IMPACT OF HEAVY METALS ASSOCIATED WITH THE COLLAPSE OF MINING DAMS ON ANTIMICROBIAL RESISTANCE: REPORTS FROM BRAZIL

L. L. F. OLIVEIRA[1], S. S. ALCANTARA[1], R. S. CALDEIRA[1], A. K. S. MACEDO[1], H. B. SANTOS[1], M. C. PAIVA[1], R. G. THOME[1], F. M. D. CHEQUER[1*]
Federal University of São João del-Rei[1]
ORCID ID: https://orcid.org/0000-0003-3514-2132[*]
farahchequer@ufsj.edu.br[*]

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ABSTRACT

Mining tailings have a strong presence of heavy metals in their composition, and these elements may be associated with the evolution and spread of antimicrobial resistance. The objective of this work was to analyze studies that describe the relationship between bacteria recovered from sites impacted by mining tailings resulting from the collapse of the Fundão and Córrego do Feijão Mine dams and the development of antimicrobial resistance. This is an integrative literature review, using the PubMed, VHL, Science Direct, and Web of Science databases, and the descriptors "antimicrobial resistance", "heavy metal", "dam" and "Brazil" (English) and "resistência antimicrobiana", "metal pesado", "barragem" and "Brasil" (Portuguese). Six articles were selected, four referring to the Fundão dam and two to the Córrego do Feijão Mine. All works suggested that environmental contamination by heavy metals, resulting from mining waste released after the dams collapsed, favored the appearance of antimicrobial resistance genes, that is, they are related to the selective pressure exerted by heavy metals. Disasters such as these raise questions about the interface of antimicrobial resistance in environments that have heavy metals as contaminants, the knowledge of which is of great relevance since antimicrobial resistance is a serious public health problem.

KEYWORDS: Bacterial Resistance to Antibiotics, Antimicrobial, Dam, Environmental contamination.

IMPACTO DOS METAIS PESADOS ASSOCIADOS AO ROMPIMENTO DE BARRAGENS DE MINERAÇÃO NA RESISTÊNCIA ANTIMICROBIANA: RELATOS DO BRASIL

RESUMO

Os rejeitos de mineração possuem forte presença de metais pesados em sua composição, sendo que estes elementos podem estar associados com a evolução e disseminação da resistência antimicrobiana. O objetivo deste trabalho foi analisar estudos que descrevam a relação entre bactérias recuperadas de locais impactados pelos rejeitos de mineração decorrentes do rompimento das barragens de Fundão e Mina Córrego do Feijão e o desenvolvimento de resistência antimicrobiana. Trata-se de uma revisão integrativa da literatura, utilizando as bases de dados PubMed, BVS*, Science Direct* e *Web of Science, e os* descritores "*antimicrobial resistance*", "*heavy metal*", "*dam*" e "*Brazil*" (inglês) e "resistência antimicrobiana", "metal pesado", "barragem" e "Brasil" (português). Foram selecionados seis artigos, sendo quatro referentes à barragem de Fundão e dois à Mina Córrego do Feijão. Todos os trabalhos sugeriram que a contaminação ambiental por metais pesados, decorrentes dos rejeitos de mineração liberados após o rompimento das barragens, favoreceu o aparecimento de genes de resistência a antimicrobianos, ou seja, estão relacionados com a pressão seletiva exercida pelos metais pesados. Desastres como estes abrem questionamentos acerca da interface da resistência antimicrobiana em ambientes que têm metais pesados como contaminantes, cujo conhecimento é de grande relevância visto que a resistência antimicrobiana se configura como um grave problema de saúde pública.

PALAVRAS CHAVE: Resistência Bacteriana a Antibióticos, Antimicrobiano, Barragem, Contaminação ambiental.

1 INTRODUCTION

Mining is one of the most important economic activities in Brazil (Penna, Martins & Silveira, 2022), where the state of Minas Gerais (MG) is a pioneer in this sector, being responsible for about 50 % of the value of mining production in the country (Passos, Coelho & Dias, 2017). During the mining and processing process, a large amount of tailings is generated (Lopes, Rodovalho & Hajj, 2022; Almeida et al., 2021; Mendes et al., 2019), which are stored in containment dams. However, due to natural events (such as earthquakes) or planning failures in construction or maintenance, dams are liable to collapse, releasing their waste into the aquatic environment (IBRAM, 2016). This becomes worrying since these wastes may contain toxic chemical elements, especially heavy metals (Paes et al., 2023).

