Antibiotic Biodegradation Mediated by Bacterial Communities in Oil-Contaminated Soils

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Abstract: Antibiotics have emerged as environmental contaminants. Since microorganisms play a crucial role in the degradation of organic pollutants, including antibiotics, the aim of the present study was to assess the potential of bacterial communities from an oil-contaminated soil to degrade antibiotics. To this end, bacterial communities from a soil with a history of oil contamination were subjected to exposure to five antibiotics: enramycin, norfloxacin, meropenem, penicillin, and oxytetracycline, and their ability to biodegrade the antibiotics was determined by using the closed bottle test, optical density measurements at 600 nm, and community structure analysis by Fourier transform infrared (FT-IR) spectroscopy and fatty acid methyl ester profiles. The experimental results demonstrated significant biodegradation of enramycin (77.36%), norfloxacin (47.94%), meropenem (68.70%), penicillin (81.27%), and oxytetracycline (70.86%). These findings suggest that, despite the known persistence of this group of antibiotics in the environment, it is feasible to enhance their degradation by using bacterial communities from oil-contaminated soils.

Keywords: *Antibiotics, Biodegradation.*

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I. INTRODUCTION

Since their discovery by Alexander Fleming in 1928, antibiotics have been used to treat infections in humans and animals. However, they have emerged as environmental contaminants because they have entered the environment and natural ecosystems through different ways (Nielsen et al., 2018, Cycoń et al. 2019). Antibiotics such as macrolides, tetracyclines, and sulfonamides were identified in environmental samples as early as in 1982 (Singh et al., 2021). These antibiotics impact on the composition of natural microbial communities and can be classified as water-soluble or lipophilic. Antibiotics that are water-soluble at different pH values can contaminate groundwater due to their mobility, while lipophilic ones can accumulate in sediments or soils (Robles-Jimenez et al 2021).

Organic pollutants, including antibiotics, can be degraded by the action of microorganisms such as bacteria (Coelho et al., 2015). Some authors have also reported biodegradation of antibiotics such as penicillin, tetracycline, aminoglycosides, and fluoroquinolones by naturally occurring fungi (Cruz-Morato et al., 2013; Rodarte-Morales et al., 2011; Liu et al., 2016).

Antibiotics can be eliminated in three main ways: by adsorption, chemical action and biological action (Oberoi et al., 2019). The presence of antibiotics in the environment impacts the microbial community structure, because they act on bacteria and select groups which can use them as carbon and energy sources or non-target organisms (Grenni et al., 2018, Zhang, et al., 2022). Bioremediation process involves the adsorption and biodegradation of antibiotics across a range of environmental matrices. The adsorption process involves the accumulation of antibiotics on the surface of microorganisms, while the biodegradation process allows for the complete removal of antibiotics from the environment through decomposition. Some antibiotics such as Fluoroquinolones, tetracyclines, and sulfonamides can be removed through abiotic process, lake photodegradation, and oxidation. On other hand Fluoroquinolones and sulfonamides can directly undergo biodegradation (Yang et al 2021)

This research aimed to investigate the potential of bacterial communities from an oil-contaminated soil to biodegrade enramycin, norfloxacin, meropenem, penicillin, and oxytetracycline (OTC) in a mineral medium.

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II. MATERIAL AND METHODS

- *Mineralization and Biodegradation Studies*

The bacterial community studied was collected from an oil-contaminated soil from a hydrocarbon basin located in the south of Argentine Patagonia. Then, 10 g of soil was placed together with 90 mL of mineral medium and each of the following antibiotics: enramycin, norfloxacin, meropenem, penicillin, and OTC (20 ppm) as carbon and energy sources. This was achieved through ten successive subcultures before incubation at 28°C on a rotary shaker. The ability of the bacterial community to biodegrade the antibiotics was measured using the closed-bottle technique, by monitoring CO_2 accumulation using NaOH to capture it. To this end, 5 mL of the bacterial community with a turbidity of 1 McFarland was poured into a brown bottle with 95 mL of mineral salt medium (K_2HPO_4 0.5 g; KH_2PO_3 0.5 g; $MgSO_4$ 0.2 g; (NH_4) NO_3 1 g; yeast extract 0.025 g; pluripeptone 0.025 g) and without other hydrocarbons or nutrients. NaOH was titrated using HCl 0.1N (Bartha et al., 1979).

