



Review

Crossiella, a Rare Actinomycetota Genus, Abundant in the Environment

Tamara Martin-Pozas ^{1,†} , Jose Luis Gonzalez-Pimentel ^{2,†}, Valme Jurado ³, Leonila Laiz ³, Juan Carlos Cañaveras ⁴, Angel Fernandez-Cortes ⁵ , Soledad Cuezva ⁶ , Sergio Sanchez-Moral ¹ and Cesareo Saiz-Jimenez ^{3,*}

¹ Museo Nacional de Ciencias Naturales, MNCN-CSIC, 28006 Madrid, Spain

² Centro Andaluz de Biología del Desarrollo (CABD, UPO-CSIC-JA), Facultad de Ciencias Experimentales, Departamento de Genética, Universidad Pablo de Olavide, 41013 Sevilla, Spain

³ Instituto de Recursos Naturales y Agrobiología, IRNAS-CSIC, 41012 Sevilla, Spain

⁴ Departamento de Ciencias de la Tierra y del Medio Ambiente, Universidad de Alicante, 03080 Alicante, Spain

⁵ Departamento de Biología y Geología, Universidad de Almería, 04120 Almería, Spain; acortes@ual.es

⁶ Departamento de Geología, Geografía y Medio Ambiente, Universidad de Alcalá, 28802 Alcalá de Henares, Spain; soledad.cuezva@uah.es

* Correspondence: saiz@irnase.csic.es

† These authors contributed equally to this work.

Abstract: The genus *Crossiella* contains two species, *C. equi*, causing nocardioform placentitis in horses, and *C. cryophila*, an environmental bacterium. Apart from *C. equi*, which is not discussed here, environmental *Crossiella* is rarely reported in the literature; thus, it has not been included among “rare actinobacteria”, whose isolation frequency is very low. After *C. cryophila*, only five reports cover the isolation of *Crossiella* strains. However, the frequency of published papers on environmental *Crossiella* has increased significantly in recent years due to the extensive use of next-generation sequencing (NGS) and a huge cascade of data that has improved our understanding of how bacteria occur in the environment. In the last five years, *Crossiella* has been found in different environments (caves, soils, plant rhizospheres, building stones, etc.). The high abundance of *Crossiella* in cave moonmilk indicates that this genus may have an active role in moonmilk formation, as evidenced by the precipitation of calcite, witherite, and struvite in different culture media. This review provides an overview of environmental *Crossiella*, particularly in caves, and discusses its role in biomineralization processes and bioactive compound production.

Keywords: *Crossiella*; biofilms; caves; moonmilk; biomineralization; rhizosphere; soils; bioactive compounds



Citation: Martin-Pozas, T.; Gonzalez-Pimentel, J.L.; Jurado, V.; Laiz, L.; Cañaveras, J.C.; Fernandez-Cortes, A.; Cuezva, S.; Sanchez-Moral, S.; Saiz-Jimenez, C. *Crossiella*, a Rare Actinomycetota Genus, Abundant in the Environment. *Appl. Biosci.* **2023**, *2*, 194–210. <https://doi.org/10.3390/applbiosci2020014>

Academic Editor: Robert Henry

Received: 4 March 2023

Revised: 24 April 2023

Accepted: 27 April 2023

Published: 6 May 2023



Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (<https://creativecommons.org/licenses/by/4.0/>).

1. Introduction

The first strain included in the genus *Crossiella* has a long history of transfers and amendments. Takahashi et al. [1] studied the soil isolate *Nocardioopsis mutabilis*, capable of producing novel antibiotics, and classified it as a new subspecies: *Nocardioopsis mutabilis* subsp. *Cryophilis* based on its growth at low temperatures (8–33 °C). This strain was subsequently transferred by Labeda and Lechevalier [2] to the genus *Saccharothrix* as *Saccharothrix cryophilis* because its morphological and chemotaxonomical properties were more typical of the genus *Saccharothrix* than *Nocardioopsis*. In another study, Labeda [3] erected the genus *Crossiella* to accommodate the species *Saccharothrix cryophilis*, which was misplaced within the genus *Saccharothrix*. The genus only contained the species *Crossiella cryophila*, which was soon accompanied by *Crossiella equi*, responsible for causing abortion cases in horses with equine nocardioform placentitis in Kentucky [4].

In the last 20 years, no other species of *Crossiella* have been described, with scarce reports on the isolation of *Crossiella* strains in the literature. Sánchez-Moral [5] isolated a few strains of *Crossiella* from Altamira Cave, Spain. Adeyemo and Onilude [6] described a strain of *Crossiella* isolated from Nigerian soil with a broad spectrum of antimicrobial

activity. Cimermanova et al. [7] isolated nine actinobacteria collected from different heavy metal-contaminated soils and found that one strain could represent a new species within the genus *Crossiella*; however, they did not provide any characterization or description other than its position in the phylogenetic tree and that the strain differed from *Crossiella cryophila* in several biochemical properties. González-Riancho [8] isolated three *Crossiella* strains from white and grey biofilms from Altamira Cave. Finally, Gonzalez-Pimentel et al. [9] studied the genomes of two *Crossiella* strains selected from 13 strains previously isolated from Altamira Cave (unpublished report).