The state of Minas Gerais is marked by tragic events related to mining activity and by the year 2022, eight mining dam collapses had occurred (Lacaz, Porto & Pinheiro, 2017; Barbosa & Amaral, 2022). Two of the most recent disasters, the collapse of the Fundão dam (Mariana-MG) on November 5, 2015 and the Córrego do Feijão Mine dam (Brumadinho-MG) on January 25, 2019, occurred within a short period of time between them, had a huge social and environmental impact, and point to the need for dam safety surveillance (Milanez, Ali & Oliveira, 2021).

The collapse of the Fundão dam caused the release of about 34 million cubic meters (m^3) of mining tailings into the Doce River basin (IBAMA, 2015), while after the failure of the Córrego do Feijão Mine dam, approximately 11.7 million m^3 of mining tailings were released into the Paraobeba River, in the São Francisco River basin (Porsani, Jesus & Stangari, 2019). After both disasters, an increase in the concentration of several heavy metals was reported along the waters of the affected rivers, especially Iron (Fe), Manganese (Mn), Aluminum (Al), and Cadmium (Cd) (IGAM, 2016; IGAM, 2019; Cionek, Alves, Tófoli, Rodrigues-Filho & Dias, 2019; Macêdo et al., 2020).

Heavy metals are highly toxic even at low concentrations and are highly recalcitrant in the environment (Guo et al., 2022). In humans, these elements may be associated with various health problems, ranging from poisoning to more serious cases related to carcinogenesis and death (Oliveira, Kuno, Nascimento & Gouveia, 2021). At the environmental level, in addition to the contamination of water, soil, and aquatic organisms (Husejnovic et al., 2018; Gwimbi, Kotelo & Selimo, 2020), these elements can promote structural changes, death, and increased expression of resistance genes to metals in microbial communities (Salam, Obayori, Ilori & Amund, 2020). In addition, they are associated with the evolution and dissemination of antimicrobial resistance (AMR), considered a serious public health problem (Stepanauskas et al., 2006; Bednorz et al. 2013; Alawi, Torrijos & Walsh, 2022; Janotto, Luciano & Evangelista, 2022).

AMR refers to the ability of microorganisms (bacteria, viruses, fungi and parasites) to change after exposure to antimicrobials, resulting in loss of activity. In this way, there is a limitation of the options for treating infections and the dissemination of resistant bacteria can be favored (WHO, 2021). Although antimicrobial resistance genes occur naturally in the environment, in low amounts, contaminants such as heavy metals are able to increase them (Edet, Bassey & Joseph, 2023). Heavy metals can enrich determinants of resistance genes through co-selection mechanisms, due to the fact that resistance to antimicrobials and heavy metals share the same or similar genetic mechanisms (Baker-Austin, Wright, Stepanauskas & McArthur, 2006; Seiler & Berendonk, 2012). Several studies have shown that antimicrobial-resistant bacteria recovered from polluted environments were also resistant to heavy metals, raising questions about the possibility of inducing antimicrobial resistance by metals present as environmental contaminants (Thomas et al., 2020; Hahn, Bahlis, Basso & Van der Sand, 2015; Matyar et al., 2014).

In view of the above, this study aims to analyze existing scientific evidence to date that describes the relationship between bacteria recovered from sites affected by mining tailings resulting from the collapse of the aforementioned dams, and the development of antimicrobial resistance.

2 METHODOLOGY

2.1 Study Design

This study is an integrative literature review, a method that provides the synthesis of various empirical or theoretical research already published, in order to provide a broader understanding of a particular area of study (Lima et al., 2023).

In this review, studies were approached that associate the presence of heavy metals as environmental contaminants, released after the collapse of mining dams, and the development of antimicrobial resistance, analyzed in bacteria recovered from these sites. To this end, the guiding question of the study was: “Can the presence of heavy metals resulting from mining tailings released after dam failures in Brazil favor antimicrobial resistance?”

From the guiding question, the "PICO" was established, with the study population (Population) being: bacteria recovered from environments contaminated by the collapse of the Fundão and Córrego do Feijão Mine dams; Intervention: exposure to heavy metals resulting from mining tailings; the control group (Control): absence of exposure to metals; and Outcome: the development of antimicrobial resistance.

