Helminth parasites of the dwarf sperm whale *Kogia* sima (Cetacea: Kogiidae) from the Mediterranean Sea, with implications on host ecology

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ABSTRACT: Limited data exist on the occurrence of the dwarf sperm whale *Kogia sima* in the Mediterranean Sea and its parasite fauna. Here, the occurrence of the anisakid species *Anisakis physeteris* and *A. pegreffii* in the stomach chambers of an adult female dwarf sperm whale, stranded in southern Italy, is reported. In addition, the occurrence of *Phyllobothrium delphini* larvae infecting the blubber of the caudal peduncle region was recorded. *A. physeteris* and *A. pegreffii* represent the 2 parasite species of the genus, mostly distributed in the Mediterranean Sea in fish and squids. The finding of *A. pegreffii* and *A. physeteris* in the dwarf sperm whale represents a new record in this host species for the Mediterranean Sea. The study of gastrointestinal content also revealed a massive presence of cephalopod beaks identified as belonging to pelagic squids including the umbrella squid *Histioteuthis bonnellii*, the reverse jewel squid *H. reversa*, the long-armed squid *Chiroteuthis veranii*, and the comb-finned squid *Ctenopteryx sicula*. The feeding habits of the dwarf sperm whale, as well as the occurrence of these squid residuals in the cetacean host, suggest that these squid species play a major role in maintaining the life cycle of anisakid parasite species and *P. delphini*.

KEY WORDS: Kogia sima · Mediterranean Sea · Anisakis physeteris · Anisakis pegreffii · Phyllobothrium delphini · Squid beaks · Host ecology

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INTRODUCTION

The genus *Kogia* comprises 2 cetacean species, the pygmy sperm whale *Kogia breviceps* de Blainville, 1838 and the dwarf sperm whale *Kogia sima* Owen, 1866, which were not recognized as separate species until the mid 1960s (Taylor et al. 2012). The dwarf sperm whale appears to be distributed widely in off-

shore waters of tropical and warm temperate zones and inhabits shelf-edge and slope waters, where it primarily feeds on deep-water cephalopods (Taylor et al. 2012). In the Mediterranean Sea, the only records of kogiid species in the past are limited to 2 stranded individuals of the dwarf sperm whale, both from Italian waters (Baccetti et al. 1991, Bortolotto et al. 2003). The first refers to a decomposed carcass

found at the Foce Chiarone located between the Latium and Tuscany regions (Tyrrhenian Sea) (Baccetti et al. 1991). The second was a male found on the western coast of Sicily in Eraclea Minoa (Agrigento) (Bortolotto et al. 2003). In both cases, there is no evidence that parasites and/or gastrointestinal content were studied, nor was a genetic analysis of the host performed. Here for the first time, records on the parasites, gastrointestinal food contents, and the genetic identification of a dwarf sperm whale stranded in the Mediterranean Sea in 2017 are presented.

MATERIALS AND METHODS

Sampling

An adult female of Kogia sp., weighing 116 kg and measuring 195 cm in total length, was found stranded on the beach of Trentova (Agropoli) (40° 20′ 56″ N,14° 58′ 29″ E) in the Salerno province of southern Italy on 4 February 2017. The whale was in a decomposition grade code 3 and showed good nutritional status. During necropsy, blubber, heart, blood vessels, trachea, lungs, urinary bladder, liver, gallbladder, kidneys, pancreas, uterus, oesophagus, stomach chamber, and intestine were examined for helminths. Organs and tissues were opened and surfaces examined visually, then washed through a 100 µm mesh screen. The remaining washed material from each organ was examined carefully under a dissecting microscope, and any helminths were collected and rinsed in saline solution. The adult, L4 larval and pre-adult forms of *Anisakis* spp. were identified to the genus level on the basis of morphological characters (Mattiucci et al. 2014, 2018). Anisakid nematodes were counted and stored at -80°C for molecular identification. Cestode larvae were preserved in 70% alcohol before identification under the light microscope following Agustí et al. (2005). Gastrointestinal content was collected in order to examine and identify any remaining prey items. Cephalopod beaks were recovered from stomach and intestine and identified following the methods used by Clarke (1986) and Xavier & Cherel (2009).

