Antibiotic-Resistant in Sea Turtles

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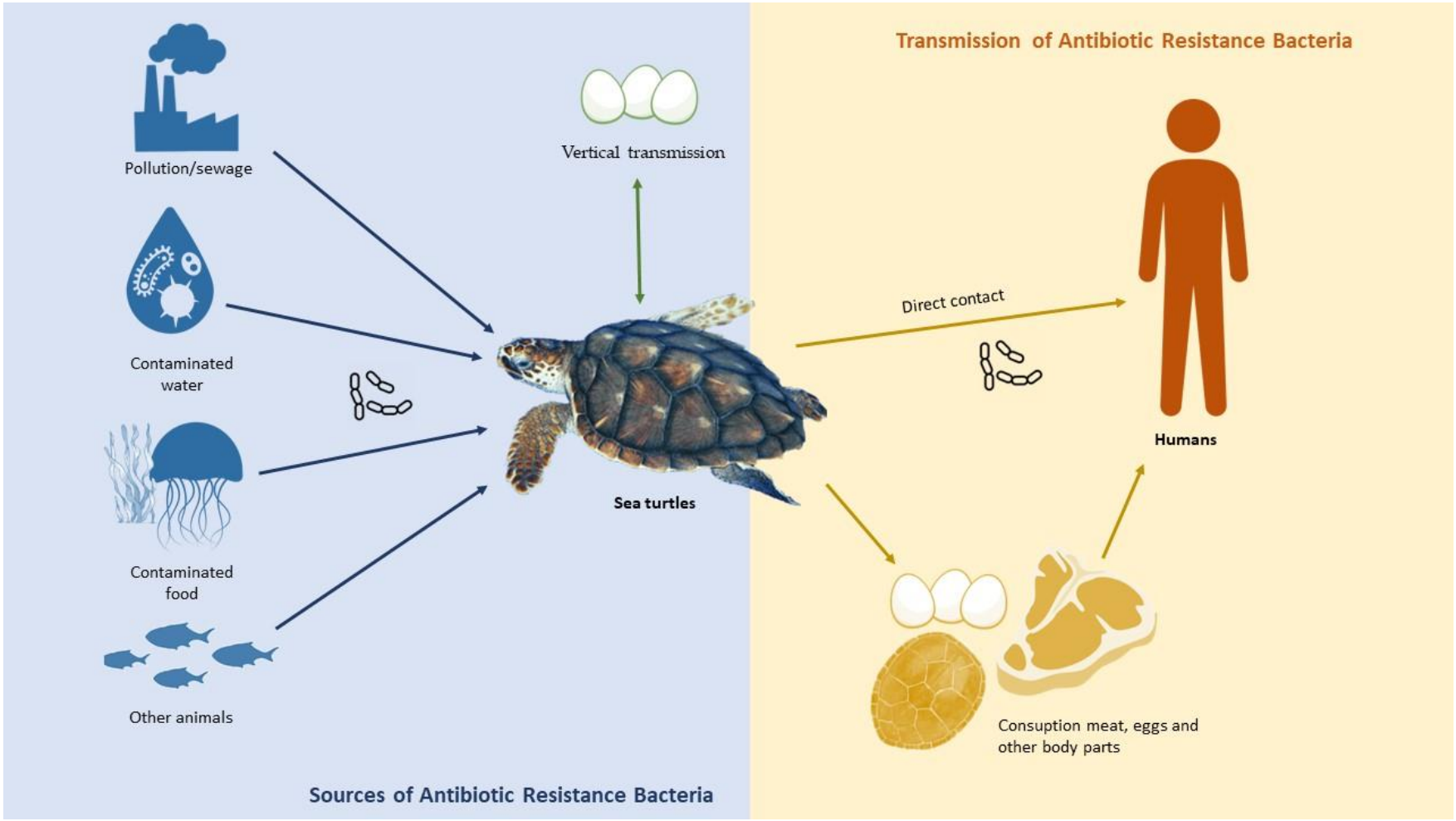
INTRODUCTION

Antibiotic-resistant bacteria (AMR) are spreading in the environment at an alarming rate, becoming one of the most significant concerns in the XXI century. Currently, it is pretty common to find antibiotic-resistance genes in the environment and in animals that have never experienced antibiotic treatment. AMR is associated with the overuse and misuse of antibiotics in human and veterinary medicine, and their uncontrolled release into waste in many parts of the world. AMR may occur due to genetic mutations or horizontal transfer of resistance genes. Horizontal transfer can even occur between non-phylogenetically related bacteria.