2.2 Search Strategy

Four databases were used to search for studies (PubMed, Virtual Health Library (VHL), Science Direct, and Web of Science), which was performed for the period from October 13, 2022 to February 2, 2023. To carry out the search, the descriptors in English "antimicrobial resistance", "heavy metal", "dam", and "Brazil", and also in Portuguese "resistência antimicrobiana", "metal pesado", "barragem" and "Brasil" were used, combined together with the Boolean operator "AND" ("antimicrobial resistance" AND "heavy metal" AND "dam" AND "Brazil") ("resistência antimicrobiana" AND "metal pesado" AND "barragem" AND "Brasil").

2.3 Selection of the Studies

After conducting searches in the aforementioned databases, duplicate publications were excluded. Next, the titles and abstracts were read, excluding articles that did not fit the theme of this review, and the remaining articles were read in full. In addition, to locate articles that had not been found in the databases used, a search was carried out in the reference lists of the selected articles.

2.4 Eligibility Criteria

Articles published in English, Portuguese, and Spanish and that answered the guiding question of the study were considered eligible. Book chapters, literature reviews, dissertations, theses, monographs, books, editorials, manuals, news, reports and comments were excluded.

2.5 Data Collection

After reading the articles in full that met the inclusion criteria, information extracted from them was recorded in Table 1, which addressed detailed information about all the studies included in this review (author, year, objective of the study, analyzed sample, methodology used, control group, main results, and limitations of the study). All steps were performed blindly and independently by three of the authors of this review.

3 RESULTS

A total of 434 articles were found in the analyzed databases, of which 22 were excluded because they were in duplicate (n=412). Of the remaining 412 articles, 384 were excluded by title and/or abstract and subsequently 28 articles were selected by title and/or abstract and read in full. After reading, 23 articles were excluded according to the eligibility criteria, and one article was found by searching the references of selected articles, with a total of six articles being included at the end of this review. Figure 1 presents the methodology used in the selection of articles included in this review.