The isolation of *Crossiella* strains on only five occasions in the last 10 years included this genus within the so-called “rare actinobacteria”. Oren and Garrity [10] considered *Actinobacteria* a synonym of *Actinomycetota*. They presented the names and formal descriptions of 42 phyla to effect valid publication in their names based on genera as nomenclatural types. However, in this paper, we maintained the original names, as previously published by each author, to avoid mistakes.

“Rare actinobacteria” are non-*Streptomyces* actinobacteria whose isolation frequency is much lower than *Streptomyces* strains, commonly isolated by conventional methods [11,12]. Tiwari and Gupta [13,14] reported 120 new genera of “rare actinobacteria” in the first decade of the 21st century. A total of 40 out of 120 genera were isolated from soils with comparatively lower percentages from other environments: marine and freshwater sediments, marine animals, plants, buildings, etc. A few reports included the rare genera *Actinomadura*, *Nonomuraea*, *Micromonospora*, *Streptosporangium*, *Nocardiosis*, and *Pseudonocardia* as most frequent in diverse environments [15–20]. It is noteworthy that an abundance of “rare actinobacteria” is in extreme environments, as exemplified in Atacama [18] and other deserts [21–24]. However, *Crossiella* has not been included among “rare actinobacteria” thus far. We have found that *Crossiella* is an abundant genus in most studied Spanish caves, whether they are gypsum, karstic, or volcanic [9,25–27], and in other terrestrial and aquatic environments.

In this paper, we review the occurrence of environmental *Crossiella*, its relative abundance in Spanish caves and other subterranean environments, as well as its involvement in caves’ mineral precipitation. The interest in *Crossiella* lies in its role in biomineralization and potential use in biotechnological processes (stone bioconsolidation, enzyme sources, bioactive compounds, etc.).

2. The Genus *Crossiella* in Caves

Table 1 shows the occurrence of *Crossiella* in different Spanish caves. The high relative abundance of this genus is in moonmilk (Figure 1), either from karstic (Pindal) or volcanic (Fuente de la Canaria and Bucara II) caves, as well as in coloured biofilms (Pindal, Altamira, Castañar, Covadura) is remarkable [27–31]. The relative humidity is near 100% in these caves. In addition, other mineral/biological formations, such as a pink formation in Bucara II, exhibit high relative abundance (38.9%). Similarly, formations such as mucous formations or brown deposits also reach relatively high abundances (6.7–12.8%) [29]. Interestingly, low percentages of *Crossiella* found in the sediments under the moonmilk indicate an aerobic behaviour for this genus [3]. *Crossiella* was also found in phototrophic biofilms from Nerja Cave [30].

Table 1. Occurrence and relative abundance (>1%) of *Crossiella* in Spanish karstic environments, as reported in NGS studies.

Cave	Relative Abundance	Genus	Type of Sample	References
Pindal	16.0–27.1	<i>Crossiella</i>	Moonmilk	[26,28,31]
	1.4–1.7	<i>Crossiella</i>	Sediment under moonmilk	
	11.3–11.7	<i>Crossiella</i>	Top-layer sediments	

Table 1. Cont.

Cave	Relative Abundance	Genus	Type of Sample	References
	6.0–9.0	<i>Crossiella</i>	Sediments	
	5.3–7.9	<i>Crossiella</i>	Yellow biofilm	
	2.0–8.0	<i>Crossiella</i>	Grey biofilms	
	7.0–8.0	<i>Crossiella</i>	Pink biofilms	
Fuente de la Canaria	12.6–12.8	<i>Crossiella</i>	Mucous formations	
	12.3	<i>Crossiella</i>	Moonmilk	[29]
	6.7	<i>Crossiella</i>	Brown and yellow deposits	
Bucara II	38.9	<i>Crossiella</i>	Pink deposit	[29]
	24.9	<i>Crossiella</i>	Moonmilk	
Nerja	0.1–1.5	<i>Crossiella</i>	Phototrophic biofilms	[30]
Castañar	15.0	<i>Crossiella</i>	Grey biofilm	[31]
Altamira	>20.0	<i>Crossiella</i>	Grey biofilms	
	27.0	<i>Crossiella</i>	White biofilms	[30]
	38.0	<i>Crossiella</i>	Yellow biofilms	
Covadura	26.4–54.1	<i>Crossiella</i>	White biofilm	
	21.8–51.9	<i>Crossiella</i>	Yellow biofilm	Unpublished data
	4.5–19.7	<i>Crossiella</i>	Sediments	
Yeso	1.3–13.3	<i>Crossiella</i>	Sediments	Unpublished data
Thyssen Museum basement	16.6	<i>Crossiella</i>	White biofilm	
	64.2	<i>Crossiella</i>	Grey biofilm	[32]
	2.8–7.4	<i>Crossiella</i>	Sediment	

