

# *Abundance and movements of sperm whales in the western Mediterranean basin*

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## ABSTRACT

1. Sperm whales in the Mediterranean are classified as ‘Endangered’ by the IUCN. They are apparently isolated from adjacent Atlantic populations, and subject to anthropogenic pressures including interactions with illegal driftnet fisheries, ship strikes, ingestion of debris and underwater noise.

2. Photo-identification data opportunistically collected from the western Mediterranean basin show that individual sperm whales regularly move in excess of 500 km across the western basin, suggesting that this area is occupied by a single population.

3. The best abundance estimate for this region is approximately 400 animals, with confidence intervals between 200 and 1000.

4. Given the mortality levels reported in the literature, this figure suggests that the conservation status of sperm whales in this region is very serious. Immediate priority should be placed both on conducting systematic surveys for abundance estimation and on measures to reduce the mortality associated with driftnet fishing.

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Received 13 February 2012; Revised 2 November 2013; Accepted 2 November 2013

KEY WORDS: sperm whale; Mediterranean; abundance; movement; photo-identification

## INTRODUCTION

The conservation status of the Mediterranean sperm whale population is an issue of concern, the population having been classified as ‘Endangered’ by the IUCN (Notarbartolo di Sciara *et al.*, 2012). Although extensive commercial whaling has ceased, there are a number of other global threats

that still remain, such as entanglement in fishing gear, high levels of contaminant accumulation, anthropogenic noise disturbance, and ship collisions (Notarbartolo di Sciara *et al.*, 2012). All of these global factors are likely to be especially concentrated in the enclosed and heavily exploited Mediterranean Sea (Reeves and Notarbartolo di Sciara, 2006). Collisions with marine traffic

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(Reeves and Notarbartolo di Sciara, 2006), interactions with fisheries (Bearzi, 2002; Tudela *et al.*, 2005), underwater noise from seismic surveys or military operations (Notarbartolo di Sciara and Gordon, 1997), and ingestion of marine debris (Viale *et al.*, 1992) are all problems for sperm whales in this region. Of particular concern is the continuing mortality attributed to entanglement in nets from illegal driftnet fisheries (Tudela *et al.*, 2005; Reeves and Notarbartolo di Sciara, 2006). For example, 15 out of 24 sperm whale strandings along the coast of Mallorca alone in the period 1993–1998 showed evidence of contact with pelagic driftnets (Lazaro and Martin, 1999). In the period 1971–2004, on the Mediterranean coasts of just Spain, France and Italy, 229 sperm whales were reported being found either dead from entanglement or entangled in nets (Reeves and Notarbartolo di Sciara, 2006).

Sperm whales are widely distributed within the Mediterranean from the Alborán Sea to the Levant basin (Cañadas *et al.*, 2002; Gannier *et al.*, 2002; Frantzis *et al.*, 2003; Lewis *et al.*, 2007; Azzellino *et al.*, 2008; Boisseau *et al.*, 2010). Sperm whale habitat in the Mediterranean comprises deep offshore waters, especially those over the continental slope (Praca and Gannier, 2008; Praca *et al.*, 2009) and those associated with oceanographic frontal systems with marked temperature discontinuities (Gannier and Praca, 2007). It is presumed that these are areas where mesopelagic squid, the main sperm whale prey worldwide, are most abundant, although evidence on the diet of sperm whales in the region is sparse. The Mediterranean consists of two main basins, the eastern and the western, separated by the Straits of Sicily and Messina. All age and sex classes appear to be present in both the east and west basins of the Mediterranean (Frantzis *et al.*, 2003; Drouot *et al.*, 2004b; Drouot-Dulau and Gannier, 2007). In the western basin, larger groups as well as calves are more common in the central zone than in the north (Drouot *et al.*, 2004b).