Samples for histological examination of all organs and tissues examined for parasites were fixed in 10% neutral phosphate-buffered formalin and processed by routine methods into paraffin blocks, which were cut into 3μ m thick sections and stained with hematoxylin and eosin. Because dolphin morbillivirus infection (DMV) represents a common cause of ceta-

cean stranding along the Mediterranean coasts (Centelleghe et al. 2017), a brain sample was examined for DMV by RT-PCR restriction fragment length polymorphism (RFLP) according to the methodology used in Verna et al. (2017).

Host identification

The cetacean was identified to species using the morphometric keys provided by Barros & Duffield (2003) and McAlpine (2009). DNA sequence analysis on a tissue sample of the cetacean was used to confirm the morphological identification. Total genomic DNA was extracted from approximately 25 mg of muscle with a NucleoSpin® Tissue kit (Machery-Nagel, Düren, Germany) following the manufacturer's recommendations. A ~700 bp fragment was amplified from the cytochrome b gene (cytb), one of the most commonly used markers for DNA-based species identification in cetaceans (Viricel & Rosel 2012), using primer pairs L14724 and H15387 (Palumbi et al. 2002). PCR reactions were carried out in 50 µl volumes using the following conditions: initial denaturation at 95°C for 5 min followed by 34 cycles of 95°C for 60 s, 49°C for 60 s, and 72°C for 60 s, followed by a final extension of 72°C for 7 min. A negative control (template-free PCR reactions) was used to test for contamination. PCR products were checked by agarose gel electrophoresis and purified using a High Pure PCR Product Purification Kit (Roche Diagnostic).

Sequence reactions were obtained with the BigDye Terminator Cycle Sequencing technology (Applied Biosystems), purified in automation using the Agencourt CleanSEQ Dye terminator removal kit (Agencourt Bioscience Corporation), and a robotic station Biomek FX (Beckman Coulter). Products were analyzed on an Automated Capillary Electrophoresis Sequencer 3730 DNA Analyzer (Applied Biosystems, ThermoFisher Scientific). Forward and reverse chromatograms were analysed and assembled using the software package SeqManII (DNASTAR). The resulting sequence was used to perform a BLAST® search (Altschul et al. 1990) in the GenBank database (www.ncbi.nlm.nih.gov/blast/).

Genetic/molecular identification of Anisakis spp.

A total of 108 *Anisakis* spp. specimens were identified to the species level by a multi-marker genotyping approach. The length of each frozen nema-

tode was first measured; cephalic and caudal ends were preserved in 70% alcohol, while a portion of tissue of the nematode was used to perform genetic/molecular identification. The last included both nuclear and mitochondrial markers: i.e. 3 diagnostic allozyme loci (Mattiucci et al. 2009), DNA sequences analysis of mitochondrial (mtDNA cytochrome C oxidase subunit II [cox2], 629 bp) (Mattiucci et al. 2014) and nuclear (elongation factor EF1 α-1 of nDNA, 409 bp) genes (Mattiucci et al. 2016). The EF1 α -1 of nDNA was analysed as a further nuclear marker to detect the possible occurrence of hybrid genotypes between A. pegreffii and A. simplex (s.s.), as indicated in Mattiucci et al. (2016). The diagnostic allozyme loci (Adk-2, Pep C-1, and Pep C-2) were analysed, according to established procedures (see Mattiucci et al. 2001), on 108 Anisakis spp. specimens.

The total DNA was extracted using the QuickgDNA MiniPrep (column format) by Zymo Research from 2 mg of homogenized tissue from each nematode following the manufacturer's protocol (Levsen et al. 2018). The mitochondrial cox2 gene was amplified using the primers 211F (5'-TTT TCT AGT TAT ATA GAT TGR TTY AT-3') and 210R (5'-CAC CAA CTC TTA AAA TTA TC-3') (Mattiucci et al. 2014). PCR was carried out according to the previously described procedures (Mattiucci et al. 2014). The sequences obtained at the mtDNA *cox2* locus for the sequenced nematodes were compared with those in GenBank: A. simplex (s.s.) (DQ116426), A. pegreffii (DQ116428), A. berlandi (KC809999), A. typica (DQ116427), A. ziphidarum (DQ116430), A. nascettii (FJ685642), A. physeteris (DQ116432), A. brevispiculata (DQ116433), and A. paggiae (DQ116434).