Although in aquatic environments the bacterial concentrations are low in comparison to the soil, marine animals which are completely immersed in this environment can be bioindicators, reservoirs and spreaders of AMR. AMR can be an index of marine pollution, that can be used to detect antimicrobial pollution in marine environments. Sea turtles play a vital role in maintaining the health of marine ecosystems. These animals have been proposed as sentinel species to determine pollution levels in marine environments.

The present study aims to present antibiotic resistance and resistance genes in sea turtles and determine how they can impact the ecosystem and human health under the One health concept.

SEA TURTLE'S DISPERSION AND CONTAMINATION SOURCE OF PATHOGENIC BACTERIA



Transmission routes of antibiotic resistance bacteria in sea turtles.

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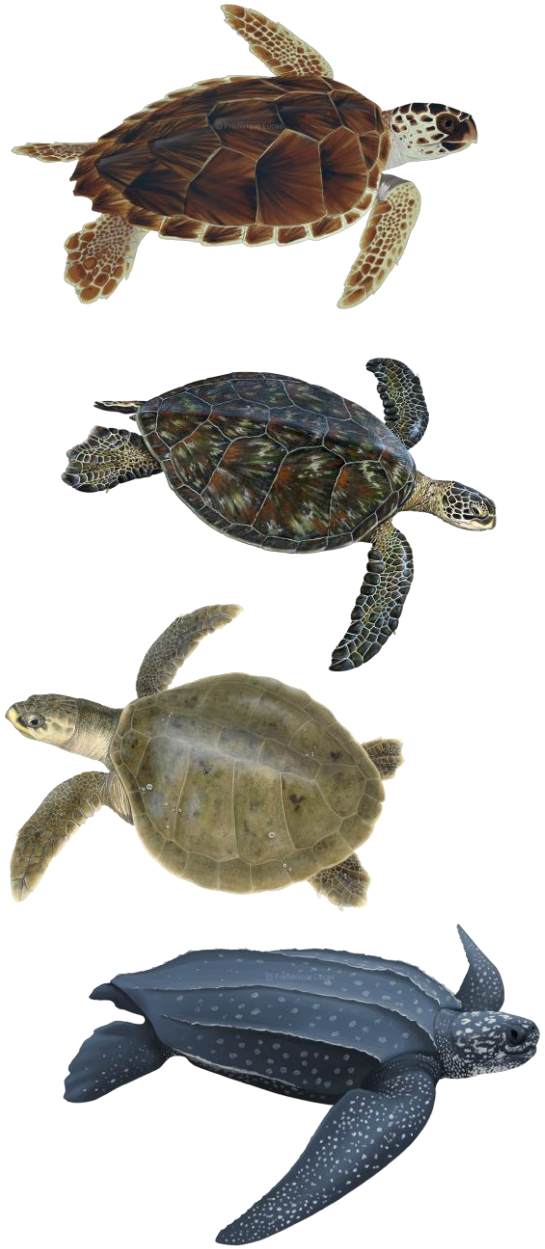
47.4 % (9/19) were performed in *Caretta caretta*, 21% (4/19*) Chelonia mydas*, 5.3 % (1/19) *Lepidochelys olivacea*, 5.3 % (1/18) *Dermochelys coriacea*.

The studies were carried out in different locations around the globe including The Gulf of Oman and the Arabian Sea, the Great Barrier Reef, Taiwan, the Gulf of California, the Pacific Ocean, the Adriatic Sea, Italy, the Mediterranean, 'Brail, the Gulf of Guinthea, St. Kitts, West Indies

Bacteria isolated were mostly Enterobacteriaceae. Regarding antibiotic resistance, the majority was observed in the classes of penicillins, tetracyclines, phenicol quinolones, and cephalosporins.