Movements of Mediterranean sperm whales are poorly understood. The Mediterranean Sea is an enclosed basin connected to the Atlantic Ocean by the narrow shelf of the Strait of Gibraltar. Several observations suggest a high degree of isolation

between Mediterranean sperm whales and those in adjacent Atlantic populations – there have been no observations of migration through the Strait of Gibraltar, and genetic evidence supports the view that there is no connection with the adjacent populations of the North Atlantic (Drouot *et al.*, 2004a; Engelhaupt *et al.*, 2009). From east to west the Mediterranean measures about 3800 km and the widest distance north to south is around 900 km, distances over which sperm whales from other populations are known to regularly move (Whitehead, 2001; Whitehead *et al.*, 2008). In the western basin, males appear to travel to and from the more northern areas of the basin in an apparently restricted version of the movements made by males in larger ocean basins (Whitehead, 2003; Drouot-Dulau and Gannier, 2007). The degree to which sperm whales move between the two basins is largely unknown. Surveys report an absence or very low density of sperm whales in the Strait of Sicily and Ionian Sea which link the two areas (Lewis *et al.*, 2007), and these transition areas are much shallower than typical sperm whale habitat. These areas are not absolute barriers, however, as a recent study documented three sperm whales having made the transition from the western to the eastern basin in the last 20 years (Frantzis *et al.*, 2011). Nonetheless, as these individuals represented about 1% of the identified animals examined in that study, and there is no evidence of east to west movements, it seems reasonable to consider movements between the basins as relatively rare events.

Mediterranean sperm whales remain poorly known, and there is no quantitative abundance estimate currently available (Reeves and Notarbartolo di Sciara, 2006; Notarbartolo di Sciara *et al.*, 2012). The IUCN ‘Endangered’ classification results mainly from consideration of the elevated threats probably faced by this population (Notarbartolo di Sciara *et al.*, 2012), informed judgements that it numbers ‘more likely in the hundreds rather than the thousands’ (Reeves and Notarbartolo di Sciara, 2006) and very likely ‘fewer than 2,500 animals’ (Notarbartolo di Sciara *et al.*, 2012), and the likelihood that it is isolated from other sperm whale populations in larger ocean basins such as the North Atlantic

(Drouot *et al.*, 2004a; Engelhaupt *et al.*, 2009). Accurate estimates of abundance are therefore important if potentially costly conservation efforts are to be justified. Photo-identification data collected from three regions across the western Mediterranean basin over 18 years were analysed to provide the first quantitative abundance estimates of sperm whales in this region.

## METHODS

### Photo-identification data

Data were collected during dedicated research cruises on board auxiliary diesel powered sailboats up to 20 m in length in the months June to October for the Ligurian Sea in the years 1990–2008, and June to August between 1993 and 2008 for the Gulf of Lions and waters around the Balearic Archipelago. Individual sperm whales were identified from photographs showing the individually unique markings on the trailing edges of their tail flukes, after they had been located acoustically or visually. Photographs were assigned a Q-value of 1–5, with 1 representing an image that could not be used for identification and 5 a high quality image in which even subtle markings would be visible. Q-values were classified based on the quality of the photograph, regardless of how well the individual was marked. Photograph quality depended on multiple factors: the percentage of the image covered by the fluke; focus; exposure (darkness–lightness); fluke orientation (angle between the ventral side of the fluke and the photographer); fluke tilt (angle between the fluke and the water surface); and percentage of fluke visible above the water (Arnboom, 1987). Only high-quality photographs ( $Q \geq 3$ ) were used for further analysis.