The EF1 α -1 nuclear gene was amplified using the primers EF-F (5'-TCC TCA AGC GTT GTT ATC TGT T-3') and EF-R (5'-AGT TTT GCC ACT AGC GGT TCC-3') (Mattiucci et al. 2016). The PCR procedures followed those reported in Mattiucci et al. (2016). In particular, because the primers at that locus are to date only available for species of the *A. simplex* (s.l.) complex, the sequencing of the EF1 α -1 gene of the nDNA was carried out on only those 18 specimens of *A. pegreffii* previosuly identified based on the allozyme diagnostic loci and mtDNA cox2 locus (see 'Results'). The sequences obtained at the EF1 α -1 locus were then compared at the diagnostic positions (i.e. 186 and 286) with those previously analysed and deposited in GenBank (Mattiucci et al. 2016).

A Bayesian inference (BI) tree, inferred from the mtDNA *cox2* gene sequences obtained, was built in relation to the *cox2* gene sequences previously se-

quenced at the same locus from other *Anisakis* spp. The analysis was performed using MrBayes 3.1 (Huelsenbeck & Ronquist 2005) with the TRN+I+G substitution model as implemented in jModelTest 2.1 (Darriba et al. 2012). The parameters for the selected model were I = 0.487 and G = 0.783, chosen with Akaike's information criterion (AIC) (Posada & Buckley 2004). For the Bayesian analysis, 4 incrementally heated Markov Chains (using default heating values) were run for 1000000 generations, sampling the Markov Chains at intervals of 100 generations. The burninfrac was fixed at 0.25. Posterior probabilities were estimated and used to assess support for each branch in the inferred phylogeny, where p = 95% is indicative of significant support (Reeder 1995); Toxocara canis and Ascaris suum were used as outgroups.

RESULTS

Sampling

A total of 1348 anisakid specimens were collected from the stomach chambers (Fig. 1). The adult anisakid specimens were first assigned morphologically to the genus Anisakis; some nematodes were L4 or pre-adult stages, with a mean (\pm SD) length of 19.5 \pm 5.6 (range: 10.0–32.0) mm. A total of 43 cestode larvae (merocercoid) found in the blubber of the caudal peduncle region were morphologically identified as $Phyllobothrium\ delphini$.

More than 100 cephalopod beaks were recovered from the whale's stomach (Fig. 1) and intestine, but just 15 of them were sufficiently well preserved for species identification. Beaks were identified as belonging to 4 species of pelagic squid including the umbrella squid Histioteuthis bonnellii (N = 4), the reverse jewel squid H. reversa (N = 9), the longarmed squid Chiroteuthis veranii (N = 1), and the comb-finned squid Ctenopteryx sicula (N = 1). Mediterranean seagrass *Posidonia oceanica* was also found in the stomach chambers (Fig. 1). No significant gross or microscopic pathological findings were seen in the carcass or sectioned tissues. No obvious specific cause of death was noticed. Results of the RT-PCR RFLP analysis of the brain for detection of DMV infection were negative.

Host identification

The provisional identification of the stranded cetacean as a dwarf sperm whale using morphologi-



Fig. 1. Stomach of the dwarf sperm whale *Kogia sima* showing numerous *Anisakis* spp. individuals (a) and squid beaks (b). Remains of Mediterranean sea grass *Posidonia oceanica* (c) are also visible

cal diagnostic features was confirmed by the DNA sequencing approach. BLAST analysis of the *cytb* sequence obtained (accession number: MG252607) provided the highest match of 100% over 596 bp to *Kogia sima* voucher SEFSC (accession number: EU517708).

Genetic/molecular identification of Anisakis spp.