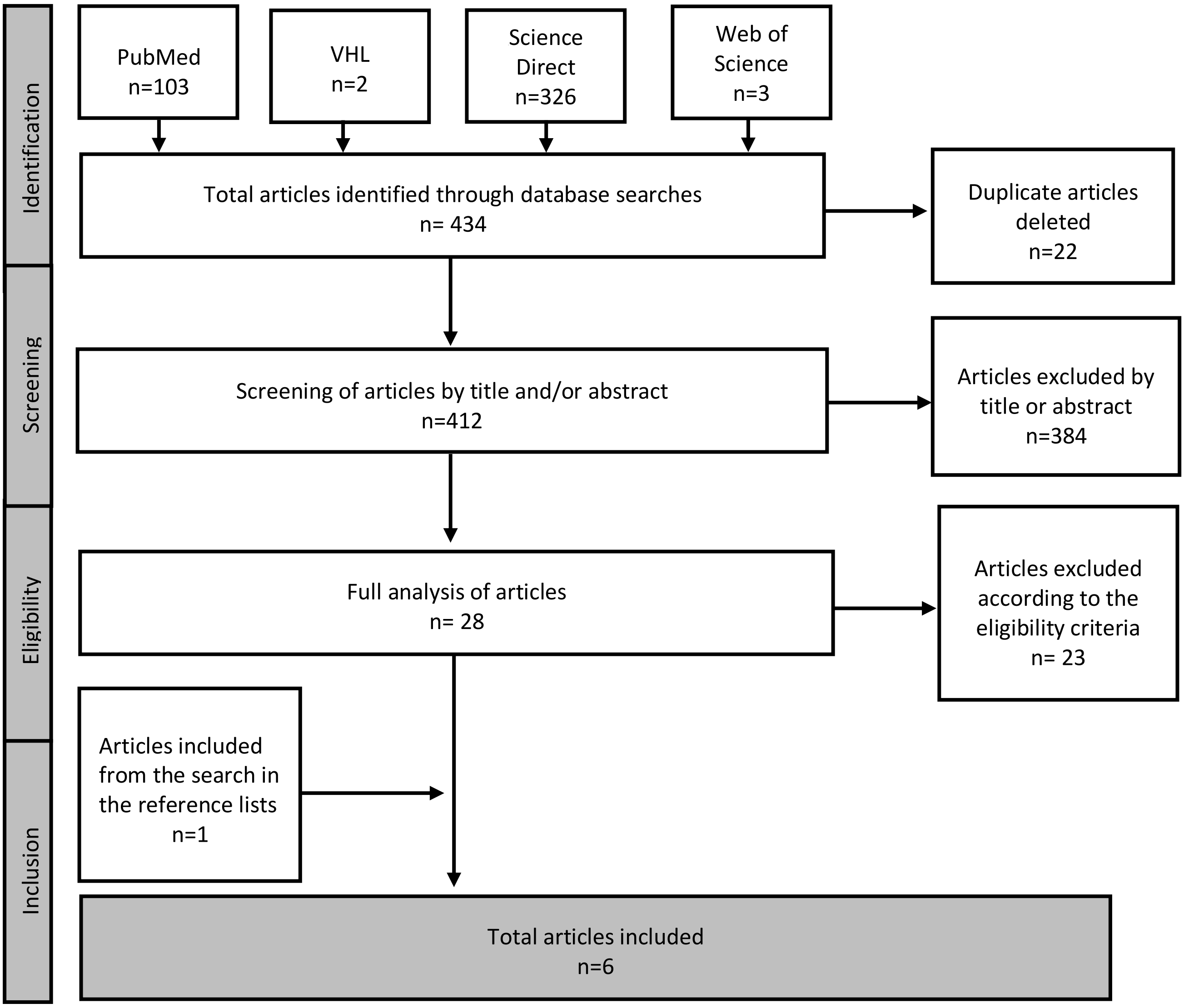

Figure 1: Flowchart that presents the methodology used in this integrative review.

All six studies were carried out in Brazil, but some of them with the collaboration of other countries such as Chile, Costa Rica, and the United States.

Table 1 presents detailed information on the selected articles. Four studies (66. 7%) referred to the Fundão dam and two (33.3 %) referred to the Córrego do Feijão Mine dam.

In general, all six studies presented in this review suggest that environmental contamination by heavy metals resulting from mining tailings released after the collapse of the Fundão and the Córrego do Feijão Mine dams favored the appearance of antimicrobial resistance genes (ARGs), that is, at least the development of bacterial resistance may be related to the pressure caused by heavy metals.

In relation to the studies referring to the Fundão dam, Suhadolnik et al. (2022) analyzed sediment samples from rivers belonging to the Doce River basin, quantified the metals present in these samples by optical emission spectrometry, extracted the DNA and, using bioinformatics techniques, performed the prediction of ARGs. The concentrations of metals were within the stipulated by the National Council for the Environment (*Conselho Nacional do Meio Ambiente* - CONAMA) with the exception of Chromium (Cr) and Cd, and the concentration of Fe, Mn, Mg, and Cr was higher in the rivers affected by the disaster. Genomic analysis resulted in 684 different resistance genes, covering all classical resistance mechanisms and classes of clinically relevant antimicrobials, including last-line compounds for the treatment of infections caused by multidrug-resistant bacteria, 38 % of which were exclusive to impacted rivers. The affected rivers had a higher proportion of unique ARGs compared to the reference river, i.e. they were more similar. Furthermore, critical antibiotic resistance genes (ARGs) such as *mcr* and *ere*A2 were significantly more common in the disturbed microbiomes. The metals Magnesium (Mg), Fe, and Copper (Cu) were those that most correlated with antimicrobial resistance, with a strong interaction between Cu and genes for resistance to β-lactams, aminoglycosides, and macrolides being reported (Table 1).

Vasconcelos et al. (2022) analyzed soil samples collected near the Doce River. Initially, the samples were placed on tryptone soy agar with nystatin and Mn, and later, susceptibility tests for β-lactams, aminoglycosides, tetracycline, quinolones, DNA extraction, and PCR were carried out. A total of 21 strains were found, 18 of which were *Bacillus* and three *Mucilaginibacter*, all with antimicrobial resistance and resistance to metals. Among them, the strain *Mucilaginibacter sp*. 21p was that which most demonstrated resistance to metals and antimicrobials. Although there were no antimicrobial residues generating selective pressure in the environment, the bacterial community was exposed to heavy metals and the development of antimicrobial resistance was attributed to the occurrence of cross-resistance with these heavy metals (Table 1).

Gaeta et al. (2022) retrieved water samples from eight different locations to investigate the occurrence of clinically important bacteria. The samples were placed on MacConkey agar plates with ceftriaxone, the strains were identified by mass spectrometry and susceptibility tests, and determination of the resistance mechanism by the double disk synergy test, as well as DNA extraction were performed. Environmental *Escherichia coli* strains co-hosting the clinically relevant bla $_{\text{CTX-M-2}}$ ESBL (extended spectrum beta-lactamase) gene and operon mer genes that confer mercury tolerance were found after the disaster. These bacteria were also resistant to a number of antimicrobials such as ceftriaxone, cefotaxime, cefepime, trimethoprim/sulfamethoxazole, amikacin, gentamicin and tetracycline) (Table 1).