Photographs were analysed using Europhlukes software (Beekmans *et al.*, 2005) complemented by the use of visual methods to confirm identity matches (Whitehead, 1990). Each image was loaded into Europhlukes Phlex 1.3.6, a program that attempts to automatically trace around the fluke's edge based on the contrast between the fluke and the background sea. Adjustments were made manually to obtain good independent fits to

the left and right margins of the photographed fluke. The Europhlukes software Match 1.5.3 (Beekmans *et al.*, 2005) was used to compare all the contours thus obtained. The program provides a coefficient (*m*-value) between 0 and 1 based on the similarity of the traces: *m*-values closer to 1 represent a higher similarity between two individual traces and indicate a possible match between those individuals. Each new fluke was visually compared with the first 20 already in the catalogue ranked by their *m*-value similarity to the new fluke. If there was no match that fluke was considered a new individual. Individual flukes were identified based on their specific mark types such as scallops, waves, nicks, distinct nicks, tooth mark scars, presence of holes and missing portions, as described by Dufault and Whitehead (1995).

### Analysis of movements

Geographically, effort was concentrated in the areas to the south and east of the Balearics Archipelago, and along the French and Italian coasts (Figure 1). Therefore, the analysis of these data began by attempting to assess whether these two concentrations represented discrete populations, to determine whether they should be analysed as a single population or as distinct units. A lagged identification rate analysis was used to

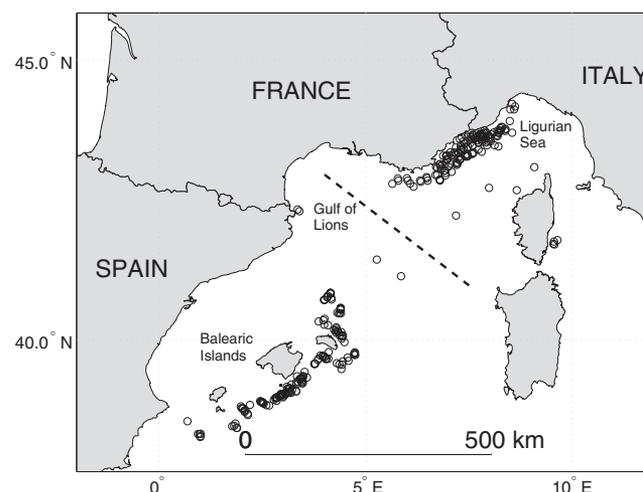


Figure 1. Identification locations (○). Dashed line shows division into areas for movement analysis.

estimate the probability that individuals would be sighted in one area at time  $t + \Delta t$  given that they had been sighted in either the same or the other area at time  $t$  (Whitehead, 2001; Whitehead and Wimmer, 2005). Analysis of movement in continuous space was also used to estimate diffusion rates and home range size, again following the methods of Whitehead (2001). If the two areas contain separate populations then we would expect much higher probabilities of individuals being identified in the same area at time  $t + \Delta t$  as they were at time  $t$  (i.e. higher resighting rates within the region of first identification), and for home range size to be smaller than the distance between the two areas. These approaches carry relatively few assumptions (Whitehead, 2001). The central assumption for the former is that the effort put into identifying each individual animal be fixed in advance, which was broadly true in this study, and for the latter it is that the probability of identifying an animal in any location is independent of the time since it was last identified, which was met by considering only a single identification of each individual within a sampling period set to one day.

carry few other assumptions, unlike the other methods, which are vulnerable to severe negative bias when identifiability is heterogeneous (Gowans *et al.*, 2000; Pledger *et al.*, 2003; Whitehead and Wimmer, 2005; Gero *et al.*, 2007). They can incorporate heterogeneity in identifiability of individuals and in mortality rates (which also incorporates emigration and mark change) by assuming two classes of individuals (A and B) that can have different identification and/or mortality rates. The two-class models have been shown by simulation to also perform well when identifiability of individuals varies continuously, for example with a continuous distribution of wariness to vessels as opposed to two age–sex classes that behave differently (Whitehead and Wimmer, 2005). The full model estimates the following parameters:  $N_m$ , the population size at the study midpoint (i.e. 1999);  $r$ , the annual rate of increase;  $\alpha$ , the proportion of individuals in class A;  $\beta$ , the ratio of identifiability of class B animals;  $\delta_A$ , the annual mortality rate of class A animals, and  $\delta_B$ , the annual mortality rate of class B animals. The parameters are estimated by maximum likelihood, with the likelihood function  $L$  defined as:

$$L = \sum_i \left\{ \sum_{j=1, \dots, I-1} \log \left[ \alpha q_{t_{i,j}t_{i,j+1}}(\text{A}) + (1 - \alpha) q_{t_{i,j}t_{i,j+1}}(\text{B}) \right] + \log \left[ \alpha s_{t_{i,I}}(\text{A}) + (1 - \alpha) s_{t_{i,I}}(\text{B}) \right] \right\}$$

### Abundance estimates

A variety of approaches were used to estimate abundance, incorporating Peterson estimators, Jolly–Seber models, and general models estimated by maximum likelihood. The general models all condition on the first identification of each individual and assumes that the overall identification rate in each year is  $n_j / N_j$ , the number of animals identified in that year divided by the estimated population size in that year, but

where individual  $i$  has an identification history  $t_{i,1}, t_{i,2}, \dots, t_{i,I}$  over  $J$  sampling periods,  $t_1 \dots t_J$ ,  $q_{jk}(\text{A})$  is the probability that an individual of class A identified in the  $j$ th sampling period is next identified in sample  $k$ , and  $s_j(\text{A})$  is the probability that an individual of class A identified in the  $j$ th sampling period is *not* identified again (for full details see Appendix A of Whitehead and Wimmer, 2005). Models assuming no trend in numbers were fitted by

fixing  $r = 0$ , models assuming no heterogeneity at all by fixing  $\alpha = 1$ , with heterogeneity in mortality only by fixing  $\beta = 1$ , with heterogeneity in identifiability only by setting  $\delta_A = \delta_B$ , and assuming a closed population by setting  $\delta_A = \delta_B = 0$  and  $r = 0$ . Note that in these analyses, the mortality term also accounts for mark change and emigration given that these causes for an animal to be 'lost' are not explicitly modelled, so parameter estimates for this term cannot be directly interpreted in terms of individuals dying. Note also that the models estimate the population size in the middle of the study period (i.e. 1999). Where possible, precision was assessed with bootstrap confidence intervals.

Uncertainty about whether samples from the northern and southern portions of the study area should be analysed as separate or unified populations was addressed by producing separate abundance estimates from identifications collected in the eastern and western portions, as well as estimates derived from the combined data set treated as a single population. In the combined analyses, both the full data set and a restricted data set that included only data collected in the period 2000–2008 (this comprised 93% of the full data set, and excluded years in which effort was low) were analysed to address the effect of uneven temporal distribution of effort. Finally, bias in the

estimates was estimated using a parametric bootstrapping procedure where 1000 data sets were produced by simulating populations with the parameters estimated from that model fitted to combined data sets with the lowest AIC and sampling from them following the sampling schedule realized for the observed data set. The bias in the estimate was then taken to be the ratio between the observed population estimates and the mean of the population estimates from the 1000 bootstrapped simulations. SOCPROG v2.4 software (Whitehead, 2009) was used to fit models without heterogeneity and custom written Matlab code to fit models with heterogeneity.

## RESULTS

The final data set contained 507 identifications of 180 individuals in the period between 2 October 1990 and 4 October 2008 (Figure 1). Effort was highly skewed toward the second half of this period, with 473 (93%) of the identifications made in the years 2000–2008 (Table 1). Discovery curves by identification and by time suggested that rates of identifying new individuals did not drop off over time (Figure 2), so all of the results that follow should be treated with caution in the knowledge that the population was unlikely to have been fully sampled.