Of the 108 *Anisakis* spp. specimens, 18 (16.6%) (all L4 or pre-adult stages) were genetically identified as *A. pegreffii* according to the alleles observed at the diagnostic loci, i.e. $Adk-2^{100}$, $Pep\ C-1^{100}$, and $Pep\ C-2^{100}$; while, based on the genotypes observed at the same loci, i.e. $Adk-2^{97}$, $Pep\ C-1^{110}$, and $Pep\ C-2^{108}$, 90 specimens (83.3%) (all adult stages) were identified as belonging to the species *A. physeteris*.

Additionally, the mtDNA cox2 sequences of those 90 specimens identified as A. physeteris by allozyme loci matched, 100 or 99% those sequences available in GenBank for that parasite species, at the same locus. Analogously, the 18 mtDNA cox2 sequences of those individuals identified by allozyme loci as A. pegreffii were a 100% match of A. pegreffii sequences, previously deposited in GenBank. Eight sequences of mtDNA cox2 were deposited in GenBank with the accession numbers: MG076944, MG076945, MG076946, MG076947 for A. pegreffii;

and MG076948, MG076949, MG076 950, MG076951 for *A. physeteris*.

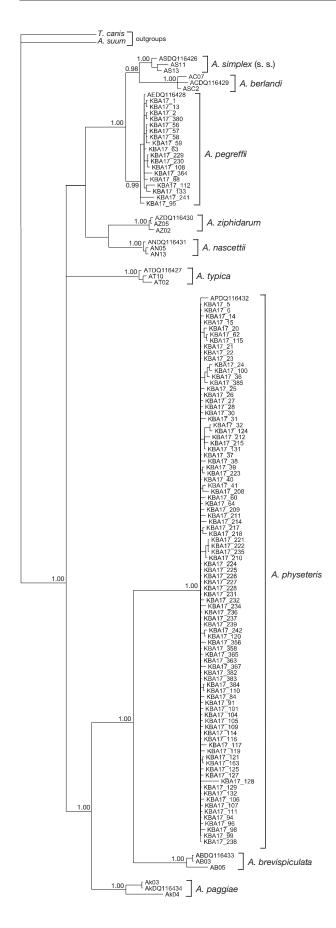
Finally, the 18 *Anisakis* spp. specimens identified as *A. pegreffii* by allozyme diagnostic loci and mtDNA cox2 were also sequenced at a further nuclear locus, i.e. the partial sequence of the EF1 α -1 gene that confirmed the homozygote genotypes of *A. pegreffii*. The 4 EF1 α -1 of nDNA gene sequences we obtained from *A. pegreffii* were deposited in GenBank (accession numbers: MG076940, MG0 76941, MG076942, MG076943).

Phylogenetic analysis inferred from BI (Fig. 2) showed that the 90 *A. physeteris* sequences and the 18 sequences of *A. pegreffii* obtained here clustered in 2 distinct and well supported phylogenetic clades, also including the previously deposited sequences of these species (Fig. 2).

DISCUSSION

This is the first parasitological study of a dwarf sperm whale stranded in the Mediterranean Sea. To date, 9 species belonging to the genus Anisakis have been identified worldwide. These species possess distinct gene pools and are reproductively isolated, as demonstrated by means of nuclear markers (allozyme data) (see Mattucci et al. 2018). The existence of 9 species as distinct phylogenetic units has been demonstrated by various phylogenetic analyses, as inferred from both nuclear and mitochondrial genes (Mattiucci & Nascetti 2008, Cavallero et al. 2011, Mattiucci et al. 2014, 2018). The nuclear and mitochondrial genetic/molecular markers used in the present study allowed the identification of the 2 species A. physeteris and A. pegreffii from the dwarf sperm whale.

Previous reports on the detection of *Anisakis* spp. in the dwarf sperm whale are scattered throughout its host range. By means of genetic/molecular tools, the dwarf sperm whale has been indeed recognized, outside the Mediterranean basin, as the main host of *A. brevispiculata* and *A. paggiae* (Mattiucci et al. 2005, 2018, Mattiucci & Nascetti 2008); while, occasionally, adult specimens of *A. typica*, *A. physeteris*, *A. ziphidarum* (Cavallero et al. 2011, Klimpel & Palm 2011, Quiazon et al. 2013, Kuhn et al. 2016, Di Azevedo et



al. 2017), and L4 of *A. berlandi* (Shamsi et al. 2012) were also identified. For instance, *A. physeteris* in the dwarf sperm whale has been reported from the Atlantic coast of the USA (Cavallero et al. 2011). Thus, the finding of *A. pegreffii* and *A. physeteris* in this cetacean is a new host record for the Mediterranean Sea.