- *Bacterial Growth*

The growth of the bacterial community was determined by measuring the optical density (OD) at 600 nm and at a specific OD for each antibiotic: 274 mm for enramycin, 273 mm for norfloxacin, 276 mm for meropenem (Mendez et al., 2003), 245 mm for penicillin and 275 mm for OTC.

- *Determination of Emulsification Index (E24) of the Biosurfactant*

The emulsification index (E24) of the biosurfactant was determined by adding 2 mL of toluene individually to the same amount of cell-free culture followed by vortexing for 2 min. The culture was then allowed to stand for 24 h at room temperature. The E24 index was determined by the following formula (Abouseoud et al. 2007):

E_{24} index (%) = [height of emulsified layer (mm)/total height of the liquid column (mm)]x 100

- *Fourier Transform Infrared (FT-IR) Spectroscopy Profiles*

To determine the FT-IR profiles, the bacterial communities (10 mL) were harvested by centrifugation at 8000 g for 10 min, washed tree times with physiological solution, suspended in 50 µL of ethanol 70%, placed in a ZnSe window, and stove-dried for 15 min at 42 °C. IR spectra were measured with a FT-IR spectroscope. Spectra were recorded over wavelengths ranging from 3500 to 700 cm^{-1}, with an interval of 1 cm and a spectral resolution of 4 cm. The final spectrum was the average of 64 scans. Digitized IR spectra (represented by a total of 1300 points) were saved for additional transformation.

- *Transformation of Spectra*

Spectra were transformed (normalization, smoothing and second derivative using the Savitzky–Golay algorithm) and recorded in ASCII format and imported into a worksheet (Mouwen et al., 2006). Five spectral windows were selected for calculation purposes: the window between 3000 and 2800 cm^{-1}, dominated by the influence of functional groups of membrane fatty acids (w1); the window between 1800 and 1500 cm^{-1}, with the influence of the amide I and amide II groups belonging to proteins and peptides (w2); the window between 1500 and 1200 cm^{-1}, a mixed region influenced by proteins, fatty acids and other phosphate-carrying compounds (w3); the window between 1200 and 900 cm⁻1, which is informative mostly for carbohydrates and polysaccharides (w4); and the window between 900 and 700 cm^{-1}, which is named "the true fingerprint" because of very specific spectral patterns (w5).

- *Closed Bottle Test*

To determine the fatty acid methyl ester (FAME) profiles, after 20 days of incubation at 28ºC, the samples were centrifuged at 4000 rpm for 30 min. The FAMEs were extracted and analyzed as described by the MIDI microbial identification system (Microbial ID, Inc, Newark, NJ, USA). This system was applied to separate FAMEs by using a gas chromatograph (HP 6890) equipped with a split/splitless injector, a flame ionization detector, an Ultra 2 capillary column (25 m, 0.2 mm, 0.33 µm), an automatic sampler, an integrator, and a software program which identifies the fatty acids (Microbial ID 6.0 version). The injector and detector temperatures were maintained at 250ºC and 300ºC respectively. The sample (2 µL) was injected in split mode, and the column temperature was raised from 170 to 270°C at a rate of 5°C/min.

The FAME profiles obtained were used to determine the bacterial and fungal groups present in the samples. The sum of i14:0, i15:0a, i16:0a, i17:0, i18, a15:0, a16:0, a17:0, a18:0, and a19:0; Actinobacteria, and the sum of 10Me16:0, 10Me17:0, and 10Me18:0; for Atinobacterias. Gram negative bacteria was the sum of cy17:0, cy19:0, 16:1ω7, 16:1ω9, 17:1ω8, and 18:1ω7; for Fungal arbuscular mycorrhiza fungi (AMF) + Zygomycota + Ascomycota and Basidiomycota + unspecific fungal AMF were 16:1ω5cb; Zygomycota was 18:1ω9cc; Ascomycota and Basidiomycota were 18:2ω6cd; Unspecific fungal was 18:3ω6,9,12d; Unspecific microbial was the sum of 14:0, 15:0, 16:0 d, 17:0, 18:0, 20:0, and 20:4ω6,9,12,15; and Total microbial: bacterial + fungal + unspecific microbial (Acuña & Pucci 2022; Joergensen, R. G. 2022).