Table 1. Capture–recapture matrix

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008
1990	1																		
1991	0	3																	
1992	0	0	0																
1993	0	0	0	1															
1994	0	0	0	0	0														
1995	0	0	0	0	0	2													
1996	0	0	0	0	0	0	4												
1997	0	0	0	0	0	0	1	3											
1998	0	0	0	0	0	0	0	1	2										
1999	0	0	0	0	0	0	0	0	0	5									
2000	0	0	0	0	0	0	1	1	1	1	11								
2001	0	0	0	0	0	0	0	1	1	0	3	14							
2002	0	1	0	0	0	0	2	0	0	1	3	3	22						
2003	0	0	0	0	0	0	0	0	0	1	2	1	5	43					
2004	0	0	0	0	0	0	0	1	0	1	2	3	4	3	28				
2005	0	0	0	0	0	0	1	0	0	0	1	0	3	3	1	15			
2006	0	0	0	0	0	0	1	1	0	0	1	2	1	1	1	3	20		
2007	0	0	0	0	0	0	1	0	0	1	2	0	4	5	4	2	4	39	
2008	0	0	0	0	0	0	0	0	0	1	2	3	3	4	4	2	5	6	37

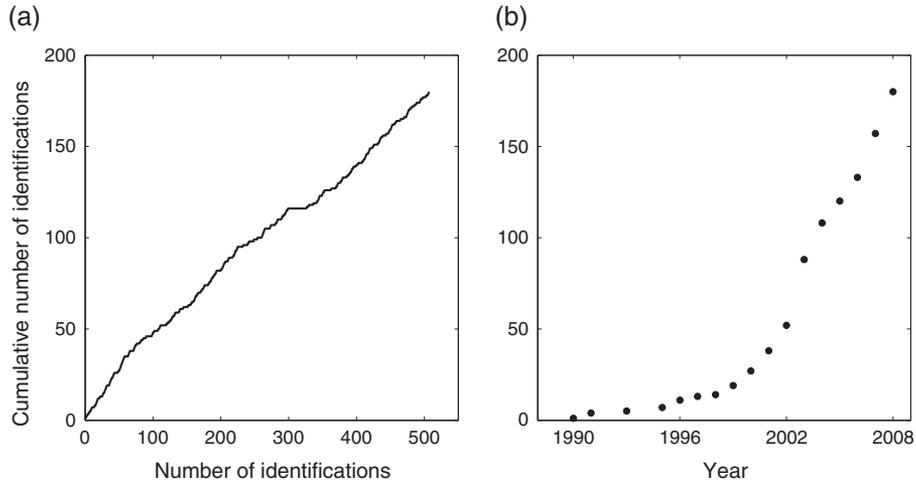


Figure 2. Discovery curves by (a) number of identifications and (b) year of study.

**Analysis of movements**

There were several re-sightings of individuals across the two geographic clusters of identification effort (Figure 3). In all, 37 (21%) of the individuals were re-sighted with at least 1 year between the first and last sightings, and of these, six (16%) were sighted in both areas. The analysis of continuous movement showed diffusion rates (a quantification of the rate a population spreads spatially) dropping to zero over time scales >1 year (Figure 4(a)) and displacements stabilizing at 400–600 km over similar time-scales

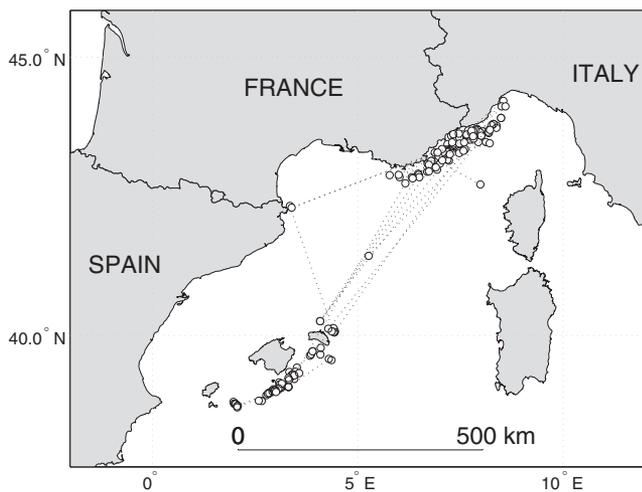


Figure 3. Movements of whales sighted in more than 1 year. Sighting locations are marked with  $\circ$ , and dashed lines link identifications of the same individual.