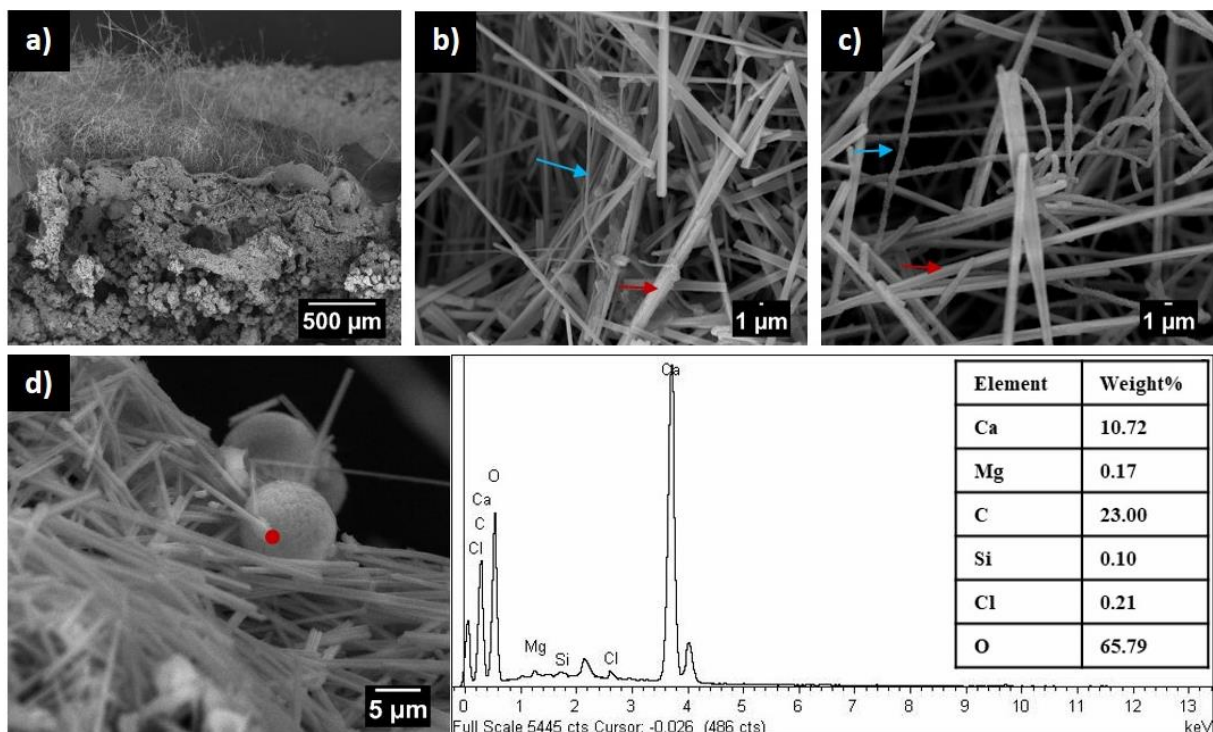


Figure 1. Scanning electron micrographs of moonmilk deposits in Pindal Cave, Spain. (a) Longitudinal view of sediment covered by moonmilk. (b,c) Crystalline calcite fibres (red arrow) and *Actinomycetota* filaments (blue arrow). (d) Scanning electron micrographs and EDX spectra of crystalline calcite fibres. Note the swelling of filaments in (c), similar to those reported for *Crossiella cryophila* [3].

Crossiella, at a relative abundance of 15.0%, was found in grey biofilms from Castañar Cave [31]. Similar grey biofilms were observed in Altamira Cave [8] and the Thyssen Museum, reaching a relative abundance of 64.2% [32]. Data from a geomicrobiological study of a Roman nymphaeum located in the archaeological basement of the Thyssen Museum in Malaga, Spain, were also included in Table 1 due to its interest.

The environmental conditions of this archaeological basement are special because they mix the characteristics of an environment heavily influenced by the natural underlying karst system with those of an enclosure located in an urban building. Apart from caves, it was remarkable that a subterranean environment, the Roman mortar pavement in the archaeological basement, was colonized by grey biofilms with a high relative abundance of *Crossiella*. This environment is characterized by permanent darkness, the absence of visits, and high relative humidity.

Table 1 shows the occurrence of *Crossiella* in moonmilk, grey, yellow, pink and white biofilms, and sediments from different caves and subterranean environments. *Crossiella* is abundant in different types of rocks, either in volcanic (Fuente de la Canaria, Bucara II), karstic (Pindal, Nerja, Castañar, Altamira) or gypsum (Covadura, Yeso) caves.

In addition to the studies in Table 1, authors have reported the occurrence of *Crossiella* using methodological approaches other than NGS. Stomeo et al. [33] found metabolically active *Crossiella* in white biofilms from Ardales Cave, Malaga, Spain. Portillo and Gonzalez [34] identified *Crossiella* as a major metabolically active bacterium in the black crust of a shelter located in Aragon, Spain, and Sanchez-Moral [5] reported *Crossiella* in Altamira Cave.

Table 2 shows the widespread occurrence of *Crossiella* in caves in the USA, France and China. Less frequent records were found in caves in Italy, Pakistan, Portugal, Serbia, and Thailand, among other countries [35–57].

Table 2. Occurrence and relative abundance (>1%) of *Crossiella* in caves all over the world.