- *Statistical Analysis*

To identify possible similarities between FAME profiles and FT-IR spectra, the data were subjected to analysis of variance using the PAST (Hammer & Harper, 2005) and Sherlock (Microbial ID 6.0 version) software.

III. RESULT AND DISCUSSION

The five antibiotics here evaluated were used by the bacterial community as carbon and energy sources with different percentages of degradation. Table 1 presents the results of the emulsification index (E_{24}), optical density (OD 600 nm), degradation percentage (Dg%), Shannon diversity Index (H), and FAME profile for the five antibiotics selected for the study. Meropenem showed the highest bacterial growth (measured as OD) followed by penicillin. Penicillin was the most degraded antibiotic (81.27%), exhibiting the highest Shannon diversity index. The main difference for this was that the bacterial community with activity in meropenem was

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composed of Gram-negative bacteria and unspecific microorganisms and the one with activity in penicillin was rich in Gram-positive bacteria and firmicutes. The remaining antibiotics showed different degradation percentages (Fig. 1) and the bacterial communities were also different (Figs. 2 and 3).

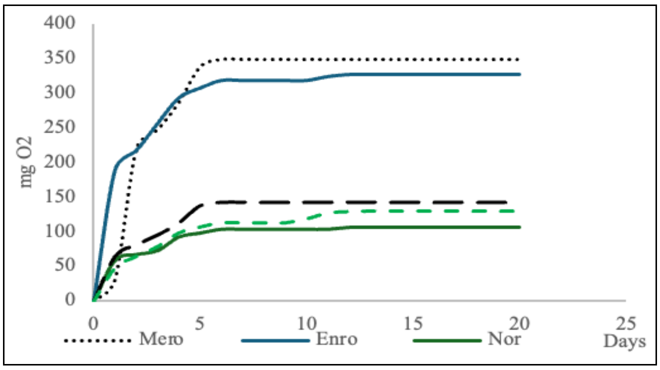

Fig 1 Closed-Bottle Test by CO_2 Accumulation

Table 1 Emulsification Index (E24), Optical Density (OD 600 nm), Degradation Percentage (Dg%), Shannon Index (H) and Fatty Acid Index for the Five Antibiotics Selected for the Study.

	Enromycin	**Meropenem**	**Norfloxacin**	**Penicillin**	**OTC**
EE 24h	12.52	81.25	-	-	-
OD 600nm	10.66	54.50	3.6	20.92	2.54
Dg %	77.36	68.70	47.94	81.27	70.80
Shannon H	3.023	2.59	2.787	3.112	2.835
Gram +	25.24	7.70	31.03	13.68	21.98
Firmicutes	25.24	7.70	29.93	13.68	21.98
Actinobacteria	-	-	1.10	-	-
Gram -	21.82	31.61	25.91	9.47	18.20
Zygomycota:	6.96	-	-	0.72	0.69
Ascomycota and Basidiomycota	10.34	-	-	2.69	2.98
Unspecific fungal	1.17	-	0.95	0.51	0.63
Unspecific microbial	18.35	29.93	23.47	14.08	10.78

It is known that bacteria susceptible to antibiotics acquire resistance genes. The information about antibiotic resistance is extensive and annually updated. However, research on antibiotic degradation is less prevalent, with even fewer studies investigating microorganisms capable of utilizing antibiotics as carbon and energy sources (Reis, 2020). Antibiotic biodegradation occurs through both biotic and abiotic processes. Biotic processes involve microbial activity, while abiotic ones encompass sorption, hydrolysis, photolysis, oxidation, and reduction reactions (Massé et al., 2014). For this reason, the present study was conducted in dark rooms to evaluate only the biodegradation process and not light oxidation.