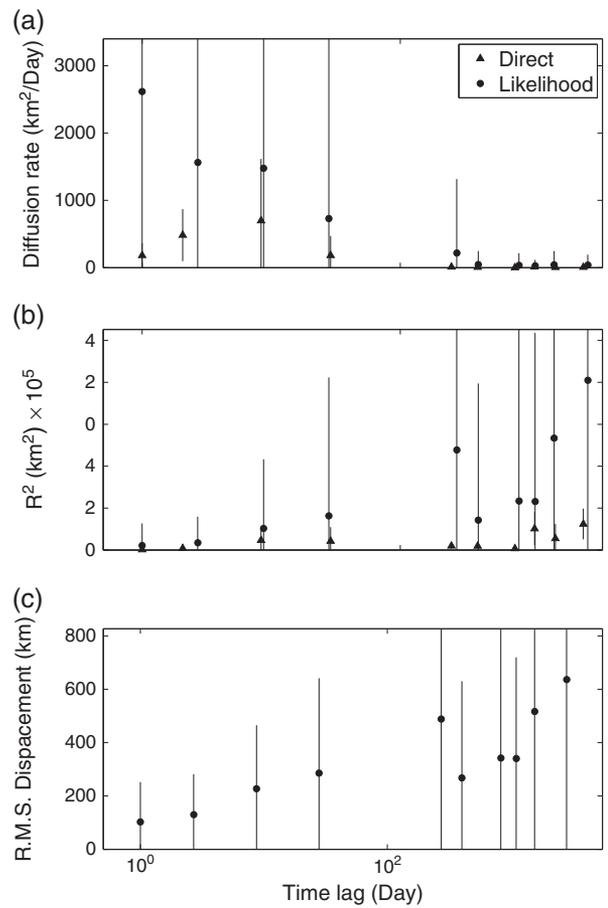


Figure 4. Movement in continuous space. Plots are of diffusion rate (a), displacement estimates (b), and root-mean-square displacement estimates (c) over increasing time-lags. Error bars show jackknife standard errors.

(Figure 4(b)), indicating home range sizes in the order of 1000 km across, very similar to estimates derived for sperm whales in the Pacific. Noting that maximum straight-line distance between any pair of identification locations reported here is 970 km, these results suggest that individuals use the entire western basin (see also Carpinelli *et al.*, 2014). The lagged identification rate analysis across areas supported this qualitative assessment in that there were non-zero probabilities of re-identification in different areas over time lags ranging up to >9 years (Figure 5), but also indicated that the probability of an individual being re-sighted in an area different from its first sighting was lower than the probability of being re-sighted in the same area, suggesting some restriction of movement between the two areas. Overall, it seems reasonable to

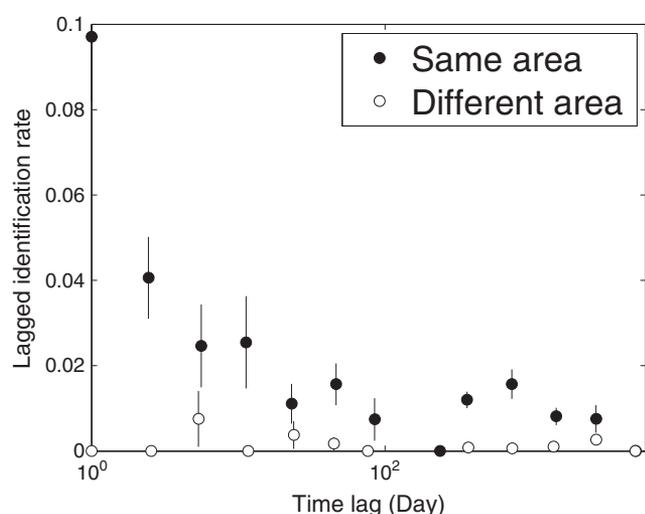


Figure 5. Lagged identification rates between areas. Error bars show jackknife standard errors.

suggest on the basis of these data that the sperm whales present in the western Mediterranean basin represent a single population, albeit with imperfect mixing in that the lagged identification rates within the same area are higher than those across areas (Figure 4).

