Supplementary Material

Evidence of a small, island-associated population of bottlenose dolphins in the Mariana Islands

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1 Individual Distinctiveness and Photographic Quality Rating Protocols

The following protocols for rating quality of photographs and distinctiveness of dolphin dorsal fins were adapted from Rosel et al. (2011).

1.1 Photographic Quality Rating

The photographic quality rating is based on the quality of the photograph independent of the distinctiveness of the fin. This rating is determined through an evaluation and summed values of the following four characteristics:

1.1.1 Focus/clarity

Description:

Crispness or sharpness of the image. Lack of clarity may be caused by poor focus, excessive enlargement, poor developing, motion blur, or poor digital resolution resulting in pixelization of fin.

Tips for evaluation:

Attempt to make the fin full frame, but do not enlarge the image to more than 200%. When the leading and trailing edges of the fin differ in focus, score according to the lowest level of focus.

Based on the scale:

2 = excellent focus (including “pretty darn good” focus)

4 = moderate focus

9 = poor focus, very blurry, pixelized fin

1.1.2 Contrast/lighting effects

Description:

Range and effect of tones in the image. Images may display too much contrast, too little contrast, or distortion from variation in tones. Contrast deals specifically with comparing the fin to its background. That is, splashing or another fin behind the focal fin is an issue of contrast.

Tips for evaluation:

Consider both edges of the fin and ask, “Does the fin sufficiently stand out from its background?” When there is something other than the water surface behind the fin (e.g., fin reflection, another fin, water spray), do not automatically consider the contrast to be compromised unless all or part of the fin edges cannot be clearly distinguished from the background. Alternatively, do not automatically assume that an image with a very dark fin has sufficient contrast, as variation in background tones could still cause distortion of the fin edges.

Regarding fin edge distortion, do not stare at an image for a long time looking for distortion. If it takes a long time to discern distortion (or if the apparent edges of the fin do not line up with the color banding in the water), then distortion is most likely not a confounding factor. The use of a contrast score of 8 should be restricted to cases when there is no contrast (i.e., the fin blends completely into the background). Finally, there is an inevitable interaction between focus and contrast. If poor focus reduces contrast in an image, evaluate the contrast as you see it (i.e., don’t try to separate the two characteristics).

Based on the scale:

1 = sufficient contrast (edges of fin sufficiently stand out from background)

3 = compromised contrast or distortion of fin from variation in background tones

8 = no contrast (fin and background are virtually the same tone)

1.1.3 Angle

Description:

Angle of the fin to the camera. Given the tapering shape of the dorsal fin (with the trailing edge thinner than the leading edge), the difference between “slight” and “oblique” may depend on whether the trailing edge is angled toward or away from the camera. That is, a fin is functionally oblique at smaller angles if the trailing edge of the fin is angled away from the camera.

Tips for evaluation:

Consider only the edges of the fin relative to the camera and not the position of the fin in the animal’s surfacing. That is, do not penalize the fin if it is not upright in the image. Evaluate each image in a surfacing independently because animal or boat movement could cause the angle of the fin to the camera to change mid-surfacing. Consider only the angle of the fin and not the animal’s body, particularly in images where much of the body is visible. The angle of the body relative to the camera can be more pronounced and thus misleading.

Based on the scale:

1 = perpendicular to the camera

2 = slight angle from the camera

8 = oblique angle from the camera

1.1.4 Extent visible

Description:

Extent of fin visible in the image. Fins obscured by water, waves, shadow, other dolphins, etc., would be evaluated by this rating. A sheet of water coming off of the fin is also considered to obscure the fin.

Tips for evaluation:

Consider the full extent of the fin, from its tip to the base. When the fin is obscured by water, use the top edge of the water stream when evaluating how much of the fin is obscured. If you are unable to tell if water spray is behind the fin or coming off of it, be conservative and consider the spray to be obscuring the fin and score accordingly. For glare/water spots, consider them only if they are actually obscuring the edge of the fin.

Based on the scale:

1 = leading and trailing edge fully visible (1-2 small glare/water spots can be present on leading edge)

3 = same as above, but 1-2 small glare/water spots are present on the trailing edge

5 = same as above, but any part of the lower ¼ of the leading edge is obscured

8 = more than the lower ¼ of the leading edge or any part of trailing edge is obscured (excludes 1-2 small glare/water spots)

1.1.5 Overall photographic quality rating

5 – 7 = Q1: Excellent quality

8 – 11 = Q2: Average quality

≥12 = Q3: Poor quality

1.2 Distinctiveness Rating

Photos of both sides of the dorsal fin are used in order to identify individuals. It is therefore important to use only those features on the leading and trailing edges of the dorsal fin and the peduncle for individual distinctiveness. The shape (and bend) of the fin is also taken into consideration. In rare cases, punctures through the fin can be seen on both sides of the fin and should be included in the rating. Scars and coloration patterns on the fin and body are used as secondary identification marks.