The FAME analysis of microbial communities (Table 2, Fig. 2) showed that the antibiotics influenced the proportion of Gram-positive and Gram-negative bacteria. Norfloxacin favored the growth of Gram-positive bacteria (31.03%), meropenem favored Gram-negative bacteria (31.60%), enramycin favored Zygomycota (6.96%) and penicillin favored Ascomycota/Basidiomycota (2.69%). Meropenem also influenced the growth of the unspecified microbial group (29.93%), reflecting its wide impact on the community. These results suggest that the antibiotics selected not only alter bacterial growth, but also the structure and diversity of microbial communities, reflecting a complex interaction between antibiotics and microorganisms in the soil studied.

The Shannon index (H') (Table 1) showed highest diversity in the soil samples exposed to penicillin (3.112), indicating a more balanced and diverse bacterial community, in agreement with that reported by Liu et al. (2016). Although both penicillin and meropenem are β-lactam antibiotics, meropenem presented a lower diversity index (2.590) than penicillin, suggesting a decrease in the richness or evenness of the species present under its influence. The remaining antibiotics impacted the microbial community structure differently: enramycin (3.023) and norfloxacin (2.787) maintained a relatively high diversity, while OTC (2.835) maintained a somewhat lower but still significant diversity, the isolated microorganism recovers were slow in comparison to β-lactam antibiotics. Several studies have indicated that antibiotics significantly impact soil microbial communities, altering their structure and activity **(**Cycoń et al. 2019**).** The effects of antibiotics on the activity and diversity of microbial communities depend on various soil physicochemical parameters, antimicrobial activity, antibiotic dosage, and exposure time. It has been demonstrated that microorganism's sensitive to different antibiotics are killed or inhibited in the presence of antibiotics (Conde-Cid et al., 2020). However, on the other hand, there is evidence suggesting that certain microorganisms can adapt to antibiotics, potentially transforming them or even growing at their expense (Ahmad et al., 2022). A possible explanation for this is that less toxic transformation products may facilitate the recovery of original microbial communities from the initial disturbances caused by antibiotic exposure. In this regards, various studies have found transient negative effects of antibiotics on the functional, structural, and genetic diversity of soil microbial communities, leading to a temporary loss of soil functionality followed by subsequent recovery (Ahmad et al., 2022).

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The fatty acid composition of the bacterial communities grown in the presence of different antibiotics showed modifications in their communities (Table 2, Fig. 2) with more than 10 Euclidean distances. The profiles showed that fatty acids were widely represented under all conditions, while others were specific to certain treatments. The 16:1 w7c fatty acid, for example, which is related to bacterial membranes, was predominant in all antibiotic treatments, reaching its highest proportion with meropenem (18.00%) and showing significant values with enramycin (11.10%) and norfloxacin (11.39%).

Table 2 Fatty Acid Prefile for the Five Antibiotics Selected for the Study.