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					metschnikovii, *V. fluvialis*, *Citrobacter freundii*, *Pseudomonas aeruginosa*, *P. putida*, *P. putrefaciens*, *Acinetobacter calcoaceticus*, *Morganella morganii*, *Proteus vulgaris*, *Enterobacter cloacae*, *Alcaligenes faecalis*, *Klebsiella oxythoca*	Pradofloxacin (82.5%), Cefotaxime (77.5%), Ceftazidime (70%), Danofloxacin (77.5%), Cefuroxime (72.5%), Moxifloxacin (67.5%), Ciprofloxacin (67.5%), Aztreonam (60%), Enrofloxacin (60%), Tetracycline (58%), Trimethoprim-sulphamethoxazole (50%), Doxycycline, (47.5%)	CTX+AmpC, bla_{ACT-2}+$TEM-236$+$SHV-12$, $bla_{CTX-M-3}$+$ACT-24$+$TEM-236$	
	Mediterranean	35	2015-2016	Oral and cloacal	*Morganella morganii*, *Citrobacter spp.*, *Proteus spp.*, *Pseudomonas aeruginosa*	Penicillins, tetracyclines, phenicols, quinolones, cephalosporins	-	(Pace et al., 2019)
	Italy	107	2016-2020	Spleen	*Salmonella enteritidis*	-	bla_{TEM} tet(D), tet(E) sulI	(Gambino et al., 2022)
	South Tyrrhenian sea, Ionian Sea	14	2006-2007	Oral and cloacal	*Citrobacter spp.*, *Proteus spp.*, *Enterobacter spp.*, *Escherichia spp.*, *Providencia spp.*, *Morganella spp.*, *Pantoea spp.*, *Pseudomonas spp.*, *Shewanella spp.*	carbenicillin (100%), cephalothin (92.6%), oxytetracycline (81.3%), amoxicillin (77.8%), colistin (72.0%), tetracycline (64.9), ampicillin (63.6%) ticarcillin–clavulanic acid (52.9%), lomefloxacine (51.9%).	-	(Foti et al., 2009)

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						(46.8%,), doxycycline (46.1%,)		
	Taiwan	28	2018-2020	Cloacal and nasal s	*Vibrio* spp.	Penicillin (74.47%), spiramycin, amoxicillin, and cephalexin		(Tsai et al., 2021)
	Gulf of Oman in the Arabian Sea	20	2015	Albumen and yolk	*Citrobacter spp.*, *Aeromonas spp.*, *Pseudomonas spp.*	Amicacyn, Trimethoprim-sulfamethoxazole, gentamicin, Ampicillin	-	(Al-Musharafi et al., 2015)
Chelonia mydas agassizii, *Lepidochely olivacea*	Gulf of California, Pacific Ocean	420	2012	Nasopharyngeal and cloacal	*Vibrio alginolyticus* (60%), *V. parahaemolyticus* (26%), *V. cholerae* (9%).	Ampicillin	29.4% tdh+ gene, 11.7% tdh+ and toxRS/new+, 100% non-O1/non-O139, 66% gene ace	(Zavala-Norzagaray et al., 2015)
Lepidochelys olivacea	Taiwan	1	2019	Abcess	*E. faecalis*	Doxycycline, enrofloxacin, erythromycin, neomycin, oxytetracycline, gentamicin, amikacin, ciprofloxacin, spiramycin, chloramphenicol, ceftiofur, azithromycin	gene tet(M)	(Tsai et al., 2019)
Caretta caretta ¶	Adriatic Sea	200	2018-2021	Oral, cloacal samples, skin wounds, biopsy	*E. coli*, *Serratia spp.*, *Moraxella spp.*, *Kluyvera spp.*, *Salmonella spp.*, *Acinetobacter spp.*, *Enterobacter spp.*, *Klebsiella spp.*, *Morganella spp.*	Ampicillin, amoxicillin + clavulanic acid, ceftazidime, cefuroxime, gentamicin, doxycycline, ciprofloxacin, enrofloxacin	- →	(Trotta et al., 2021b)
	Italy	52	2016-2019	Clinical samples	*Aeromonas hydrophila*, *Vibrio vulnificus*, *V. alginolyticus*, *V.*	Ampicillin (97.5%), Amoxicillin + Clavulanic acid (90%), Cephalexin (90%),	bla_{ACT-24}, bla_{ACT-2}, bla_{ACT-17}, bla_{DHA-4}, bla_{CMY37},	(Trotta et al., 2021a)