The distinctiveness rating of an individual fin is determined by the number, size, and shape of the features located on the leading and trailing edges of the dorsal fin and peduncle. There are 4 categories of distinctiveness D-1 (high), D-2 (moderate), D-3 (low), D-4 (clean fin with no peduncle scars).

Only those fins with a distinctiveness of D-1 or D-2 (and a quality rating of Q-1 or Q-2) are entered into the catalog.

D-1: High distinctiveness; features evident even in a distant or poor quality photograph. In some cases the fin may have only 1 major feature that has a uniquely identifiable shape or is large (deep and > ¼ of the fin edge) or is located on a fin that has a unique shape.

D-2: Moderate distinctiveness; 2 features or 1 major feature are visible on the fin. In some cases the fin may have more than two features but they may be subtle (e.g. shallow marks, small nicks).

D-3: Low distinctiveness; very little information content on leading and trailing edges (e.g. a single nick). Features are too subtle to distinguish unless you have a Q-1 photo or you zoom in on the fin (more than 100%) to make out the features. In some cases an individual may have a clean fin with an obvious peduncle scar just behind the dorsal fin (within 12 inches).

D-4: No distinctiveness; fin is completely clean. No features on the leading or trailing edges. No punctures. There are no peduncle scars near the dorsal fin (within 12 inches).

2 Abundance Estimation Sensitivity Analysis Methodology

Sensitivity analyses were conducted to assess the robustness of the estimates of N_i from the full data set (i.e., yearly encounters of distinctive individuals in all sampling months and locations from 2011–2018) to sampling variability and bias. These analyses reduced an element of bias by estimating abundance from subsets of the full data set using the same process and models. First, a summer-only (May–September) data set was used to reduce potential bias from the non-instantaneous yearly capture occasions. A second reduced data set was used to address variability in sampling extent and included all months during which surveys occurred but only included years when all locations were surveyed (2011–2016). Rota was not surveyed in 2017–2018 (Table 1). A third reduced data set from a single sampling location (3-Islands area from 2011–2018) was considered to further minimize bias related to spatial variability in sampling, but the resulting data subset was insufficient for abundance estimation. As with the full dataset, model $\varphi(.)\ p(t)\ b(t)\ N(.)$ was replaced with the constrained model, $\varphi(.)\ p(t^*)\ b(t)\ N(.)$, in each reanalysis prior to averaging.

3 Supplementary Tables and Figures

Table S1. Model-averaged estimates of mark-recapture parameters resulting from the POPAN abundance estimation of the full southern Marianas bottlenose dolphin data set 2011–2018 ('All') and sensitivity analyses using data subsets, including data only from summer (May–September) in 2011–2018 and spatially-comparable data from 2011–2016. Parameters (with standard errors, SE) include annual survival probability (φ), capture probability (*p*), probability of entry (*b*), and the super-population size estimate (*N*) of distinctive individuals.

	All		Summer		2011-2016	
Parameter	**Estimate**	**SE**	**Estimate**	**SE**	**Estimate**	**SE**
φ	0.79	0.06	0.80	0.07	0.82	0.06
*p*2011	0.38	0.13	0.37	0.12	0.39	0.15
*p*2012	0.56	0.13	0.49	0.15	0.51	0.10
*p*2013	0.56	0.12	0.48	0.13	0.53	0.10
*p*2014	0.48	0.09	0.38	0.09	0.48	0.09
*p*2015	0.47	0.09	0.41	0.10	0.49	0.10
*p*2016	0.31	0.12	0.29	0.13	0.39	0.13
*p*2017	0.30	0.11	0.27	0.12	-	-
*p*2018	0.27	0.12	0.27	0.13	-	-
*b*2012	0.11	0.05	0.09	0.05	0.18	0.14
*b*2013	0.10	0.03	0.09	0.03	0.12	0.09
*b*2014	0.09	0.03	0.08	0.03	0.07	0.06
*b*2015	0.09	0.02	0.08	0.03	0.08	0.05
*b*2016	0.09	0.03	0.08	0.03	0.06	0.05
*b*2017	0.10	0.05	0.09	0.05	-	-
*b*2018	0.09	0.04	0.08	0.03	-	-
N	111	12	111	14	79	8

Table S2. Model selection results from the POPAN sensitivity analyses. The notation of the models (n = 6) and parameters (n = 4) is explained in the text. AICc is the Akaike's information criterion corrected for small sample size; ΔAICc is the difference in the AICc of a given model from the AICc of the best model; AICc weight is the Akaike weight used for model averaging; $\hat{c}$ is the variance inflation factor, with a $\hat{c} > 1$ indicative of overdispersion in the data requiring the use of quasi-AICc values.