	Enramycin	**Meropenem**	**Norfloxacin**	**Penicillin**	**Oxytretracycline**
8:0 3OH	-	0.39	-	-	-
10:0 iso	0.52	-	-	-	-
10:0	0.78	0.65	0.71	0.38	0.57
11:0 iso	0.68	0.24	1.14	0.25	0.13
12:0 alde	-	-	-	0.16	-
10:0 3OH	1.99	3.32	2.59	6.90	9.71
12:0 iso	-	1.95	0.40	1.70	0.47
12:0	4.42	9.35	1.55	8.49	13.92
11:0 3OH	-	-	0.97	0.22	0.22
13:0 iso	-	7.00	4.67	9.46	1.85
13:0 anteiso	-	1.67	1.17	2.25	-
13:0	-	0.46	-	-	0.32
12:0 2OH	1.65	2.11	1.76	5.86	8.75
12:0 3OH	2.67	2.44	1.98	4.18	5.37
14:0 iso	2.00	1.40	1.15	1.46	0.47
14:0	4.67	8.21	3.41	2.54	3.86
15:0 iso	5.35	1.94	17.23	4.10	1.21
15:0 anteiso	6.13	0.71	4.25	1.72	1.21
15:1 w5c	-	-	-	2.81	-
14:0 iso 3OH	-	-	-	0.17	-
16:0 iso	3.54	3.39	1.39	0.54	15.34
16:0 N alcohol	-	-	-	0.76	0.41
16:0 anteiso	3.70	-	-	1.24	1.38
16:1 w9c	-	-	1.81	-	-
16:1 w7c	11.10	18.00	11.39	8.30	9.91
16:1 w5c	-	0.23	-	-	0.16
16:0	11.08	20.96	17.95	10.78	6.37
15:0 iso 3OH	-	-	-	6.59	0.40
17:1 iso w10c	0.44	-	-	-	0.12
16:0 10Methyl	-	-	1.10	-	-
15:0 3OH	-	-	-	0.84	0.36
17:0 iso	0.75	0.27	3.50	1.19	0.40
17:0 anteiso	3.77	-	0.69	2.92	1.96
17:1 w8c	-	-	0.53	-	0.38
17:0 cyclo	0.72	6.55	-	0.55	2.23
17:0	-	0.34	-	-	-
18:1 iso	-	-	0.64	-	-
16:0 3OH	-	0.21	-	-	-
18:3 w6c (6.9.12)	1.17	-	0.95	0.51	0.63
18:2 w6.9c	10.34	-	-	2.69	2.98
18:1 w9c	6.96	-	-	0.72	0.69
18:1 w7c	8.85	5.87	12.70	-	5.62
18:1 w5c	-	-	-	-	0.18
18:0	2.14	0.42	2.12	0.76	0.55
17:0 2OH	-	0.58	-	-	-
19:1 iso I	-	-	-	0.21	-
17:0 3OH	-	-	0.63	-	-
19:0 iso	1.16	-	1.09	0.34	-
19:1 w6c	0.47	-	-	-	-
19:0 cyclo w10c	-	-	-	7.02	-
19:0 cyclo w8c	1.14	1.18	-	0.61	0.44

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18:0 2OH	0.40	0.17	-	0.22	0.54
20:4 w6.9.12.15c	-	-	0.52	-	-
18:0 3OH	0.95	-	-	0.56	0.77
20:1 w9c	-	-	-	-	0.12
20:0	0.47	-	-	-	-

The biomarker 10:0 3OH, associated with Gram-negative bacteria (Norris et al., 2023), also varied significantly, reaching its highest proportion under the effect of OTC (9.71%) and penicillin (6.90%). As shown in Table 3, Pseudomonas sp. was isolated only in the treatment with OTC. This correlates with the data in Table 1, where the proportion of Gram-negative bacteria was also high under grown conditions. On the other hand, branched fatty acids, such as 15:0 iso, typical of Gram-positive bacteria, were especially abundant in the samples exposed to norfloxacin (17.23%), consistent with the higher proportion of Gram-positive bacteria observed under this treatment (Table 3).

Table 3 Bacteria Isolated from Different Media with the Five Antibiotics Selected for the Present Study

Enramycin	**Meropenem**	**Norfloxacin**	**Penicillin**	**Oxytretracycline**
Bacillus cereus	Bacillus cereus /thuringiensis	Stenotrophomonas maltophilia	Bacillus sp	Pseudomonas aeruginosa
Bacillus cereus	Microbacterium barkeri	Achromobacter xylosoxidans Achromobacter denitrificans	Cellulomonas fimi	Pseudomonas aeruginosa
	Paenibacillus polymyxa	Achromobacter xylosoxidans Achromobacter denitrificans	Virgibacillus pantothenticus	
	Curtobacterium flaccumfaciens		Cellulomonas fimi	
	Kokuria rhizophila		Pseudomonas aeruginosa	
			Mycobacterium	

Branched fatty acids such as 15:0 iso and 17:0 iso are characteristic of Gram-positive bacteria such as Bacillus sp. and Paenibacillus polymyxa, while unsaturated fatty acids such as 16:1 w7c and 18:1 w7c, here present in greater abundance, are typical of Gram-negative bacteria such as Pseudomonas aeruginosa and Stenotrophomonas maltophilia (Rodriguez et al., 2006). These results highlight the importance of integrating taxonomic characterization with lipid analysis to understand the adaptive responses of microbial communities to external stimuli like as antibiotics. These results indicate that antibiotics modulate not only the growth of microbial communities, but also their ecological complexity, which may have important implications for the resilience and functionality of these communities.