Karstic Caves	Relative Abundance%	Genus	Type of Sample (Method)	References
Heshang	n.d.	<i>Crossiella</i>	Weathered rocks (NGS)	[35]
Laugerie-Haute	4.0	<i>Crossiella</i>	Salt efflorescences (clones)	[36]
Sorcerers	30.0	<i>Crossiella</i>	Salt efflorescences (NGS)	[37]
Pillier	n.d.	<i>Crossiella</i>	Wall rock (NGS)	[38]
Yixing Shanjuan	3.9	<i>Crossiella</i>	Speleothem (NGS)	[39]
Shuanghe	9.5	<i>Crossiella</i>	Rock (NGS)	[40]
Manao-Pee	4.1	<i>Crossiella</i>	Soil (NGS)	[41]
KN14	27.1–52.3	<i>Crossiella</i>	Rock/Clay (NGS)	[42]
RN5	1.0–17.9	<i>Crossiella</i>	Rock/Clay/Mud (NGS)	[42]
Maijishan Grottoes	n.d.	<i>Crossiella</i>	Walls paintings (NGS)	[43]
Heshang	n.d.	<i>Crossiella</i>	Weathered rocks (NGS)	[44]
Kashmir and Tiser	11.9–36.6	<i>Crossiella</i>	Soil (NGS)	[45]
Zhijin	4.1	<i>Crossiella</i>	Wall rock (NGS)	[46]
Rouffignac	~70.0	<i>Crossiella</i>	Wall rock (NGS)	[47]
Stiffe	9.9	<i>Crossiella</i>	Biofilms (NGS)	[48]
Heshang	n.d.	<i>Crossiella</i>	Weathered rocks (NGS)	[49]
Cave Church	0.1–4.9	<i>Crossiella</i>	Fresco (NGS)	[50]
Volcanic Caves				
Azorean caves	18.6	<i>Crossiella</i>	Biofilms (clones)	[51]

Table 2. Cont.

Karstic Caves	Relative Abundance%	Genus	Type of Sample (Method)	References
Hawaiian caves	n.d.	<i>Crossiella</i>	Biofilms (NGS)	[52]
Californian caves	n.d.	<i>Crossiella</i>	Biofilms (NGS)	[53]
Idahoan caves	n.d.	<i>Crossiella</i>	Biofilms (NGS)	[54]
Sicilian caves	62.5–77.6	<i>Crossiella</i>	Biofilms (NGS)	[55]
Other Cave Types				
Carlsbad Cavern	n.d.	<i>Crossiella</i>	Rocks (clones)	[56]
Imawari Yeuta	n.d.	<i>Crossiella</i>	Patina/Speleothems (NGS)	[57]

n.d. Not determined.

Apart from the high abundance in Spanish caves, the high relative abundance of *Crossiella* in Italian caves is also remarkable. In this regard, Nicolosi et al. [55] recorded high relative abundances in four Etna volcano caves. One of them ranged from 62.5 to 77.6%. Other notable abundances were found in the salt efflorescences of a French shelter [37] and in caves in the USA [42], France [47], Pakistan [45], and the Azores, Portugal [51].

Crossiella has been identified as one of the dominant bacterial phylotypes, with an increasing prevalence when global humidity conditions rise, in a research covering 1050 cave microbiomes worldwide (manuscript in preparation).

3. *Crossiella* in the Environment

Supplementary Table S1 lists papers in the literature that use the keyword “*Crossiella*”, including *Crossiella* misspelling [58–146]. The occurrence of the genus *Crossiella* in different environments is significant. Papers reporting *Crossiella equi* and its involvement in animal diseases [4] were excluded.

The papers listed in Supplementary Table S1 rely on molecular methods, except for five articles describing the properties of isolated strains [5–9]. The genus *Crossiella* shows a ubiquitous and extensive geographical distribution on all continents, including Antarctica, but not in Australia/Oceania, likely due to a lack of relevant studies.

Fewer reports locate *Crossiella* in mines and reclaimed mine soils [7,120–124]. However, the number of studies on its presence in soils and the rhizospheres of diverse plants is considerable. Several *Crossiella* findings in stones and building stones were also confirmed [125–138]. Finally, a few records in sea sediments and freshwaters were significant [139–146] because they included aquatic environments among *Crossiella* habitats.

From Supplementary Table S1, we can conclude that *Crossiella*, in addition to caves, is relatively abundant in diverse environments, namely soils, plant rhizospheres, mines, building stones, and other occasional habitats, but is rarely isolated.

Considering the abundance of reports on *Crossiella* in soils [58–96] and plant rhizospheres [97–119], the presence of this genus in caves and other subterranean environments could be attributed to its transport to the subsurface via percolation waters. In this regard, *Crossiella* in percentages <1% have been found in drip waters from Pindal Cave [28]. It may be possible that once transported to the caves, the environmental conditions favour and increase the colonization and growth of *Crossiella* on different mineral substrata.

4. *Crossiella* Isolates

Only five reports shed light on *Crossiella* isolates. A screening of Nigerian soils resulted in the isolation of *Crossiella* sp. strain EK18. The 16S rRNA nucleotide sequence showed 98% similarity to *C. equi*. This strain grew well in different culture media and exhibited broad-spectrum antimicrobial activity [6]. The authors studied the effects of pH, temperature, carbon and nitrogen sources, sodium chloride concentration, and incubation time on antimicrobial activity. In addition, they reported a list of 12 so-called antimicrobial

metabolites, including alkanes, alkenes, commonly synthesized by bacteria, and phthalates, which are contaminants from materials and impurities from products used in culture media. Therefore, no conclusive data on the real bioactive compounds produced by the *Crossiella* strain can be derived from this study.