Knowledge concerning cetacean distribution and ecology in the Mediterranean Sea is limited. Therefore, any information on a cetacean species, including its parasite fauna, may help elucidate its ecology. Identification of anisakid species from a given host provides useful insights into the geographical distribution, definitive host preference and life cycles of genetically identified species of the genus Anisakis (Mattiucci & Nascetti 2008, Mattiucci et al. 2009, 2014). Indeed, the life cycles of Anisakis spp. involve crustaceans, fish, and squid as intermediate/ paratenic hosts and marine mammals as definitive hosts (Mattiucci & Nascetti 2008, Klimpel & Palm 2011). Sea turtles and birds are also reported as accidental hosts, being infected when ingesting fish hosts harbouring larval stages of Anisakis spp. (Santoro et al. 2010a,b, Shamsi et al. 2017). A host-parasite association likely resulting from co-evolutionary processes between the parasite A. physeteris and its main host, the sperm whale *Physeter macrocephalus*, has been previously suggested (Mattiucci & Nascetti 2008). Also, a host-parasite association between the sperm whales of the family Kogiidae (i.e. Kogia breviceps and K. sima) and the other 2 species of the A. physeteris (s.l.) complex (i.e. A. brevispiculata and A. paggiae) has been postulated (Mattiucci & Nascetti 2008). In the Mediterranean Sea, several hundred A. physeteris have been observed in a few stranded sperm whales P. macrocephalus (Mazzariol et al. 2011, Mattiucci et al. 2018), whose gastric contents also included several hundreds of cephalopod beaks belonging to the same squid species identified in the present study. Additionally, A. physeteris, like other larval type II Anisakis species of the 'physeteris clade', may use squids rather than fishes as primary intermediate/paratenic hosts (Mattiucci & Nascetti 2008, Mattiucci et al. 2018). Angelucci et al. (2011) found a mixed infection of A. pegreiffii and Anisakis type II larvae (presumably A. physeteris) in the flying squid Todarodes sagittatus in the waters off Sardinia,

Fig. 2. Bayesian inference tree based on mtDNA cox2 gene sequences of A. physeteris and A. pegreffii collected from dwarf sperm whale, shown in relation to other known Anisakis spp. sequences

Mediterranean Sea. *Anisakis* type II larvae, in mixed infection with type I larvae, were also found in the Humboldt squid Dosidicus gigas off the Chilean coast (Pardo-Gandarillas et al. 2009) and in some Argentine shortfin squid Illex argentinus samples from Falkland waters (P. Cipriani unpubl. data). Therefore, the finding of adult A. physeteris in a dwarf sperm whale suggests that this nematode species is adapted to host species belonging to the Physeteroidea clade. As the ecology of the dwarf sperm whale in the Mediterranean Sea is similar to that of the sperm whale, infection with A. physeteris may have been acquired by preying upon those squid species (Spitz et al. 2011) that occur in the deeper water layers of the southern Tyrrhenian Sea, as well as in other basin waters of the Mediterranean Sea (Bello 2008, Romeo et al. 2012). Further, in 2 sperm whales stranded in successive events during 2011 and 2013 along the Adriatic coast (Mazzariol et al. 2011, S. Mattiucci & P. Cipriani unpubl. data), several hundred A. physeteris was found and, interestingly, also a very high number of beaks belonging to the same squid species as those identified in the present study (S. Mattiucci & P. Cipriani unpubl. data). The presence of 4 pelagic squid species (umbrella, reverse jewel, long-armed, and comb-finned squids) identified on the basis of their beak morphology, together with a massive presence of Anisakis spp. specimens, suggests that these cephalopod species play a role in transmitting the nematodes to the dwarf sperm whale. To date, the recognized intermediate/paratenic squid hosts included only the lesser flying squid Todaropsis eblanae, the Angolan flying squid Todarodes angolensis, the flying squid, and the southern shortfin squid *Illex coindettii* for A. pegreffii; and the umbrella squid, the Humboldt squid, the southern shortfin squid, the flying squid, and the angel squid Ancistroteuthis lichtensteinii for A. physeteris (Mattiucci et al. 2018).