Model	No. parameters	AICc	ΔAICc	AICc weight	c-hat
All					
φ(.) *p*(t) *b*(.) *N*(.)	11	342.47	0.00	0.69	1.00
φ(.) *p*(.) *b*(.) *N*(.)	4	345.84	3.38	0.13	1.00
φ(.) *p*(eff) *b*(.) *N*(.)	5	346.61	4.14	0.09	1.00
φ(.) *p*(.) *b*(t) *N*(.)	10	348.26	5.80	0.04	1.00
φ(.) *p*(eff) *b*(t) *N*(.)	11	348.83	6.36	0.03	1.00
φ(.) *p*(t*) *b*(t) *N*(.)	16	349.23	6.76	0.02	1.00
Summer					
φ(.) *p*(t) *b*(.) *N*(.)	11	242.18	0.00	0.49	1.39
φ(.) *p*(.) *b*(.) *N*(.)	4	243.07	0.89	0.32	1.39
φ(.) *p*(eff) *b*(.) *N*(.)	5	244.63	2.46	0.14	1.39
φ(.) *p*(.) *b*(t) *N*(.)	10	248.23	6.05	0.02	1.39
φ(.) *p*(eff) *b*(t) *N*(.)	11	249.46	7.28	0.01	1.39
φ(.) *p*(t*) *b*(t) *N*(.)	16	249.86	7.68	0.01	1.39
2011-2016					
φ(.) *p*(t) *b*(.) *N*(.)	9	265.74	0.00	0.45	1.00
φ(.) *p*(.) *b*(t) *N*(.)	8	266.78	1.03	0.27	1.00
φ(.) *p*(.) *b*(.) *N*(.)	4	268.29	2.55	0.13	1.00
φ(.) *p*(eff) *b*(t) *N*(.)	9	268.88	3.14	0.09	1.00
φ(.) *p*(eff) *b*(.) *N*(.)	5	270.47	4.72	0.04	1.00
φ(.) *p*(t*) *b*(t) *N*(.)	12	271.66	5.92	0.02	1.00

Table S3. Full sighting histories for all individuals used in the abundance estimation are provided in a separate supplementary file.

Table S4. Fraser's dolphin haplotype frequencies by sample collection location. Sample sizes are given in parentheses. Chen et al. haplotype refers to haplotype designations provided in Supplemental Table 1 of Chen et al. (2020). Because Chen et al.'s haplotypes were longer than those reported here, there were three instances where our haplotypes were identical to two haplotypes from Chen et al. over the area of overlap.

Accession no.	Haplotype	Maldives (4)	Philippines (25)	Taiwan (3)	Hawai‘i (3)	N. Pacific (3)	ETP (1)	Chen et al. haplotype
OR146773	Lh1		3		2			Hap_4
OR146774	Lh2	1	3	1				Hap_2/Hap_7
OR146775	Lh3		1					
OR146776	Lh4		3					Hap_25
OR146777	Lh5						1	Hap_45
OR146778	Lh6		2					Hap_30
OR146779	Lh7		1					
OR146780	Lh8		1					
OR146781	Lh9		2					Hap_27, Hap_35
OR146782	Lh10		1					
OR146783	Lh11		2					Hap_21
OR146784	Lh12		1					Hap_29
OR146785	Lh13		1					
OR146786	Lh14		1					Hap_19
OR146787	Lh15				1			Hap_47
OR146788	Lh16		1					Hap_14
OR146789	Lh17		1					Hap_26
OR146790	Lh18	1						
OR146791	Lh19					1		
OR146792	Lh20					1		
OR146793	Lh21					1		Hap_24, Hap_33
OR146794	Lh22		1					Hap_28
OR146795	Lh23			1				Hap_17
OR146796	Lh24			1				Hap_32
OR146797	Lh25	1						
OR146798	Lh26	1						

Table S5. Estimates of the posterior probability for each value of K (*L(K)*) and the second order rate of change of the likelihood function with respect to K (*ΔK*) from STRUCTURE runs. *L(K)* and *ΔK* were calculated as described in Evanno et al. (2005).

K	Bottlenose dolphins		Bottlenose and Fraser's dolphins	
	L(K)	*ΔK*	*L(K)*	*ΔK*
1	-7753.92	--	-9831.41	--
2	-7778.73	1.54	-8962.08	2448.94
3	-7755.77	3.58	-8802.52	314.29
4	-7916.8	1.32	-8751.63	--
5	-8164.09	1.22		
6	-8310.61	--		

Table S6. Summary of STRUCTURE results for the Marianas bottlenose dolphin samples (n = 14) when all other bottlenose dolphins were subsampled to n = 25. The column 'Proportion Fraser's ancestry' shows what proportion of an individual's nuclear genome is estimated to be derived from Fraser's dolphins, based on the analysis that used an uninformative species prior for all Marianas bottlenose dolphin samples. The columns labeled 'Assignment probability' show the probabilities that an individual has a Fraser's dolphin parent (F1 hybrid) or grandparent (F2 hybrid) based on the analysis that used an informative species prior, with all Marianas samples presumed to be bottlenose dolphins. The sum of the two Assignment probability columns shows the overall probability of an individual having a Fraser's dolphin ancestor in the previous two generations.