Cimermanova et al. [7] isolated *Crossiella* sp., strain S2, from mining wastes, with a 16rRNA gene sequence similarity of 99.1% to *C. cryophila*. The authors suggested that it may represent a novel, never described species, based on its location in the phylogenetic tree. The strain also exhibited high heavy metal resistance.

González-Riancho [8] found relative abundances of *Crossiella* >20% in white, yellow, and grey biofilms from Altamira Cave. She isolated two strains from white and one strain from grey biofilms with similarities of 99.0–100.0 to *C. cryophila* using the medium Actinomycete Isolation Agar (AIA).

Gonzalez-Pimentel et al. [9] studied two of the thirteen *Crossiella* strains previously isolated from grey biofilms colonizing Altamira Cave, Spain (unpublished report). In vitro and in silico analyses showed the inhibition of pathogenic bacteria and fungi. The exclusive combination of gene clusters involved in the synthesis of lanthipeptides, lasso peptides, nonribosomal peptides and polyketides indicates that these two strains represent a source of new bioactive compounds. The taxonomical distance of both strains from their closest relative, *C. cryophila*, suggests that they represent a new species of *Crossiella*, which will be described in future works.

So far, the low number of isolated *Crossiella* strains indicates that most of the culture media used are inadequate to reproduce their growth in the laboratory. The environmental conditions of their ecological niche should also be considered when designing specific culture media, which are superior to conventional ones.

5. Biomineralization in Caves Induced by *Crossiella*

Biomineralization or crystal formation is a general phenomenon caused by soil bacteria, as reported by Boquet et al. [147]. These authors isolated 210 bacteria that could form calcite crystals in a medium with calcium acetate and stated that their occurrence depended on the composition of the medium used.

The role of bacteria in speleogenesis has been discussed for decades. Barton and Northup [148] stated that in the 1960s, a few authors proposed that microbes played a role in forming cave deposits. Banks et al. [149] confirmed the link between calcium metabolism in bacteria and calcification using cave isolates. They suggested that the toxicity of Ca^{2+} ions to bacteria promoted the need to remove Ca^{2+} ions from the cell via calcification as a detoxification mechanism.

Further evidence of biomineralization has been reported in recent decades that sheds light on microbially induced mineral precipitation [150–153]. This precipitation has been attributed to several causes: the modulation of environmental pH, nucleation sites on cell surfaces, or enzymatically driven processes involving carbonic anhydrase, urease, etc. [154].

Grey biofilms from Altamira Cave were studied, and scanning electron microscopy (SEM) revealed an abundance of bioinduced calcite crystals in addition to moonmilk [152]. The biofilms mainly comprised *Actinomycetota* filaments promoting carbon dioxide uptake and formation of calcite deposits. A model for bioinduced calcite formation, supported by scanning and transmission electron microscopy data, was proposed by Cuezva et al. [152].

Apart from the precipitation of calcite by *Crossiella*, another experiment (Figure 2) with two strains of *Crossiella* isolated from Altamira Cave [9] revealed that both strains induced the formation of different crystals when incubated in a culture medium with barium acetate, yeast extract, and agar (Ba1). Two crystal types were identified on the plates: witherite (barium carbonate) and struvite (magnesium ammonium phosphate), with distinct abundances that were higher for witherite and scarcer for struvite. Witherite precipitation is due to an abundance of barium in the medium. Occasional struvite crystals can be derived from the amino acids and minor amounts of phosphorus and magnesium in the yeast extract [155].