The FT-IR analysis (Fig. 3) showed significant differences in the spectral profiles of bacterial communities treated with different antibiotics, evidencing changes in their biochemical composition. The spectra highlight specific variations in regions corresponding to functional groups, such as bands associated with proteins (1700–1500 cm^{-1}) and carbohydrates (1200–900 cm^{-1}). This suggests that antibiotics may cause alterations in bacterial macromolecules. Enramycin and norfloxacin presented more differentiated spectral patterns than the other antibiotics, which could indicate a different impact on bacterial communities.

The dendrogram from the results of the FT-IR spectra (Fig. 3) is congruent with the FAMEs dendrogram (Fig. 2), except for OTC, grouping enramycin and norfloxacin in a cluster separated from the rest of the antibiotics evaluated. On the other hand, OTC showed a greater distance than the other treatments, suggesting a unique response in the exposed microbial communities.

These patterns suggest that antibiotics not only affect the diversity and composition of microbial communities, as indicated by the Shannon index and baseline data, but also induce changes in the lipid composition of cell membranes. Although both methods (FT-IR and FAMEs) showed similar results, it is important to highlight that obtaining FT-IR spectra is more inexpensive and faster than obtaining the FAME profiles.

These results reflect specific adaptive strategies of bacteria against antibiotic stress, such as modifications in membrane fluidity or integrity, depending on the type of antibiotic used (Schumacher, 2023).

The mineralization process (Fig. 1) shows significant differences in the ability of microbial communities to use antibiotics. Meropenem exhibited the highest mineralization rate, reaching a maximum value close to 350 mg O_2 in only 5 days, indicating that the communities associated with this antibiotic possess high metabolic activity and degradation ability. Enramycin showed intermediate mineralization, with stabilization at approximately 200 mg CO_2. Both meropenem and enramycin showed emulsification activity (Table 1).

According with Mohammed (2020) found successful extraction (up to 97 %) with no significant emulsion breakage, and the stripping efficiency was more than 96 % in our case the system with OTC has not EE24hs but can be the reason has a less degradation for bacterial communities. Norfloxacin and penicillin showed a lower degree of mineralization, with values around 100-150 mg CO_2 after 10 days. OTC showed the lowest mineralization rate, suggesting a more limited metabolism or greater structural resistance of the compound.

The present results also showed that more than 70.8 % of OTC was successfully removed after 20 days of culture (Table 1), indicating excellent ability of bacteria to degrade

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this antibiotic. According to previous results, the removal of OTC by different bacteria was similar to or higher than 99.9 % by the cyanobacterium Spirulina platensis (Zhou et al., 2021), 92.6 % (100.0 mg/L) by Chlorella sorokiniana (Wu et al., 2022), and 39.2 % (10.0 mg/L) by Scenedesmus obliquus (Yang et al., 2020). OTC consumes minimal oxygen and is necessary for antibiotic mineralization; however, this antibiotic is predominantly degraded by fungi, with partial cleavage of its stable four-ring core structure. This degradation mechanism has not yet been correlated to the actual mineralization rate reported by Reis (2020) (Fig. 2). Antibiotics like tetracyclines, quinolones and sulfonamides, are photo sensitive. Regarding these antibiotics, Cetecioglu et al. (2014) observed biodegradation of approximately 46%.