Gaeta et al. (2020) analyzed the microbiota of the nasopharynx, rumen, and rectum of 16 dairy cows belonging to a farm where the water consumed by the animals was affected by mining waste. Although the animals did not demonstrate clinical manifestations, by molecular approach, about 200 different genera of bacteria were found in the experimental group cows compared to the control group. In addition, on the farm that had water impacted by heavy metals, a higher prevalence and abundance of antimicrobial resistance genes was reported, with a high frequency of active efflux mechanisms. Differences in the diversity of the aquatic microbiota suggest that exposure to water contaminated with heavy metals can interfere with the microbiota of dairy cattle, and consequently, interfere with animal productivity (Table 1).

Regarding the dam at the Córrego do Feijão Mine, Thompson et al. (2023) analyzed samples collected one week (February/2019) and four months (May/2019) after the disaster, in eight locations along the Paraopeba River. Total DNA was extracted from the samples and subsequently quantified, and metagenomic analyzes were performed. In addition, bacteria present in the water samples were isolated and resistance was tested for a series of antimicrobials. The most abundant phyla in the studied areas after the disaster were Proteobacteria (29–73 %), Firmicutes (0–54 %), Bacteroidetes (0–50 %), Actinobacteria (4–22 %) and Cyanobacteria (0–23 %), with the predominance of Firmicutes, mainly *Bacillus* (71 %) and Proteobacteria, mainly *Acinetobacter* (28 %), and directly implies pollution by heavy metal contamination.

In addition, *Pseudomonas* (n = 26), *Enterobacter* (n = 26), *Raoultella* (n = 7), and *Klebsiella* (n = 5) bacteria were the most abundant in the samples, these bacteria are reported to be multi-resistant to numerous antibiotics. Resistance analyzes showed that all isolates were resistant to at least one type of antibiotic, the main ones being: ampicillin, ampicillin/sulbactam, amikacin and meropenem, but also ceftriaxone, cefuroxime, cefepime, ciprofloxacin and gentamicin. This increase in resistance suggests a possible influence of tailings sludge on the spread of antibiotic resistance in the Paraopeba River (Table 1).

The study by Furlan et al. (2020) analyzed 30 samples, including soil, sediment, and water from the Paraopeba River, affected by mining tailings. The physical-chemical conditions of the water were determined, the DNA of the samples was extracted, and the antimicrobial resistance genes researched by PCR. Samples from affected sites showed high turbidity, in addition to values of Mn, Al, Fe, and Cu above those allowed by law (CONAMA 357/05) for water bodies, and high concentrations of Fe, Al, Cu, Mn, and Cd for soils and sediments. The averages of ARGs found in unaffected sites and in affected sites were 29 and 45, respectively, being detected 1.55 times more in sites affected by the disaster, with ARGs being associated with resistance to β-lactams, quinolones, aminoglycosides, sulfonamides, phenicols and glycopeptides the most increased. After the disaster, resistance genes were detected for important classes of antimicrobials such as: β-lactams (bla$_{\text{CMY}}$, bla$_{\text{SHV}}$, bla$_{\text{TEM}}$, bla$_{\text{CTX-M-Gp1}}$, bla$_{\text{CTX-M-Gp9}}$), quinolones (qepA, oqxA, oqxB, qnrB, qnrS), aminoglycosides (aadA, aac(6')-lb, aph(3')-la, aph(3')-VI), tetracyclines (tet(B), tet(C), tet(D)), phenicols (floR, cmla), sulfonamides (sul1, sul2, sul3), glycopeptides (vanC1, vanC2/3), and macrolides (erma, ermB, ermC, mefAE). It is noteworthy that the presence of heavy metals was responsible for greater selective pressure, favoring the emergence of bacteria with a multi-drug resistant (MDR) phenotype (Table 1).

Table 1: Information from the selected articles about the development of antimicrobial resistance after the collapse of mining dams in Minas Gerais.

