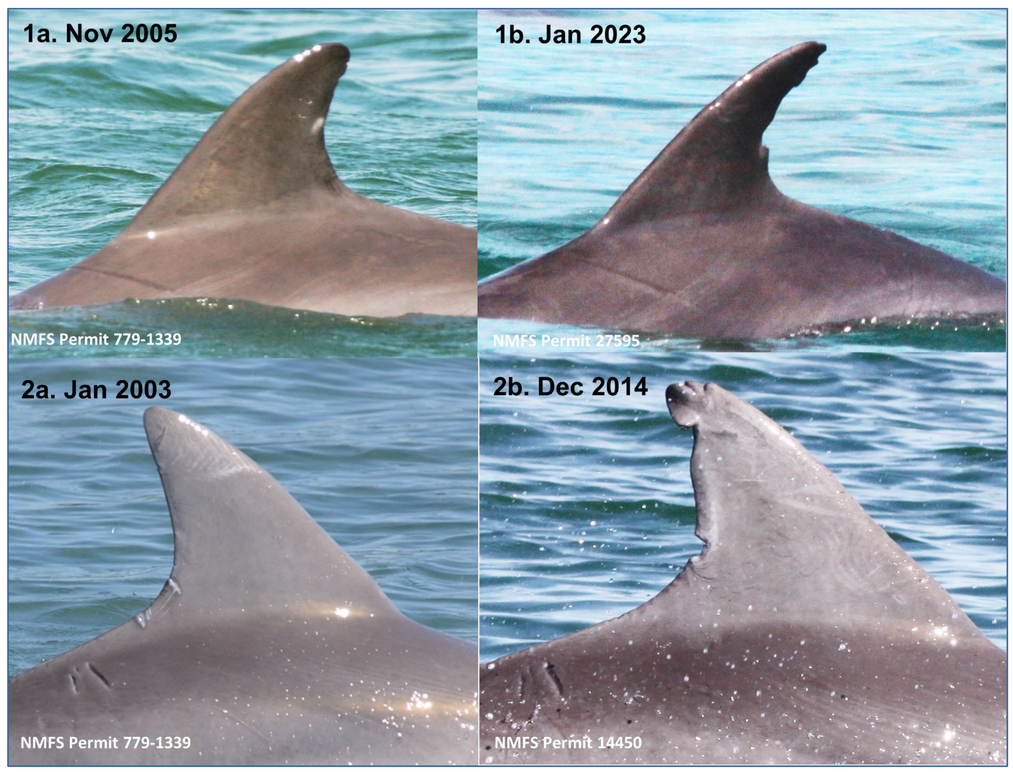
INTRODUCTION AND BACKGROUND

Previous photo-identification and genetic data suggest that resident bottlenose dolphins in Biscayne Bay form a demographically distinct population. Within this population, two communities* have been identified based on individual ranging patterns: a "northern" community and a "southern" community. Sightings in the southernmost extent of the Biscayne Bay study area have included animals previously sighted in Florida Bay raising questions about the full extent of the southern community's range. This study aims to identify the home range of bottlenose dolphins sighted across two management units in South Florida (Biscayne Bay and Florida Bay stocks) to inform questions about population connectivity.

To explore these connections, we compared photo-ID catalogs from Biscayne Bay (NOAA) and Dolphin Research Center's catalog from the Middle Florida Keys.

METHODS

Scar pattern analysis was incorporated to aid in identifying matches.



1a and 1b. Note the linear scar anterior to the dorsal fin. This along with other scars not pictured, was used to identify the fin changes in this animal.

2a and 2b. The scar pattern posterior to the dorsal fin was used to identify the fin changes in this animal. Biopsy samples collected in 2003 and 2014 confirmed this match.

Home range analysis: Kernel density estimates (KDE) were calculated for each individual to estimate total (95% KDE) and core (50% KDE) home ranges. A *k*-means cluster analysis (Hartigan & Wong, 1979; MacQueen, 1967) was used to determine community structure. The number of optimal clusters was determined using the average silhouette method (Rousseeuw, 1987). Cluster results were used to produce group total and core home range maps. The following parameters were used:

- Mean latitude and longitude values
- 95% and 50% KDEs
- Latitude and longitude of the 95% and 50% KDE centroids
- Standard distance deviation (S_{XY}) of 95% and 50% KDE centroids