### Abundance estimates

When analysed as a single population, no upper confidence bound for the abundance estimate for any method exceeded 400 individuals, although there was considerable variance among estimating methods (Table 2). For both the full and restricted data sets, the model convincingly preferred by AIC was that incorporating heterogeneity in identifiability, with very similar population estimates of 231 (95% C.I. 164–363) and 232 (150–373) for full data set and restricted data sets, respectively (Table 2). Heterogeneity in mark–recapture models typically leads to estimates that are biased low, and when bootstrap simulations of populations with these parameters were sampled as described in the Methods, this proved to be the case with bias estimates of 0.63 (95% C.I. 0.51–0.84) and 0.59 (0.42–0.82) for the full and restricted data sets respectively. Dividing the original population estimates by these bias values, and combining the lower confidence bound of the population estimates with the higher confidence bound of the bias estimates (and vice versa) to construct a conservative confidence range gives final estimates of 365 (194–716) and 396 (183–892) for the full and restricted data sets respectively. Analysing the data as two separate

Table 2. Population estimates – single population. All ranges in parentheses represent 95% bootstrap confidence intervals. Note that estimates are not adjusted for bias – see text for bias-adjusted estimates

Method	Full data set		Restricted data set (2000–2008)	
	Population estimate	AIC	Population estimate	AIC
Peterson	7–254 <sup>a</sup>	-	44–254 <sup>a</sup>	-
Jolly-Seber	12–280 <sup>a</sup>	-	57–227 <sup>a</sup>	-
Model: Closed (Schnabel)	310 (268–391)	473	300 (241–390)	391
Model: Mortality only	157 (110–249)	454	152 (103–235)	377
Model: Mortality with trend	89 (58–185)	451	150 (107–245)	378
Model: Heterogenous mortality	113 (87–154)	441	111 (83–158)	369
Model: Heterogenous identifiability	231 (164–363)	<b>437</b>	232 (150–373)	<b>366</b>

<sup>a</sup>These ranges represent the range of estimates from consecutive pairs of sampling periods. i.e. years.

Table 3. Population estimates – two populations. All ranges in parentheses represent 95% bootstrap confidence intervals. Note that estimates are not adjusted for bias – see text for bias-adjusted estimates

Method	Western population		Eastern population		Summed estimates
	Population estimate	AIC	Population estimate	AIC	
Peterson	5–199 <sup>a</sup>	-	2–144 <sup>a</sup>	-	7–343
Jolly-Seber	19–91 <sup>a</sup>	-	14–138 <sup>a</sup>	-	33–229
Model: Closed (Schnabel)	320 (241–541)	80	162 (135–226)	343	482 (376–767)
Model: Mortality only	184 (52–558)	81	77 (103–235)	317	261 (155–793)
Model: Mortality with trend	50 (0–97)	248	47 (29–111)	316	97 (29–208)
Model: Heterogenous mortality	155 (48–401)	84	66 (48–98)	315	221 (96–499)
Model: Heterogenous identifiability	184 (69–411)	85	112 (76–180)	305	296 (145–591)

<sup>a</sup>These ranges represent the range of estimates from consecutive pairs of sampling periods, i.e. years.

populations gave very similar results (Table 3), although summing the abundance estimates generally gave higher figures than the combined analysis – this is not surprising, given that some of the same individuals would have contributed to both of the geographically restricted analyses.