Meropemen and penicillin are both β-lactam antibiotics but possess different oxygen contents and distinct community selections. Degradation of these antibiotics primarily occurs through hydrolysis of the β-lactam ring, producing degradation products that can frequently be detected at higher concentrations than the parent form. To date, only a limited number of strains have been reported to further degrade degradation products, a process probably associated with certain enzymes and their coding genes. β-lactam antibiotics can be degraded not only by β-lactamases, but also by enzymes from different classes. In a previous study, Al-Ahmed et al., 1999 found in the closed-bottle test demonstrated that penicillin G is degraded more extensively than ciprofloxacin, meropenem, sulfamethoxazole, and cefotian dihydrochloride. Penicillin is degraded in the presence of β-lactamase or penicillinase under acidic or alkaline conditions, and even in the presence of weak nucleophiles such as water and metal ions (Popovich et al., 2020). Several studies have demonstrated that Penicillin and cephalosporins are degraded in the presence of metal ions such as mercury, copper (Bischoff et al., 2018), zinc, cadmium, and cobalt (Saitoh and Shibayama, 2016). These metal ions facilitate the opening of the β-lactam ring and catalyze the inactivation rate by forming intermediate complexes with penicillin and cephalosporins. Enzymatic strategies represent an excellent green technology with non-toxic effects on target and non-target organisms (Shah et a 2024). Regarding the degradation of fluoroquinolones such as norfloxacin, some authors have reported that they are recalcitrant compounds. Degradation and transformation occur predominantly at the piperazine moiety, whereas certain fungal species have demonstrated the ability to cleave the stable quinoline core and partially mineralize some of these antibiotics. In the present study, norfloxacin exhibited the lowest oxygen utilization rate. In this regard, de Souza Santos et al. (2014) observed norfloxacin degradation of 12-18% in treatments with activated sludge and anaerobic biodigesters.

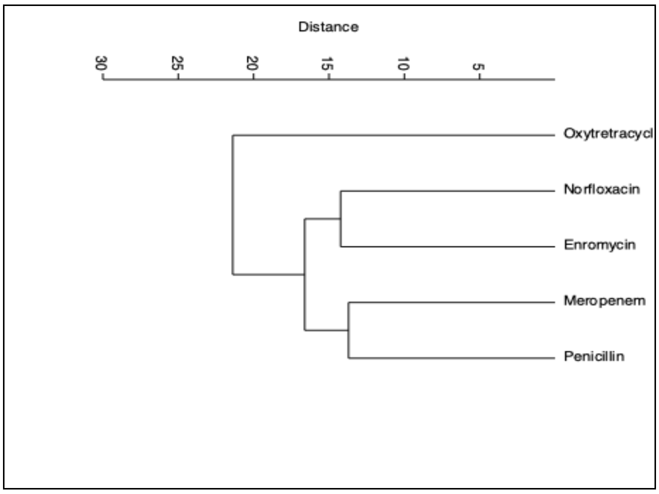

Fig 2 Dendrogram Obtained from All Fatty Acid Methyl Esters (FAMEs)

Enramycin and macrolides mineralization have been reported to some extent in soil and demonstrate favorable utilization by bacterial communities (Topp et al 2016), with 77.36% in an FT-IR occurring in the same location as meropenem but possessing different fatty acids with distinct Shannon indices. The underlying mechanism is likely related to the action of esterases, which have been shown to partially hydrolyze the stable 14-membered lactone ring of this antibiotic.

Reis (2020) reported that antibiotic degraders may protect susceptible members of the microbiota by reducing antibiotic concentrations, thus eliminating the need for susceptible bacteria to acquire resistance genes, a phenomenon known as indirect resistance. According to this author, the utilization of antibiotic-degrading organisms to biodegrade antibiotics shows promise from a biotechnological perspective. However, the risks associated with the direct application of these antibiotic degraders for bioremediation and bioaccumulation purposes must be carefully considered. Some bacteria identified as degraders exhibit antibiotic resistance, which can become rapidly established in microbial populations through compensatory mutations and co-resistance events.

Together, these findings highlight the complex interplay between microbial diversity, biochemical composition, and functional capacity of bacteria for the degradation of specific antibiotics.

IV. CONCLUSION

Enramycin, norfloxacin, meropenem, penicillin and oxytetracycline were susceptible to biodegradation and biotransformation reactions by bacteria from an oil-contaminated soil. The selected bacterial groups differed from those of the original bacterial community. We suggest that future work on soil bioremediation should be focused on enzymatic remediation, and that biological techniques should be preferred over antibiotic treatments.