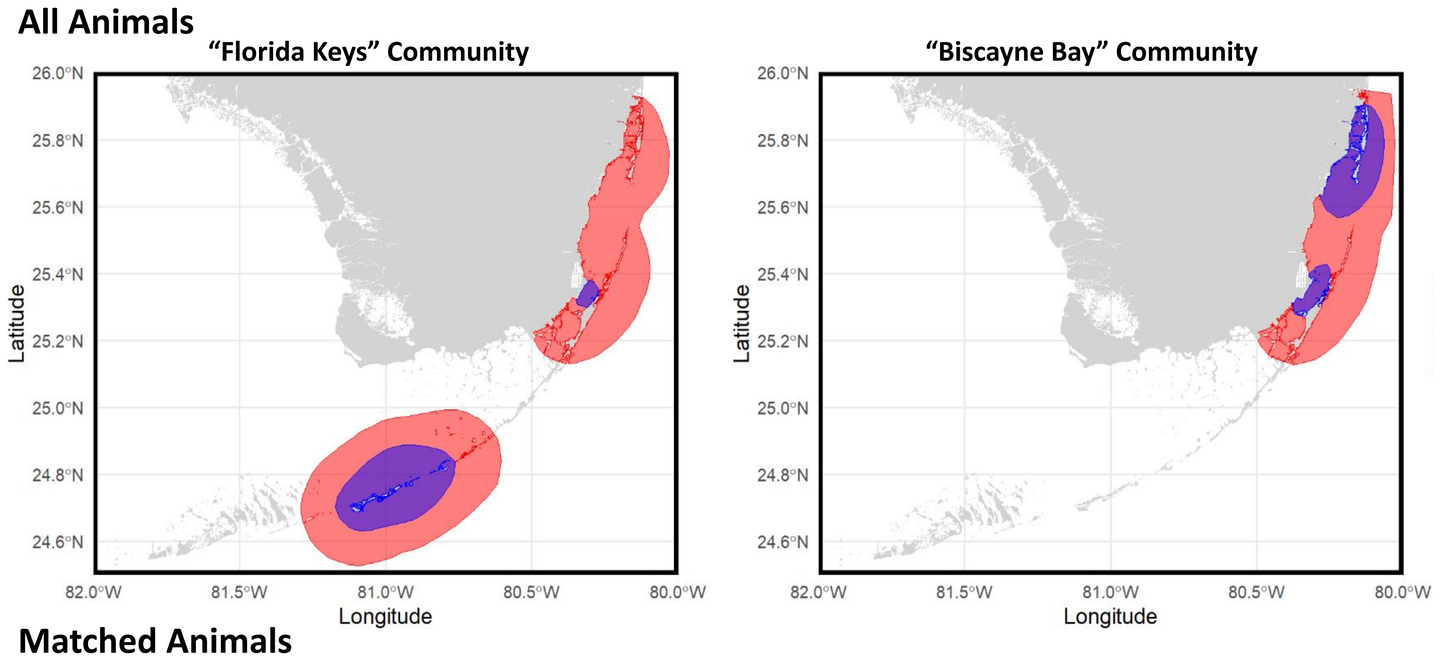
Social association analysis: The half-weight association index (HWI) was used to quantify association patterns among individuals. Monte Carlo permutation tests (*n*=10,000) were run to test for preferred associations and avoidances, and community-specific patterns were analyzed using a two-sided Mantel test.

- To reduce the impact of transient individuals, a sighting threshold of at least five sightings between 2013 and 2023 was set for all analyses. Both the home range and social association analyses were performed using two data sets: the full combined catalogs and a catalog limited to matched animals only.
- Data was analyzed using the *adehabitatHR* package in R version 4.4.1 and the social network analysis program SOCPROG 2.9 (Whitehead, 2009).