A. pegreffii is the dominant species of its genus in the Mediterranean Sea, being widespread in several pelagic and demersal fish and rarely found in squid species (Mattiucci & Nascetti 2008, Anastasio et al. 2016, Cipriani et al. 2018a,b). In Atlantic waters, the northern limit of its geographical range is the Spanish–Portuguese border (Mattiucci & Nascetti 2008, Klimpel & Palm 2011, Kuhn et al. 2016). Infection by A. pegreffii may have been acquired by the dwarf sperm whale through consumption of squid species or fish species such as the Atlantic horse mackerel Trachurus trachurus or the European hake Merluccius merluccius, which are infected by this parasite in the Mediterranean Sea (Spitz et al. 2011, Mladineo &

Poljak 2014, Blažeković et al. 2015, Cipriani et al. 2018b, Levsen et al. 2018).

The presence of A. pegreffii in the stomach chambers of the dwarf sperm whale in our study, and the absence of A. simplex (s.s.), whose geographical range is mostly in Atlantic waters, suggests that the dwarf sperm whale had recently been feeding in the Mediterranean Sea. However, the possibility that some of the food remains found in the stomach came from species consumed in Atlantic waters cannot be completely excluded. All the identified specimens of A. pegreffii were at L4 or pre-adult stage with a mean length of 19.5 (10.0-32.0) mm, much smaller than the 41.6 (33.0–55.0) mm described for the adult stage of A. pegreffii (Mattiucci et al. 2014, 2018). This finding could be explained as a recent infection of the cetacean before it stranded. Alternatively, kogiids may be an unsuitable host for the full development of A. pegreffii into the adult reproductive stage, as adult A. pegreffii have only been found in oceanic dolphins and baleen whales (Mattiucci et al. 2018), likely a result of host-parasite co-adaptation and coevolutionary processes (Mattiucci & Nascetti 2008, Mattiucci et al. 2018).

Furthermore, taking into account that cephalopod species are considered as the second intermediate host of *Phyllobothrium delphini*, our data suggest that the recovered squid species from the dwarf sperm whale could also play a role in the life cycle and transmission of this parasite in the Mediterranean Sea. P. delphini merocercoids are common in offshore cetaceans feeding on fish and/or cephalopods (Aznar et al. 2007). Although the life cycle of P. delphini has not yet been elucidated, marine mammals may act as intermediate host for this parasite, and large predatory and/or scavenger pelagic sharks are the most likely definitive host (Agustí et al. 2005, Aznar et al. 2007). Since tetraphyllideans are usually found at the plerocercoid stage in fish, cephalopods, and other marine invertebrates, and since dwarf sperm whales feed intensively on cephalopods, it is plausible that the P. delphini infection was acquired by the consumption of squid prey.

In conclusion, the species of anisakids found in this study, together with previous stranding events of dwarf sperm whales in the Mediterranean Sea, suggest the existence of a dwarf sperm whale population in this basin. Also, we conclude that *A. physeteris* maintains its life cycle in the Mediterranean Sea by using both physeteroid species as hosts, i.e. the sperm whale (Mazzariol et al. 2011, Mattiucci et al. 2018, S. Mattiucci & P. Cipriani unpubl. data) and the dwarf sperm whale (present study). Further, the mas-

sive presence of *A. physeteris* in this dwarf whale, similar to that previously observed in stranded sperm whales (Mazzariol et al. 2011, Mattiucci et al. 2018, S. Mattiucci & P. Cipriani unpubl. data), coupled with the massive accumulation of squid beaks in the stomach of these cetacean hosts, suggests that the life cycle of the parasite is well established and maintained in the Mediterranean Sea. Thus, the occurrence of *A. physeteris* could be used as an ecological indicator to monitor the stability of trophic webs, which include the above-mentioned physeteriids and squid species, in the Mediterranean Sea ecosystem (Mattiucci & Nascetti 2008).

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