LABID	Sex	Haplotype	Proportion Fraser's ancestry	Assignment probability	
				F1 hybrid	F2 hybrid
104035	M	32	0.092	0	0
104066	F	Lh1	0.109	0	0
104067	M	34	0.271	0	0.008
104070	M	32	0.110	0	0.000
108172	M	32	0.192	0	0.003
108183	M	39	0.168	0	0.012
108207	F	Lh1	0.181	0	0.001
108208	F	Lh1	0.242	0	0.004
116858	F	32	0.173	0	0.002
116866	M	32	0.172	0	0.001
116867	M	Lh1	0.428	0.010	0.041
116868	M	Lh1	0.301	0	0.003
116869	M	32	0.242	0	0.002
116881	M	33	0.065	0	0
Mean			0.196	0.001	0.006

Table S7. Estimates of apparent survival using a Cormack-Jolly-Seber model with different parameterizations. All - all yearly encounters of individuals; models tested included φ(.), *p*(.), *p*(eff), and *p*(t). Two age-class (time-since-marking) - first year for all cohorts was assigned as the first age class (included "transients" - individuals encountered only once in the dataset), all other years were assigned as the second age class (so-called "residents"); models tested included φ(tsm), *p*(.), *p*(eff), and *p*(t). Ad hoc - the first occurrence for each individual was removed prior to running models (Pradel et al. 1997); models tested included φ(.), *p*(.), *p*(eff), and *p*(t); apparent survival is only estimated for the assumed "resident" population.

Apparent Survival	**All**		**Two Age-Class**		**Ad Hoc**	
	Estimate	**SE**	**Estimate**	**SE**	**Estimate**	**SE**
φ all	0.78	0.06	-	-	-	-
φ "transient"	-	-	0.75	0.09	-	-
φ "resident"	-	-	0.81	0.09	0.91	0.07

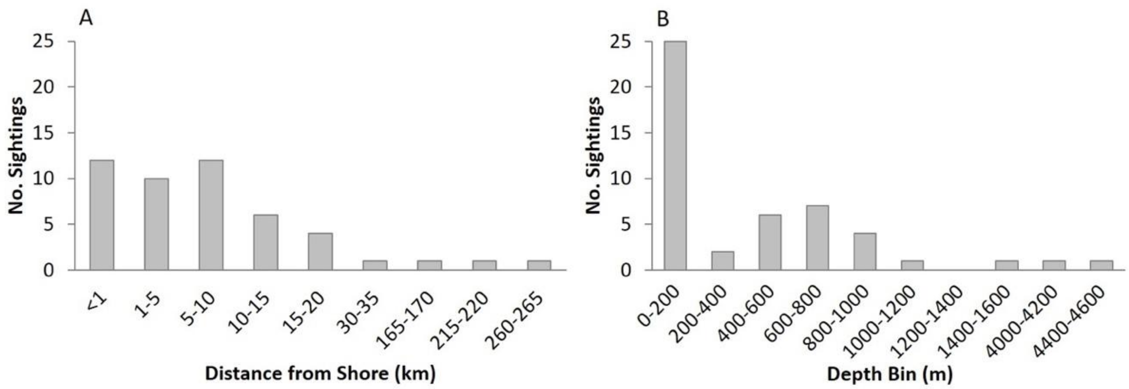


Figure S1. Number of bottlenose dolphin group sightings (n = 48) by distance to shore (km) (A) and depth bin (m) (B) across all ship and small-boat surveys in the Marianas.