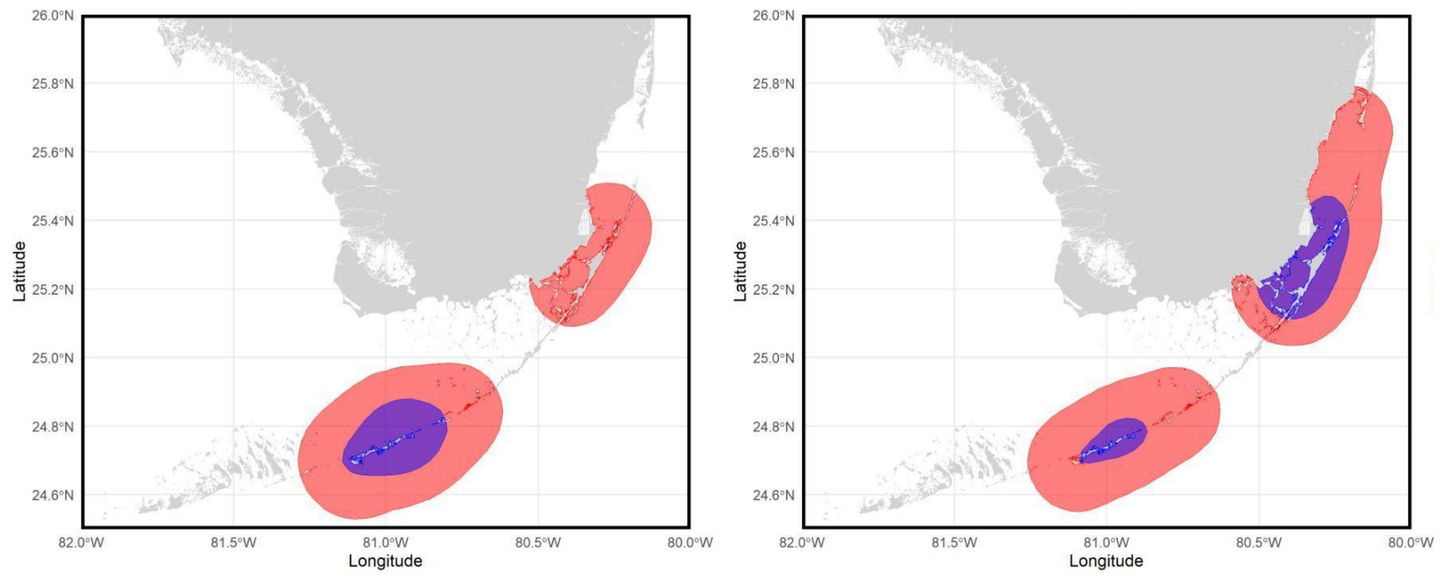
*Here we define community as "an assemblage of individuals belonging to the same species who share a common home range and exhibit social interactions (Goodall, 1986; Wrangham,1986)

RESULTS

All Animals



Matched Animals



Above: Total (95% KDE) and core (50% KDE) home range patterns for each "community" identified by *k*-means cluster analysis. **Top:** Total and core home ranges for ALL animals. **Bottom:** Total and core home ranges for only MATCHED animals (*N*=33).

Matched Individuals: 40 individuals were matched between NOAA's Biscayne Bay catalog and the Dolphin Research Center catalog.

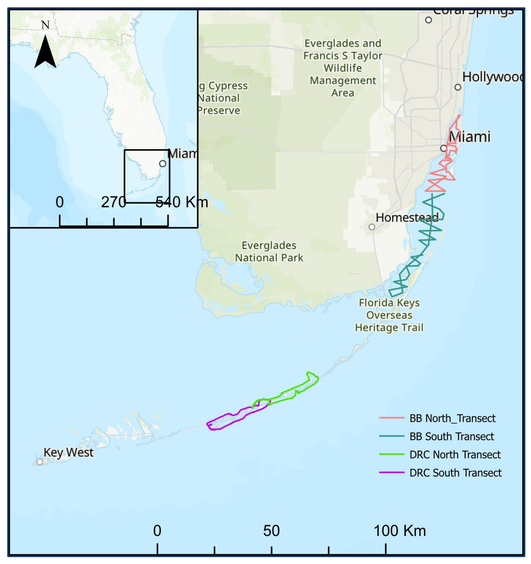
- 33 of these individuals were observed ≥5 times from 2013-2023.
- 7 of the 40 matched individuals were only observed in Biscayne Bay before 2013 and were not included in this analysis

Catalog Comparisons:

- 28% of the 145 individuals in NOAA's southern Biscayne Bay community matched with the Dolphin Research Center's (Middle Florida Keys) catalog.
- 24% of the 167 individuals identified in the Dolphin Research Center's (Middle Florida Keys) catalog matched with NOAA's Biscayne Bay catalog

Matched Animals (n=33)			
"Community"	# of Individuals	95% KDE	50% KDE
"Florida Keys"	14	3316.7 km^2	605.8 km^2
"Biscayne Bay"	19	3837.3 km^2	707.3 km^2
All Animals (n=241)			
"Florida Keys"	32	1786.7 km^2	528.4 km^2
"Biscayne Bay"	209	4099.0 km^2	831.2 km^2

Photo-ID Survey Areas



Social Associations:

- Within-Group Associations: Max HWI: 0.33 ± 0.13.
- Between-Group Associations: Max HWI: 0.21 ± 0.10
- Statistical Test: Two-sided Mantel test, $t = 5.14$, $P < 0.01$.

CONCLUSIONS AND FUTURE DIRECTIONS

Conclusions

- Two distinct "communities" were identified among matched individuals:
  - One with a core range in the middle Keys and one with a core range spanning both the middle Keys and Biscayne Bay.
  - The southern boundary of the Biscayne Bay stock may extend further than previously thought.
- Social analysis revealed significantly stronger associations within their primary regions (Biscayne Bay or FL Keys) than with individuals outside their community.

Future Directions

- Conduct additional studies on genetic and genomic population structures.
- Integrate data from neighboring Photo-ID survey areas between Biscayne Bay and the Middle Keys to further examine the connectivity between the communities.

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