Study		Method			Results	
Author and Year	**Study Objective**	**Sample Analyzed**	**Methodology**	**Control**	**Main results**	**Limitations**
Fundão Dam (Mariana –MG)						
Suhadolnik et al., 2022 (32)	Characterization of resistance to antibiotics and metals and virulome of bacteria from rivers affected by the Fundão dam failure disaster, in addition to determining the mobility of ARG, MRG and VFG and hosts	Sediments collected in the Carmo and Casca rivers, 7, 30, 150 and 390 days after the rupture of the Fundão dam (November 2015 to December 2016)	Verification of amino acids, resistance to metals and antimicrobials, taxonomy through total DNA extracted from collected samples	Sediments collected in the Água Fria River	Presence of 684 resistance genes and all classic antimicrobial resistance mechanisms; Although the amount of metals is below the limits, antimicrobial resistance was enhanced under the environmental conditions presented	Need for studies with a larger number of samples and shorter sampling periodicity
Vasconcelos, et al., 2022 (33)	Isolation and identification of native bacteria with resistance to metal (metalloid) in estuarine soils, in addition to exploring the mechanism of resistance of native bacteria to metal exposure through the genome	Soils collected in the Doce River estuary, in December 2018	Isolation, and identification of the mechanism of antimicrobial resistance of bacteria resistant to metals	Not specified	*Bacillus* and *Mucilaginibacter* genera were identified, both showing resistance to metals and antibiotics; Presence of efflux pump and production of capsules in addition to a new species (*Mucilaginibacter* sp. 21p) resistant to antibiotics	Need for more studies to know about the ability to transfer resistance

					related to high concentration of heavy metals	
Gaeta, et al., 2022 (34)	Genomic and microbiological investigation of WHO priority bacteria recovered from a river affected by the mining dam disaster	Water samples collected along 84 km of the Doce river basin, during 2018	Isolation and identification of species; Genome sequencing; Antibiotic susceptibility testing of multi-drug resistant *Escherichia coli* strain	Not specified	A broad resistome (antibiotics and heavy metals) was predicted including the presence of the clinically relevant extended-spectrum β-lactamase (ESBL) blaCTX-M-2 gene, efflux pump genes of quacEΔ1 and operon mer (resistance to mercury), which prove to be biomarkers of mining activity in nature	The methodology used did not allow obtaining the complete nucleotide sequence of the plasmids, due to their being too short.
Gaeta, et al., 2020 (35)	To investigate the consequences of long-term exposure to drinking water contaminated by the mining dam collapse disaster on the microbiome and resistome of dairy cattle	Nasopharyngeal microbiota, rumen and fecal fluids from cows living in an environment contaminated by heavy metals	Sequencing and analysis of the genome of bacteria present in the nasopharyngeal microbiota, rumen and fecal fluids of cows	Nasopharyngeal microbiota, rumen and fecal fluids of cows living in an environment without contamination	Contaminated environment samples showed greater abundance and prevalence of metal and antimicrobial resistance genes; Samples collected from cows had a higher prevalence of genes that confer resistance to multiple drugs and metals; Heavy metals interfere with the microbiota of dairy cows, helping to generate bacterial resistance to antimicrobials	Further research is needed to determine whether resistance can be transferred through the food chain and whether it will affect human health

Córrego do Feijão Mine Dam (Brumadinho - MG)						
Thompson et al., 2023 (36)	Analyze possible changes in microbial diversity and increased antibiotic resistance in the Paraopeba River	Water samples from the Paraopeba River, collected in February and May 2019	DNA isolation and metagenomic analyzes (16S rRNA)	Water sample collected from a site in the Paraopeba River upstream of the disaster	Analyzes demonstrated changes in microbial diversity immediately after the disaster with the presence of metal indicator bacteria (*Acinetobacter*, *Bacillus*, *Novosphingobium* and *Sediminibacterium* ; There was a significant increase in antibiotic resistance to ampicillin, ampicillin/sulbactam, amoxicillin/clavulanate, ceftriaxone, and cephalothin following the disaster	Not specified
Furlan, et al., 2020 (37)	Detection and quantification of clinically relevant ARGs in environmental samples after the Brumadinho dam failure	Soils, sediments and water collected in the Paraopeba river affected by the dam failure, 30 days after the disaster	Total DNA extraction and determination of ARGs by PCR	Soils, sediments and water collected at sites unaffected by the dam failure	About 387 amplicons of 29 ARGs were detected, which confer resistance to β-lactams, quinolones, aminoglycosides, tetracyclines, sulfonamides, phenicols, macrolides, glycopeptides and polymyxins, including genes encoding β extended-spectrum -lactamases, and mcr-7.1; A greater amount of ARGs were detected in	Not specified

	environmental samples from places close to the disaster, reinforcing that the occurrence of metals in the environment exerts a selective pressure for ARGs

Legend: MG: Minas Gerais; WHO: World Health Organization; ARGs: antibiotic resistance genes; MRG: metal resistance genes; VFG: virulence factor genes; DNA: deoxyribonucleic acid; β: beta; ESBL: extended-spectrum β-lactamase; PCR: polymerase chain reaction; rRNA: ribosomal ribonucleic acid.