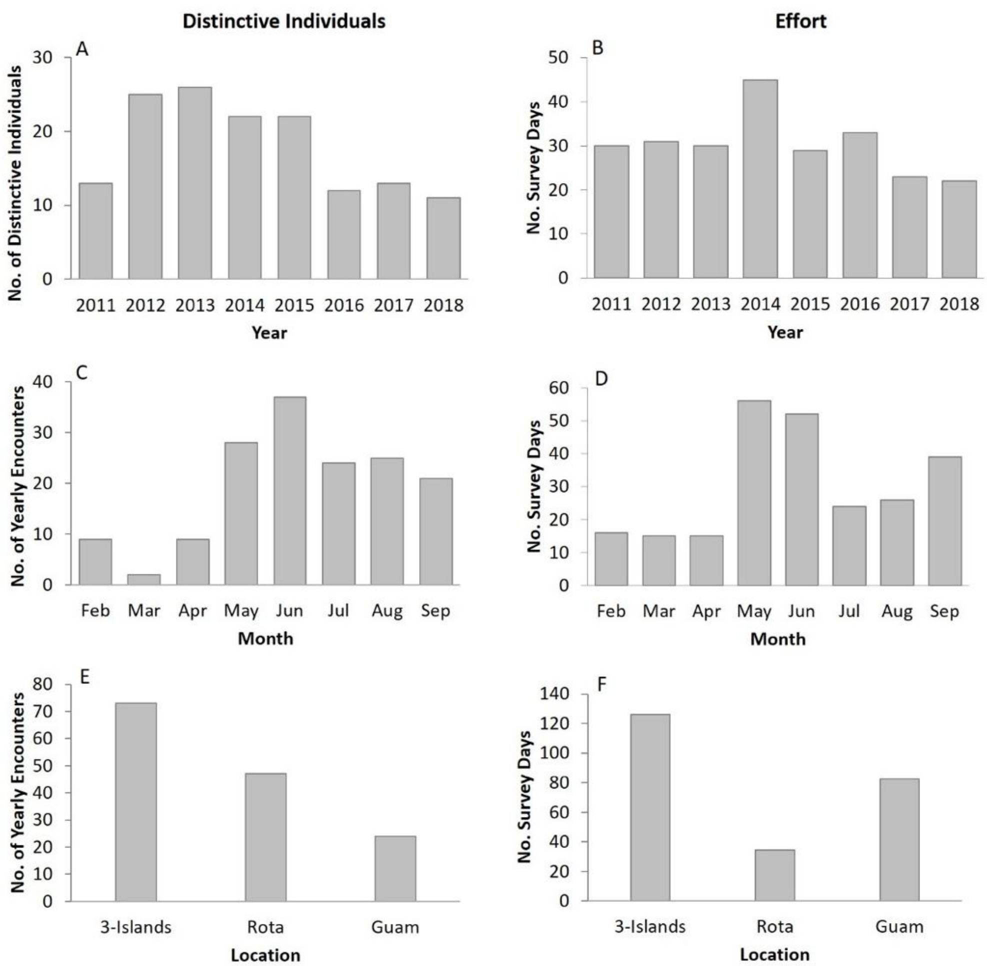


Figure S2. Encounter histories of distinctive bottlenose dolphins (n = 76) and survey effort in the southern Marianas study area during 2011–2018. Encounters of distinctive individuals used in the mark-recapture abundance estimation and survey effort (days) are summarized by year (A and B), month (C and D), and location (E and F).

