



Wildlife and Antibiotic Resistance: Exploring the Case of Bears

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INTRODUCTION

Antibiotic resistance in bears, while not as widely studied as in humans or livestock, has gained attention in recent years [1]. This phenomenon primarily arises from human activities introducing antibiotic-resistant bacteria into wild ecosystems, where animals like bears can be exposed. Due to habitat destruction and lack of available food is very common for bears to rummage through landfills, where they might ingest bacteria that have developed resistance from exposure to antibiotics used in human medicine or agriculture [2,3]. Another source of contamination is when water systems are contaminated, and these bacteria can spread into natural habitats (Figure 1) [4].

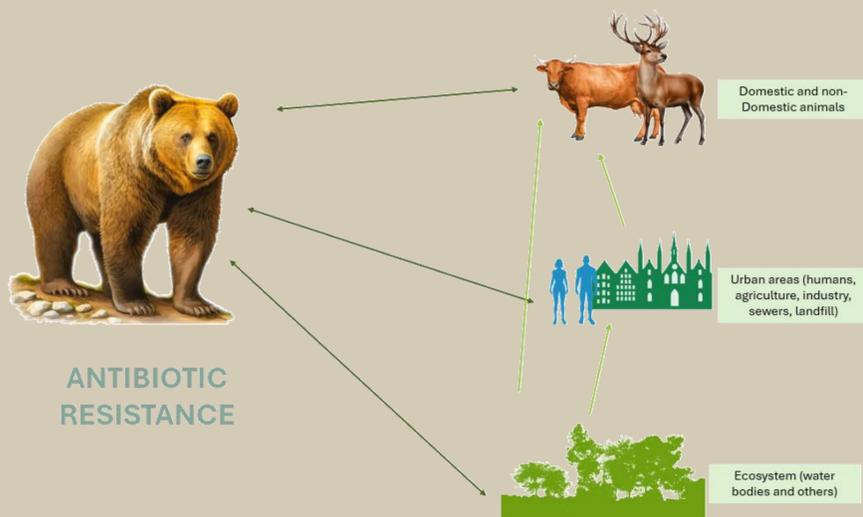


Figure 1: Bear dispersion and contamination source of pathogenic bacteria

AIMS AND METHODS

The objective of this review is to describe the presence of antibiotic resistance bacteria in bear species, their sources and their possible impact on the population.

For this review, the inclusion criteria were studies only performed in free range animals, and studies that included bacteria, phenotypic resistance and/or resistance genes

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RESULTS

A total of 8 papers were included, from 2004 to 2017. Five different species of bear were analysed. The most observed species of bacteria were *Escherichia coli*. Table 1 shows antibiotic resistance in animals from the Family Ursidae regarding species, country, year, type sample, bacteria isolated, antibiotic resistance and resistance genes.



Polar bear (*Ursus maritimus*)



Brown bear (*Ursus arctos*)



Giant Panda (*Ailuropoda melanoleuca*)

Table 2. Antibiotic resistance in animals from the Family Ursidae regarding species, country, year, type sample, bacteria isolated, antibiotic resistance and resistance genes.¶

Species	Country	Year	Type of sample	Isolated bacteria	Antibiotic resistance*	Resistance genes	Ref.
Polar bear (<i>Ursus maritimus</i>)	Svalbard	2014	Faecal	<i>Clostridiales</i>	-	blaTEM	[1]
		2004-2006	Faecal	<i>Clostridiales</i> , <i>Firmicutes</i> , <i>E. coli</i>	-	blaTEM	[2]
Brown bears (<i>Ursus arctos</i>)	Slovenia	2010-2012	Faecal	<i>E. coli</i>	-	fimH, ompT, kpsMT, ibeA, traT	[3]
		Slovakia	2020	Faeces	<i>Enterococcus spp</i>	TE, AMP, VAN, E	-
black bears (<i>Ursus americanus</i>)	USA	2014-2017	Feces and rectal and nasal swab	<i>Listeria monocytogenes</i>	TE	tet(M), tet(S)	[5]
		2014	Oral and nasal swabs	<i>E. coli</i>	TE, STR	-	[6]
	China	2016-2017	Faeces	<i>Escherichia coli</i>	STR, AMK	aph(30)-IIa, ant(300)-Ia, aac(3)-IIa, aadA1, StrB	[7]
Sloth bear (<i>Melursus ursinus</i>)	India	2015-2016	Faeces	<i>Escherichia coli</i>	GEN, CTX, CAZ	blaCTX-M, blaTEM-1, blaAmpC, qnrA, qnrB, qnrS, tetA, tetB, sulI	[8]

*AMP: ampicillin, E: erythromycin, TE: tetracycline, VAN: vancomycin, STR: streptomycin, AMK: amikacin, GEN: gentamicin, CTX: cefotaxime, CAZ: ceftazidime.¶

DISCUSSION AND CONCLUSIONS

While the direct impact of antibiotic resistance on bear populations is still unclear, the presence of resistant bacteria in wild bears is concerning. It could make them more susceptible to infections that are difficult to treat, potentially affecting their overall health and survival. Antibiotic resistance in bears is an emerging area of study that highlights the far-reaching consequences of antibiotic overuse in humans and livestock. It illustrates how environmental contamination can spread resistance even to remote wildlife populations, underscoring the need for responsible antibiotic use and better waste management to limit this global problem