4 DISCUSSION

The evolution and spread of antimicrobial resistance may be associated with factors that are independent of the use of antimicrobials in humans and animals, such as environmental pollution resulting from human activities. In this context, contamination by heavy metals stands out as one of the main selectors of organisms resistant to antimicrobials (Stepanauskas et al., 2006; Bednorz et al., 2013), being important in the maintenance and proliferation of AMR (Wales & Davies, 2015; Lin et al., 2017).

Heavy metals are associated with the spread of AMR since phenotypes of resistance to antimicrobials and heavy metals share the same or similar genetic mechanisms, such as: (i) co-resistance: when mechanisms of resistance to metals and antimicrobials are encoded in the same mobile genetic element; or (ii) cross-resistance: when the same mechanism simultaneously confers resistance to metals and antimicrobials (Baker-Austin et al., 2006; Seiler & Berendonk, 2012). This similarity in resistance pathways can cause microorganisms in contact with one of these substances to develop resistance to metals or antimicrobials, or even to both, and this resistance is usually associated with mobile genetic elements, especially plasmids (Chattopadhyay & Grossart, 2011).

Several studies have shown that antimicrobial-resistant bacteria recovered from polluted environments were also resistant to heavy metals (Matyar et al., 2014; Hahn et al., 2015; Thomas et al., 2020). Matyar et al. (2014) examined a river in Turkey, and observed that the recovered bacteria showed resistance to a range of β-lactam antimicrobials and also resistance to metals Mn, Nickel (Ni), Zinc (Zn), Lead (Pb), Cd, and Fe. Hahn et al. (2015) evaluated the resistance profile of bacteria isolated from Rio dos Sinos (Brazil) and identified microorganisms resistant to several antimicrobials, mainly vancomycin, and also to heavy metals, especially Cu, Ni, and Cr. Thomas et al. (2020) analyzed soil samples collected from a polluted river in the United States and demonstrated that the samples exhibited a high profile of antimicrobial resistance genes and also heavy metal resistance genes such as Arsenic (As), Cu, Fe, Ni, and Zn.

When present as pollutants in aquatic environments, these elements can be highly associated with the development of AMR, as demonstrated by Chen et al. (2019). In their study, soil samples collected from a river located near a copper tailings dam in northern China were analyzed, and it was observed that the abundance of antimicrobial resistance genes was positively correlated with the concentration of metals present in the water as contaminants, these being As, Zn, and mainly Cd (Chen et al., 2019).

In this context, disasters involving mining dams cause the release of large amounts of waste, which contributes to the contamination of the aquatic environment by heavy metals, which may lead to changes in AMR-related phenotypes, as demonstrated in all six studies presented in the present review.

Some studies and reports have shown that the return of the environment to pre-collapse conditions takes a long period of time, and may often not even be estimated (Serra, 2018; IBAMA, 2015), thus making the environment a potential for development, maintenance, and spread of antimicrobial resistance.

Something of concern is that bacteria present in the aquatic environment contaminated by heavy metals that acquire antimicrobial resistance can contaminate fish and other aquatic organisms that live in these environments (Seiler & Berendonk, 2012). This can pose a serious risk to public health, as antimicrobial resistance genes can be transferred from environmental bacteria to human-associated bacteria through consumption of food contaminated with resistant strains (Enciso-Martínez et al., 2022).

Another important topic is the *One Health* approach, the collaborative effort of various health science professions to achieve optimal health for people, animals, and the environment (McEwen & Collignon, 2018). In the context of antimicrobial resistance, it is mainly driven by the use and abuse of these compounds in the human and animal sectors. Antimicrobials used clinically are not completely metabolized by the body, causing active molecules to be secreted through feces and urine, flowing into wastewater and can be shared between bacteria, including environmental bacteria. In this way, it is crucial to identify and characterize the sources of antimicrobial resistance emissions into the environment and, therefore, great importance has been given to this issue, considering an efficient collaboration between all the players involved (humans, animals, and the environment) to combat this very serious problem (Serna & Gonzalez-Zorn, 2022).