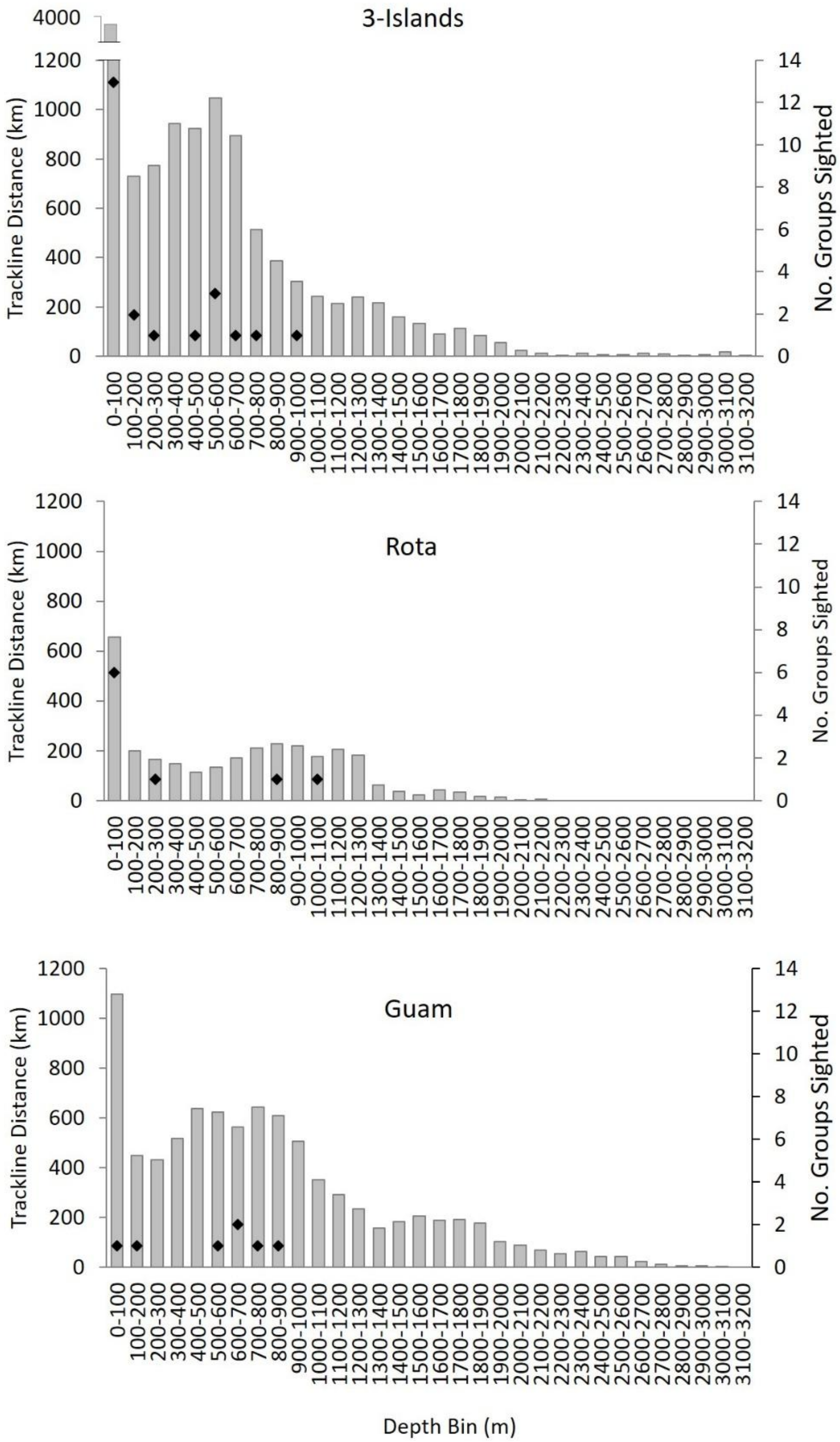


Figure S3. Survey effort (gray bars, trackline distance, km) and bottlenose dolphin group sightings (black diamonds, no. groups sighted) by depth bin (m) and location (3-Islands, Rota, and Guam) within the southern Marianas study area during 2011–2018. Note: there is a break in the 3-Islands trackline distance plot for the 100 m depth bin to accommodate the visual comparison between plots.

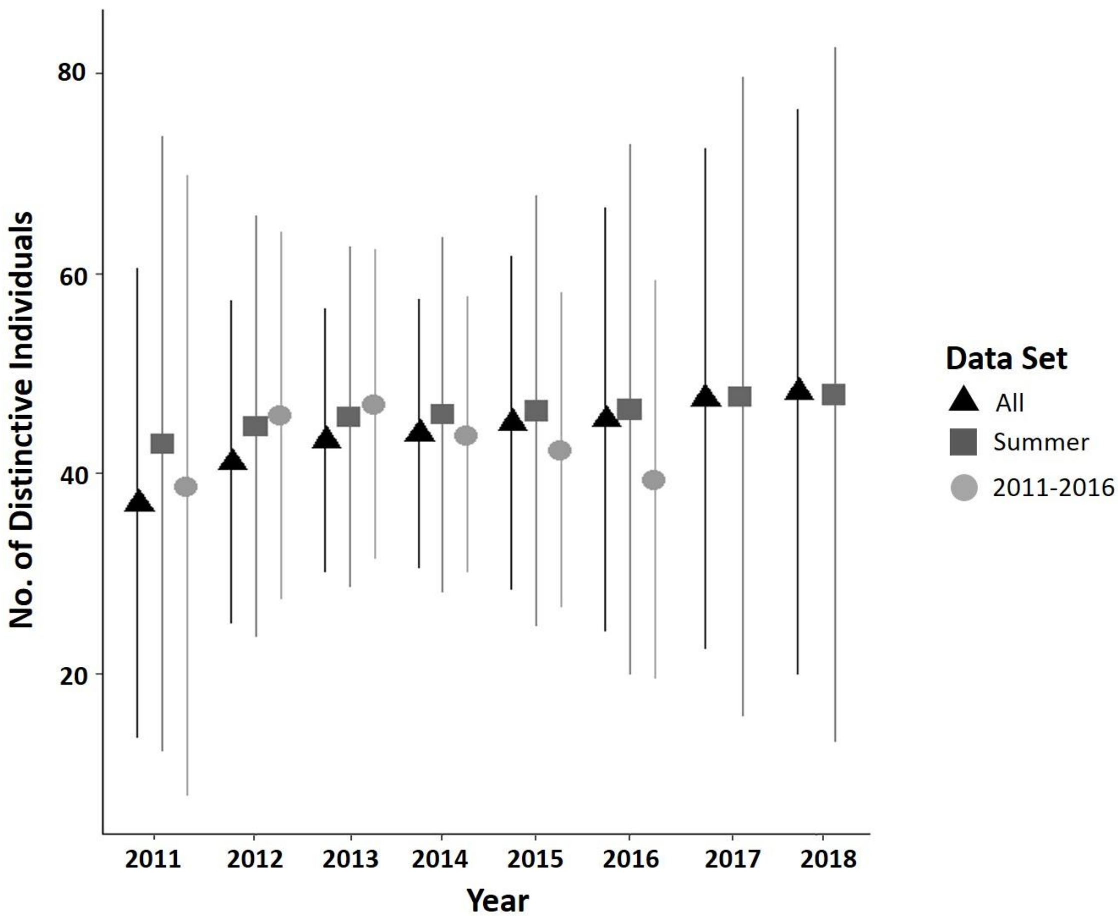


Figure S4. Comparisons of the annual estimates of distinctive individual abundance (N_i) within the southern Marianas study area from the mark-recapture analysis of the full Marianas bottlenose dolphin data set ('All') to N_i estimates from sensitivity analyses using subsets of data from summer (May–September) in 2011–2018 and spatially-comparable data from 2011–2016. Estimates of N_i at each year are jittered for clarity; error bars represent 95% CIs.