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	Island of Maio	33	2021	Cloacal (oviductal fluid), oral, and egg content	*Shewanella putrefaciens, Morganella morganii, Vibrio alginolyticus, Enterobacter cloacae, Aeromonas hydrophila/caviae, Brevundimonas vesicularis, Burkholderia cepacia, and Citrobacter spp.*	Imipenem, Enrofloxacin, Tetracycline, Piperacillin	-	(Fernandes et al., 2021)
	Italy	1	2021	Organs	*Listeria monocytogenes*	Fosfomycin, quinolones, sulfamethoxazole, oxacillin, and cephalosporins	fosX, lin, mprF, norB, sul	(Di Renzo et al., 2022)
	Mediterranean	33	2014	Cloacal	*Enterobacteriaceae (59%), Shewanellaceae (31%), Vibrionaceae families (5%)*	ampicillin (70%), sulfamethoxazole/trimethoprim (30%), tetracycline, ciprofloxacin, chloramphenicol, kanamycin, streptomycin, nalidixic acid	-	(Blasi et al., 2020)
Eretmochelys imbricata, Chelonia mydas	Brazil	17	2012-2014	Faecal samples	*Enterococcus spp.*	Tetracycline, rifampin, enrofloxacin, norfloxacin	-	(Prichula et al., 2016)
Eretmochemys imbricata, Chelonia mydas,	Gulf of Guinea	12	2010	Oral and cloacal	*P. aeruginosa, P. stutzeri, and P. mendocina, Alcaligenes faecalis*	Ticarcillin, ticarcillin + clavulanic acid, aztreonam,	-	(Oliveira et al., 2017)
Dermochelys coriacea	St. Kitts, West Indies	21	2011	Cloacal	*S. enterica*	-	-	(Dutton et al., 2013)

CONCLUSION

Based on the papers analyzed in the present study, it is possible to conclude that sea turtles are hosts of AMR. They have undoubtedly an important biological indicator of environmental health, particularly in the case of AMR in marine environments. Nevertheless, there are still gaps in knowledge about the dynamics and mechanisms routes of these agents. Wild animals such as sea turtles are often not included in epidemiological surveillance disease control. Due to their status as an endangered species, it is even more complicated to access samples. Sometimes, it is only possible in a rehabilitation centre when they are already contacted with other contaminated animals or are exposed to the antibiotic.

It is thus important to control the prevalence and diversity of antibiotic-resistant bacteria among sea turtles, as well as the sources and mechanisms of resistance. To mitigate the risks of antibiotic resistance in sea turtles, it is essential to implement strategies that promote the responsible use of antibiotics in animal and human medicine, as well as in aquaculture and other sectors. The use of antibiotics in aquaculture is a worrying situation because the regulation is rare. Such strategies can include reducing antibiotic use, strengthening hygiene and biosecurity practices, and promoting the development of alternative therapies and treatments.

Without a doubt, antibiotic resistance is a worldwide problem that impacts even the most isolated wild animals. It is important to advise the coastal populations to be careful with these animals when manipulating them or consuming their meat or eggs. Although ESBL or MRSA have not yet been reported in these animals is very likely that they are carriers of these agents but has not been performed enough investigation. In the future, further studies are needed under the One Health system to determine the role of sea turtles in disseminating and acquiring AMR in the marine ecosystem.

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