The present study had some limitations, such as the low number of studies found and the analysis of samples only in periods immediately after the disaster, making it not possible to identify chronic effects related to antimicrobial resistance. In this way, studies such as those exposed in this review are essential to better understand the effects that disasters involving mining dams, such as those in Minas Gerais, can cause to the environment, and also to human health, and it is important to carry out more research on the subject.

5 CONCLUSION

All studies presented in this review identified changes in the antimicrobial resistance profile of bacteria isolated from environments contaminated by metals after disasters. Disasters such as these open up questions about the possibility of inducing antimicrobial resistance by metals present as environmental contaminants, and further studies are essential, since antimicrobial resistance is a serious public health problem.

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ABOUT THE AUTHORS

Lara Luiza Freitas de Oliveira
Mestre em Biotecnologia pelo Programa de Pós-graduação em Biotecnologia, da Universidade Federal de São João del-Rei, Campus Centro-Oeste Dona Lindu (UFSJ/CCO) e Bacharel em Bioquímica pela mesma instituição.
E-mail: luizalara422@gmail.com
ORCID ID: https://orcid.org/0000-0002-2115-0943

Shara Sevesquim Alcantara
Estudante de graduação em Farmácia pela Universidade Federal de São João del-Rei, Campus Centro-Oeste Dona Lindu (UFSJ/CCO).
E-mail: sharasevesquim@gmail.com
ORCID ID: https://orcid.org/0009-0001-0943-1064

Rafael Sotero Caldeira
Graduado em Farmácia pela Universidade Federal de São João del-Rei, Campus Centro-Oeste Dona Lindu (UFSJ/CCO).
E-mail: faelsotscaldeira@gmail.com
ORCID ID: https://orcid.org/0009-0008-1602-2630

Anderson Kelvin Saraiva Macêdo
Doutor e Mestre em Biotecnologia, pelo Programa de Pós-graduação em Biotecnologia, da Universidade Federal de São João del-Rei, Campus Centro-Oeste Dona Lindu (UFSJ/CCO). Graduado em Ciências Biológicas pela Universidade Estadual da Paraíba (UEPB).
E-mail: andersonkelvinsm@gmail.com
ORCID ID: https://orcid.org/0000-0002-0404-1681

Hélio Batista dos Santos
Doutor e Mestre em Biologia Celular pela Universidade Federal de Minas Gerais (UFMG). Graduado em Ciências Biológicas pela Universidade Estadual de Minas Gerais (UEMG). Professor Associado III na Universidade Federal de São João del-Rei, Campus Centro-Oeste Dona Lindu (UFSJ/CCO).
E-mail: hbsantos@ufsj.edu.br
ORCID ID: https://orcid.org/0000-0001-6813-8522

Magna Cristina de Paiva
Doutora em Ciências Biológicas e Mestre em Microbiologia pela Universidade Federal de Minas Gerais (UFMG). Graduada em Farmácia pela mesma instituição. Professora do curso de Farmácia na Universidade Federal de São João del-Rei, Campus Centro-Oeste Dona Lindu (UFSJ/CCO).
E-mail: magnacpaiva@ufsj.edu.br.
ORCID ID: https://orcid.org/0000-0001-9375-7261.

Ralph Gruppi Thomé
Doutor e Mestre em Biologia Celular pela Universidade Federal de Minas Gerais (UFMG). Graduado em Ciências Biológicas pela mesma instituição. Professor na Universidade Federal de São João del-Rei, Campus

Centro-Oeste Dona Lindu (UFSJ/CCO) e Coordenador do Programa de Pós-graduação em Biotecnologia da UFSJ/CCO.
E-mail: ralph@ufsj.edu.br.
ORCID ID: https://orcid.org/0000-0002-1779-5036.

Farah Maria Drumond Chequer
Doutora em Ciências e Mestre em Toxicologia pela Faculdade de Ciências Farmacêuticas de Ribeirão Preto da Universidade de São Paulo (FCFRP-USP). Graduada em Farmácia/Bioquímica pela Universidade Federal de Alfenas (UNIFAL). Professora na Universidade Federal de São João del-Rei, Campus Centro-Oeste Dona Lindu (UFSJ/CCO) e é credenciada no Programa de Pós-graduação em Ciências Farmacêuticas da UFSJ/CCO.
E-mail: farahchequer@ufsj.edu.br.
ORCID ID: https://orcid.org/0000-0003-3514-2132.

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