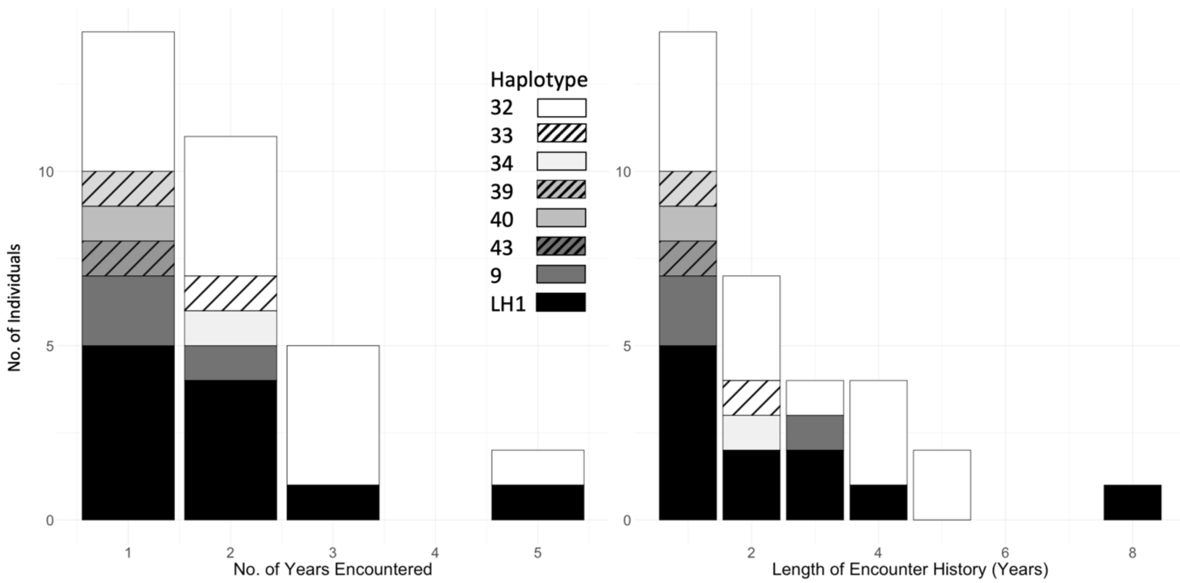
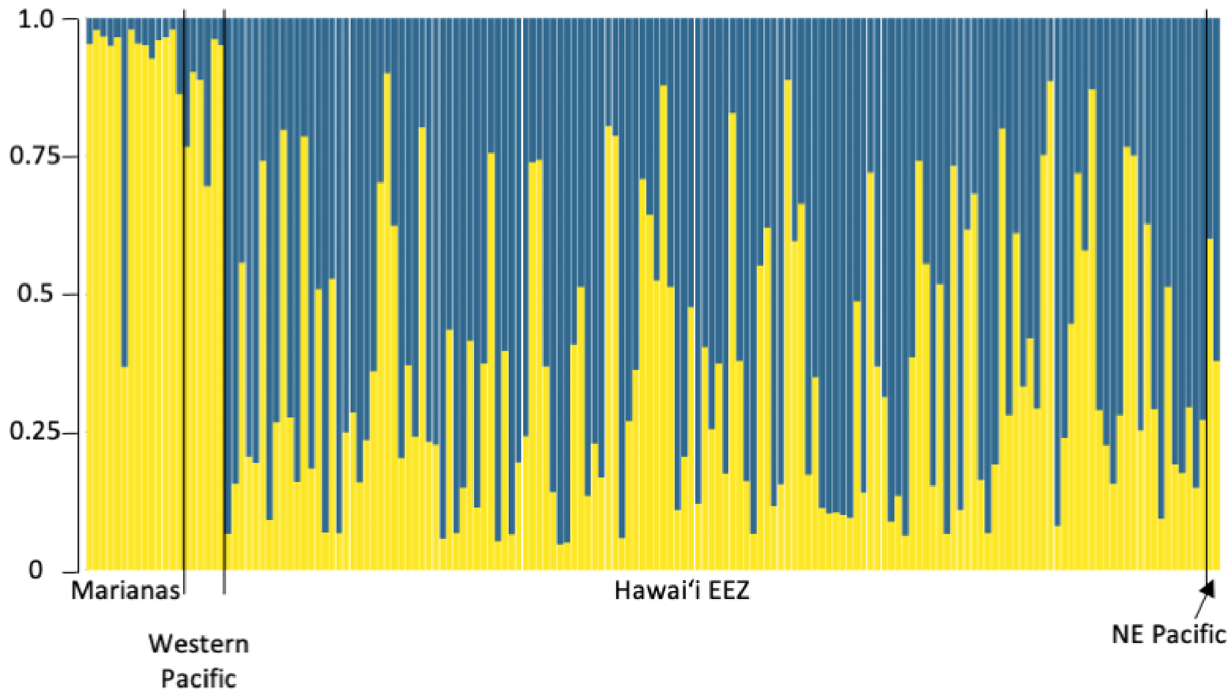


Figure S5. Summary of encounters with biopsied bottlenose dolphins in the Marianas from 2011 to 2018 showing (A) the frequency of yearly encounters and (B) frequency of encounter history lengths, color-coded by haplotype of the biopsied individual.