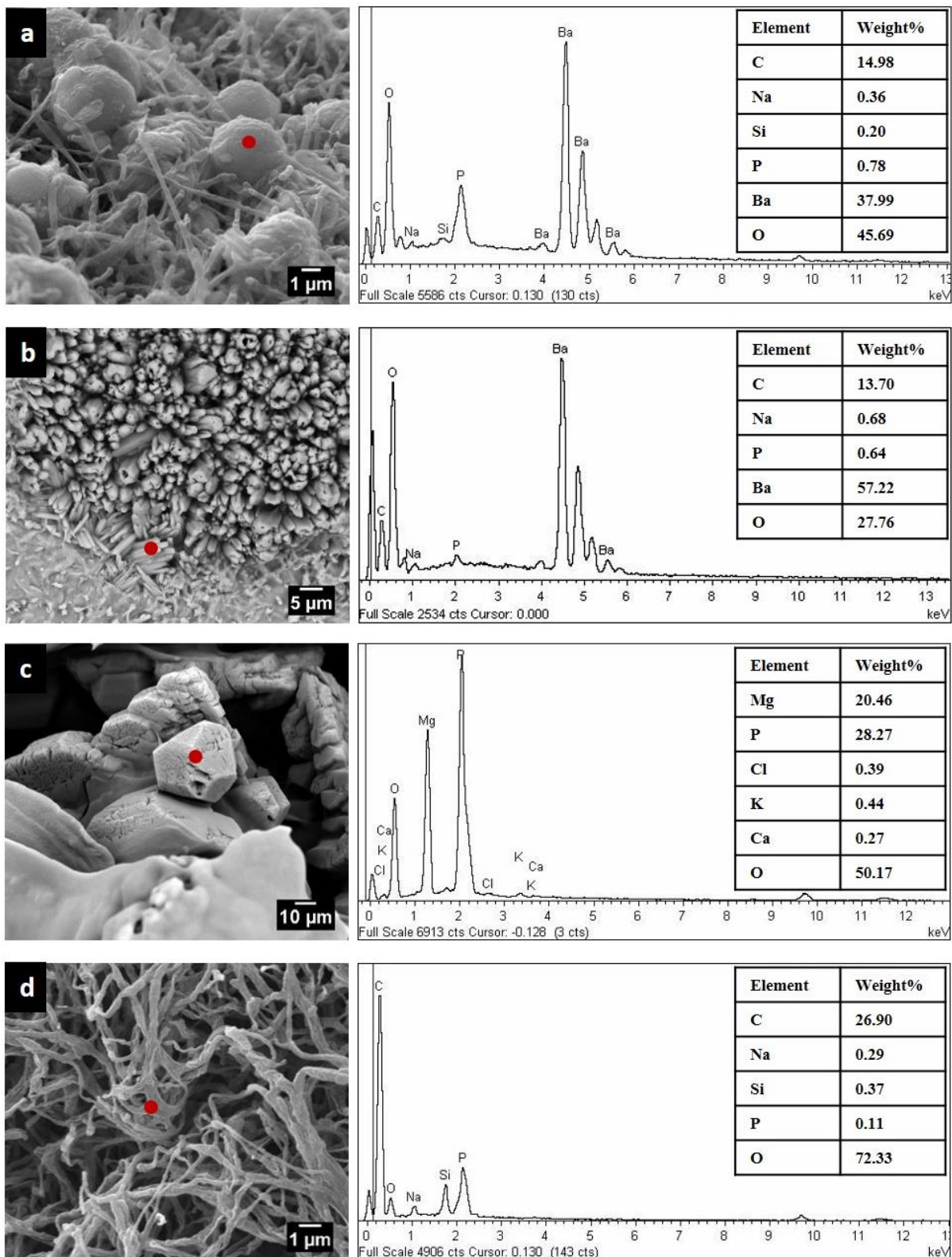


Figure 2. Scanning electron micrographs and EDX spectra of barium carbonate and phosphate crystals from two strains of *Crossiella* sp. (Cross-1 and Cross-2) [7]. (a) Witherite (barium carbonate) crystals and *Crossiella* filaments in culture medium Ba1 (Cross-1). (b) Witherite crystals in culture medium Ba1 (Cross-2). (c) Struvite (magnesium ammonium phosphate) crystals in culture medium Ba1 (Cross-1). (d) *Crossiella* filaments without crystal formation in tryptic soy agar medium (Cross-2).

Baryte (barium sulphate) precipitation by bacteria was previously reported by Joubert et al. [156]. Sanchez-Moral et al. [157] found that baryte was associated with filamentous bacteria in altered volcanic rocks. *Agromyces* spp., *Bacillus* spp., *Lysobacter* spp., *Ralstonia* sp., *Stenotrophomonas maltophilia*, and *Streptomyces* sp. were isolated from the volcanic rocks and precipitated witherite or calcite/vaterite in media with barium or calcium acetate, respectively. The occurrence of baryte, but not witherite, in volcanic rocks was due to the presence of sulphate ions that easily transform witherite into barite. This transformation was not produced on the *Crossiella* plates without sulphate ions.

Struvite precipitation is not as widespread as calcite or witherite in bacteria. Sanchez-Moral et al. [158] tested eight bacteria isolated from the Roman catacombs of St. Callixtus and Domitilla and reported that *Agromyces ramosus* precipitated calcite, magnesium calcite, witherite, and struvite, depending on the media composition. Other bacteria precipitating struvite were *Bacillus* sp. and *Ralstonia metallidurans*.

Rivadeneira et al. [159] found that only 20.8% of the tested bacterial isolates precipitated struvite and that calcium acetate appeared to inhibit struvite precipitation in culture media, whereas ammonium ions triggered it [160]. Manzoor et al. [161] stated that urease-producing bacteria play a key role in struvite precipitation, controlling nucleation, and modulating crystalline phases and crystal shapes. Urease is present in the strain type of *Crossiella*, *C. cryophila* [3], and urease genes have been identified in the genomes of the two *Crossiella* strains from Altamira Cave [9].

Sánchez-Román et al. [162] reported that carbon and phosphorus cycles are interrelated during biomineralization. They also demonstrated the co-precipitation of carbonate and struvite, which we also found in *Crossiella* strains.

The data reported show that biomineralization by *Crossiella* is an active process in the presence of different ions, confirming its role in moonmilk formation. *Crossiella* strains' ability to induce carbonate precipitation, which is used to consolidate cultural heritage stones and buildings, should be explored.