## DISCUSSION

The primary aim of this study was to provide an abundance estimate for western Mediterranean sperm whales. The analysis shows that photo-identification data collected in the period 1990–2008 is inconsistent with population sizes of greater than 1000 animals or lower than 200, with the best estimates suggesting that the population using the study area numbers around 400. This estimate is a step toward a proper understanding of the conservation status of this population. Analysis of movements also shows that individual sperm whales frequently make movements on a scale consistent with the western Mediterranean basin being occupied by a single, albeit imperfectly mixed, population. Such movements are consistent with data from populations in other regions (Whitehead, 2001; Gero *et al.*, 2007; Whitehead *et al.*, 2008) and with previous studies of movements in this region based on a subset of the data presented here (Drouot-Dulau and Gannier, 2007).

It is important to understand the limitations of these data and the estimates derived from them. Although 21% of the identified individuals were re-sighted on occasions more than 1 year apart, the discovery curves of the photo-identification

records show little sign of the levelling off that one would hope to see for a fully characterized population. This is a result of a combination of incomplete coverage in any of the regions surveyed, especially in the earlier part of the study period, a lack of effort in other regions of the western Mediterranean, and a lack of effort outside the summer months. The geographic and temporal distribution of the sampling was uneven, biased toward areas thought to contain high densities of sperm whales, and toward the most recent part of the study period. While large-scale surveys of the western basin have not suggested the existence of major un-sampled areas of higher density (Boisseau *et al.*, 2010), it is important to highlight the possibility that such areas, which would have been missed in the current study, may exist. If, for example, major areas of concentration were to be discovered between the Balearics and northern Africa, and whales from these areas did not regularly move into the north-west Mediterranean, then this would render the analysis incomplete. Similar considerations also hold for the Tyrrhenian Sea, between Corsica/Sardinia and mainland Italy, in that if sperm whales were present in this area and did not move into and out of the sampling area during the study, then even if their density were low, the Tyrrhenian could hold some hundreds of animals that would not be included in the current estimate.

Despite these caveats, this is the only quantitative abundance estimate for this region that we are aware of, and while its precision and accuracy can certainly be improved upon, it represents an important first assessment. It is largely consistent

with previous expert judgements that the population in the whole Mediterranean may number less than 1000 and our data certainly support the classification of this population as 'Endangered'. If the figure is accurate, then concern about the conservation status of this population is appropriate, especially given the number of animals reported dead on the shores of Spain, Italy and France (Reeves and Notarbartolo di Sciara, 2006; Notarbartolo di Sciara *et al.*, 2012), which is itself probably an underestimate of true mortality levels. It is therefore important that the validity of our estimate be tested, and we hope our results will encourage a much larger and more systematic effort to understand the true size of this isolated population that will also be capable of tracking the effectiveness of any conservation measures taken. Such an effort will, however, take time, and the results by themselves should be sufficient to prompt a more vigorous deployment of conservation measures, particularly with respect to the acute threats of drift-nets and shipping that are major sources of mortality in this population.

#### ACKNOWLEDGEMENTS

Balearics fieldwork was supported by One World Wildlife, and the Whale and Dolphin Conservation Society. We would like to thank all the research assistants, collaborators, volunteers, and skippers who contributed to data collection in the field by Tethys, GREC and the Balearics Sperm Whale Project, and to Marina degli Aregai, Portosole, the CRAM Foundation, and the Balearic Government Office of Fisheries Management for logistical support of the same. We are also grateful to the International Fund of Animal Welfare (IFAW) for the use of the software LOGGER. LR was supported by a NERC postdoctoral fellowship (NER/I/S/2002/00632) and the MASTS pooling initiative (The Marine Alliance for Science and Technology for Scotland) and their support is gratefully acknowledged. MASTS is funded by the Scottish Funding Council (grant reference HR09011) and contributing institutions. We are very grateful to Hal Whitehead and Phil Hammond for statistical advice and discussion of our results.

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