A



B

Figure S6. Graphical representation of the results of STRUCTURE analyses that only included bottlenose dolphins. Each vertical bar represents an individual and is colored to show the proportion of the individual's ancestry that is attributable to each of the groups defined by STRUCTURE. Results are shown for models with (A) K = 2 groups and (B) K = 3 groups.

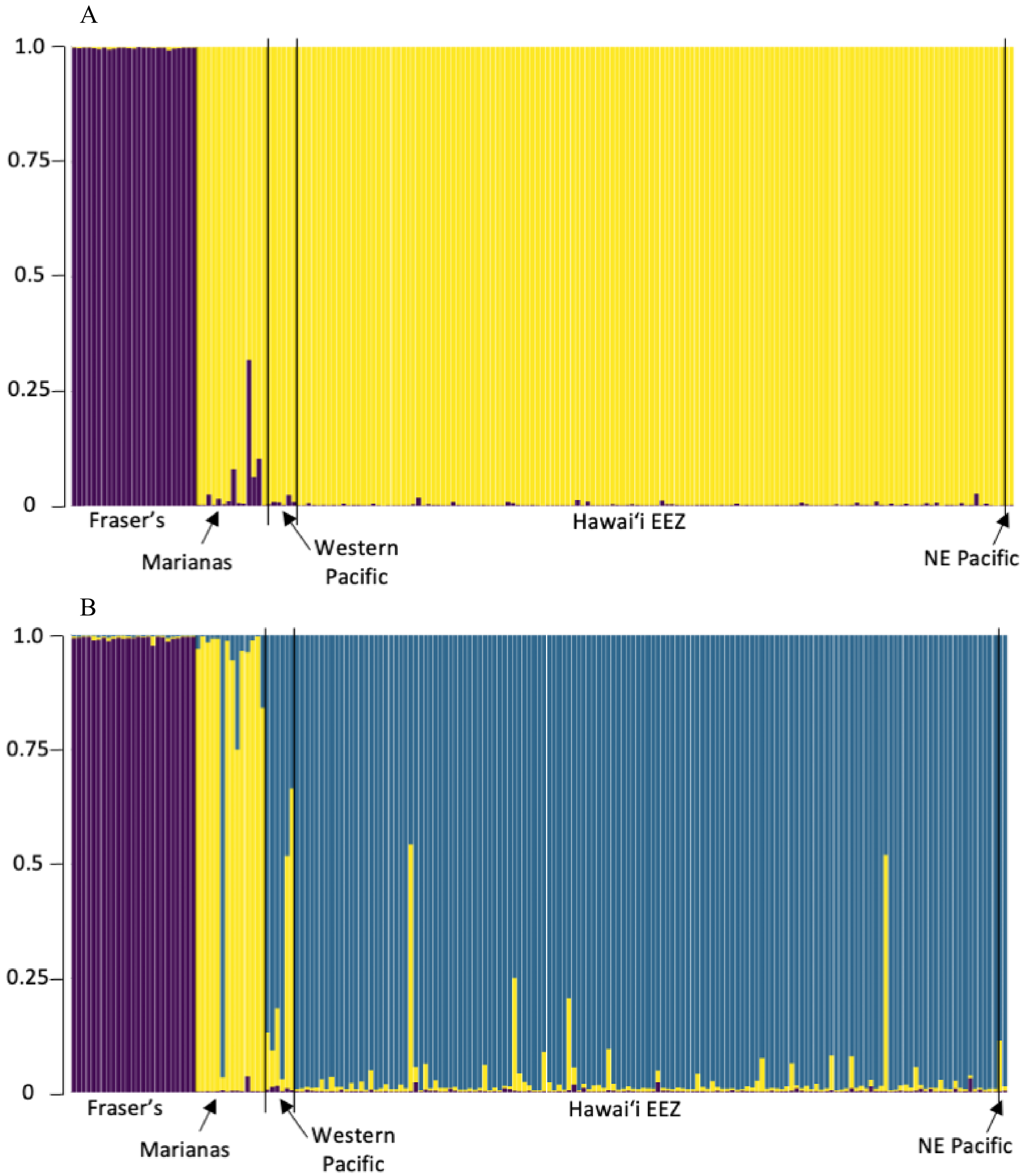


Figure S7. Graphical representation of results of STRUCTURE analyses that included both bottlenose and Fraser's dolphins. Each vertical bar represents an individual and is colored to show the proportion of the individual's ancestry that is attributable to each of the groups defined by STRUCTURE. Results are shown for models with (A) K = 2 groups and (B) K = 3 groups.