6. Moonmilk Formation

Moonmilk formation has been discussed in the literature for a long time [150,163–168]. The question: Is moonmilk an abiotic process driven physicochemically, or is it biotic, mediated by microorganisms? A biological origin currently prevails; even a combination of physicochemical and biogenic processes is being considered [166]. Cañaveras et al. [150,165] indicated that bacteria influenced the physicochemistry of calcite precipitation. They observed that cave moonmilk comprises a network of calcite crystals and active filamentous bacteria. They also found that hydromagnesite and needle-fibre aragonite deposits were associated with bacteria in Altamira Cave, predominantly *Streptomyces*, for which they demonstrated their ability to precipitate calcite/vaterite in the laboratory. The association between bacteria and mineral crystals was reported in other papers and described using SEM [152,153,165,168–170]. In addition, different bacterial genera such as *Agromyces*, *Amycolatopsis*, *Brachybacterium*, *Nocardioides*, *Nocardioopsis*, *Paenibacillus*, and *Rothia* precipitated vaterite/calcite and Mg-calcite [171].

Maciejewska et al. [153] found that all the *Streptomyces* strains tested could promote calcification and biomineralization. The metabolic activities involved in the precipitation were amino acids ammonification and ureolysis, which increased environmental pH. Sanchez-Moral et al. [169] stated that microbial activity induces carbonate precipitation in the early stages of deposition. However, as carbonate accumulates, a progressive decline in microbial activity occurs, as deduced from the RNA/DNA ratio, which is used as a marker of metabolic activity. The decreased metabolic activity is due to the progressive accumulation of carbonate and bacterial entrapment in mineral deposits.

The high relative abundance of *Crossiella* in moonmilk from different caves indicates that this genus is active in moonmilk formation (Table 1). Enzymatic processes induce this mineralization, and several enzymes have been linked to *Crossiella* activity in moonmilk. Martin-Pozas et al. [26] suggested that moonmilk formation is related to syntrophic

relationships between *Crossiella* and nitrifying bacteria, and Cuezva et al. [27] associated *Crossiella* with the ability to capture CO₂ from the atmosphere and precipitate calcium carbonate as a by-product of carbonic anhydrase action, as observed in cave moonmilk.

7. Is Moonmilk a Source of Bioactive Compounds?

Caves and moonmilk are colonized by complex bacterial communities. Maciejewska et al. [153] reported that *Proteobacteria* was the dominant phylum of moonmilk from a Belgian cave, followed by *Actinobacteria*, *Acidobacteria*, *Chloroflexi*, *Nitrospirae*, *Gemmatimonadetes*, and *Planctomycetes*. These seven phyla accounted for 85.8–90.2% of the total community. Martin-Pozas et al. [26] investigated the moonmilk composition from Pindal Cave in Spain. They found that *Proteobacteria* and *Actinobacteria* dominated the community with over 30% of relative abundance for each phylum, followed by *Acidobacteria*, *Chloroflexi*, *Planctomycetes*, *Gemmatimonadetes*, and *Nitrospirae*. These phyla accounted for 93.1–93.9% of the total community. The similarities between the phylum compositions of moonmilk from two different caves are remarkable. Moonmilk from a geographically distant cave [172] and another subterranean environment [173] also showed relatively similar phylum compositions.

Moonmilk has been a promising reservoir for novel bacteria producing bioactive compounds, and a few novel species have been isolated, namely *Streptomyces lunaelactis* [174], *Pseudomonas karstica*, and *Pseudomonas spelaei* [175]. Several studies have stressed the great diversity of unknown bacteria inhabiting moonmilk and the isolates' production of bioactive compounds [176–178].

The high abundance of *Actinomycetota* (= *Actinobacteria*) and *Pseudomonadota* (= *Proteobacteria*) in moonmilk has prompted researchers to test a series of strategies to isolate hard-to-culture "rare actinobacteria" and discover novel bioactive compounds [13,14]. Adam et al. [176] obtained 40 isolates represented by *Agromyces*, *Amycolatopsis*, *Kocuria*, *Micrococcus*, *Micromonospora*, *Nocardia*, *Streptomyces*, and *Rhodococcus* species. The *Streptomyces* isolates displayed strong inhibitory activities against Gram-positive and Gram-negative bacteria and fungi [179]. Genome mining of *Streptomyces lunaelactis* revealed 42 biosynthetic gene clusters [180] and the production of the antibiotics bagremycins and lunaemycins [180,181]. The genome of *Crossiella*, abundant in moonmilk [26], showed the presence of a combination of gene clusters involved in synthesising different bioactive compounds [9]. The data suggest the possibility of finding other moonmilk bacteria involved in synthesising bioactive compounds.

8. Conclusions

The genus *Crossiella* is widely distributed in all environments, reaching a relative abundance of up to 78% in a Sicilian cave. Its occurrence in soils, plant rhizospheres and caves is especially important. The last case is probably due to its transport to the subsurface by percolating waters. Despite this abundance, the strains isolated were scarce.

The data suggest that more environmental *Crossiella* species are waiting to be described, apart from *Crossiella cryophila* and *Crossiella equi*. The increasing number of metagenomic sequence data from all environments offers clear opportunities to guide the isolation and cultivation of *Crossiella*. Therefore, further efforts are required to design suitable isolation culture media. They should consider the environmental conditions of the niches where *Crossiella* thrives, namely alkaline pH and high mineral concentrations.

Crossiella has an important role in carbon sequestration in subterranean environments. Metagenomic studies and isolating more *Crossiella* strains and/or species are the only way to advance knowledge of *Crossiella* functions in different ecosystems. Furthermore, its role in biomineralization and moonmilk formation is also apparent.

Finally, *Crossiella* appears to be a promising source of active compounds, and the isolated strains deserve more attention regarding their potential use in biotechnological processes.