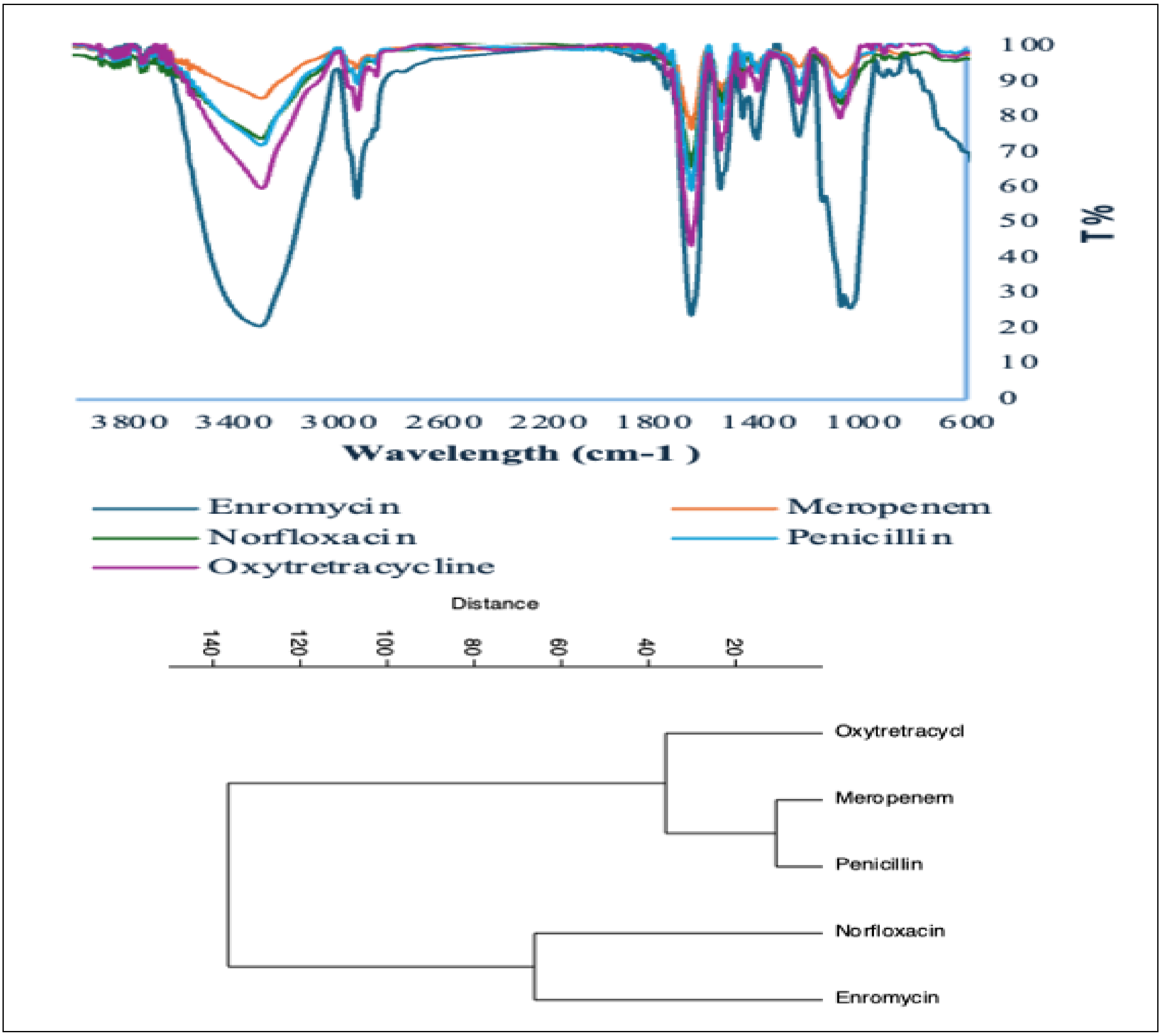

Fig 3 Dendrogram Obtained from All Fatty Acid Methyl Esters (FAMEs)

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