Supplementary Materials: The following supporting information can be downloaded at: <https://www.mdpi.com/article/10.3390/applbiosci2020014/s1>, Table S1: Occurrence of the genus *Crossiella* in different environments.

Author Contributions: Conceptualization, C.S.-J. and S.S.-M.; investigation, T.M.-P., J.L.G.-P., V.J., L.L., J.C.C., A.F.-C. and S.C.; writing—original draft preparation, C.S.-J., S.S.-M. and T.M.-P.; writing—review and editing, C.S.-J. and S.S.-M. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by the projects PID2020-114978GB-I00 and PID2019-110603RB-I00. The Malaga City Council financed data from the archaeological basement of the Thyssen Museum of Malaga through a conservation contract for this Roman site.

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: All data reported in this review can be found in the relevant papers cited. Scanning electron micrographs, EDX spectra, and unpublished data are available on request from Sergio Sanchez-Moral.

Acknowledgments: This is a contribution from CSIC Interdisciplinary Thematic Platform Open Heritage: Research and Society (PTI-PAIS).

Conflicts of Interest: The authors declare no conflict of interest.

References

1. Takahashi, A.; Hotta, K.; Saito, N.; Morioka, M.; Okami, Y.; Umezawa, H. Production of novel antibiotic, dopsisamine, by a new subspecies of *Nocardioopsis mutabilis* with multiple antibiotic resistance. *J. Antibiot.* **1986**, *39*, 175–183. [[CrossRef](#)] [[PubMed](#)]
2. Labeda, D.P.; Lechevalier, M.P. Amendment of the genus *Saccharothrix* Labeda et al. 1984 and descriptions of *Saccharothrix espanaensis* sp. nov., *Saccharothrix cryophilis* sp. nov., and *Saccharothrix mutabilis* comb. nov. *Int. J. Syst. Bacteriol.* **1989**, *39*, 420–423. [[CrossRef](#)]
3. Labeda, D.P. *Crossiella* gen. nov., a new genus related to *Streptoalloteichus*. *Int. J. Syst. Evol. Microbiol.* **2001**, *51*, 575–579. [[CrossRef](#)]
4. Donahue, J.M.; Williams, N.M.; Sells, S.F.; Labeda, D.P. *Crossiella equi* sp. nov., isolated from equine placentas. *Int. J. Syst. Evol. Microbiol.* **2002**, *52*, 2169–2173.
5. Sánchez-Moral, S. *Estudio Integral del Estado de Conservación de la Cueva de Altamira y su Arte Paleolítico (2007–2009). Perspectivas Futuras de Conservación*; Monografías N° 24; Museo Nacional y Centro de Investigación de Altamira: Santillana del Mar, Spain, 2014.
6. Adeyemo, O.M.; Onilude, A.A. Antimicrobial potential of a rare actinomycete isolated from soil: *Crossiella* sp.-EK18. *J. Adv. Microbiol.* **2018**, *11*, 1–15. [[CrossRef](#)]
7. Cimermanova, M.; Pristas, P.; Piknova, M. Biodiversity of actinomycetes from heavy metal contaminated technosols. *Microorganisms* **2021**, *9*, 1635. [[CrossRef](#)]
8. González-Riancho Fernández, C. Análisis Descriptivo y Funcional de Las Colonias Microbianas Visibles Que Crecen en la Cueva de Altamira, Enfocado al Diseño de Medidas de Control. Ph.D. Thesis, Universidad de Cantabria, Santander, Spain, 2021.
9. Gonzalez-Pimentel, J.L.; Dominguez-Moñino, I.; Jurado, V.; Laiz, L.; Caldeira, A.T.; Saiz-Jimenez, C. The rare actinobacterium *Crossiella* sp. is a potential source of new bioactive compounds with activity against bacteria and fungi. *Microorganisms* **2022**, *10*, 1575. [[CrossRef](#)]
10. Oren, A.; Garrity, G.M. Valid publication of the names of forty-two phyla of prokaryotes. *Int. J. Syst. Evol. Microbiol.* **2021**, *71*, 005056. [[CrossRef](#)] [[PubMed](#)]
11. Berdy, J. Bioactive microbial metabolites. *J. Antibiot.* **2005**, *58*, 1–26. [[CrossRef](#)]
12. Subramani, R.; Aalbersberg, W. Culturable rare Actinomycetes: Diversity, isolation and marine natural product discovery. *Appl. Microbiol. Biotechnol.* **2013**, *97*, 9291–9321. [[CrossRef](#)]
13. Tiwari, K.; Gupta, R.K. Rare actinomycetes: A potential storehouse for novel antibiotics. *Crit. Rev. Biotechnol.* **2012**, *32*, 108–132. [[CrossRef](#)]
14. Tiwari, K.; Gupta, R.K. Diversity and isolation of rare actinomycetes: An overview. *Crit. Rev. Microbiol.* **2013**, *39*, 256–294. [[CrossRef](#)] [[PubMed](#)]
15. Seong, C.N.; Choi, J.H.; Baik, K.-S. An improved selective isolation of rare actinomycetes from forest soil. *J. Microbiol.* **2001**, *39*, 17–23.
16. Bredholdt, H.; Galatenko, O.A.; Engelhardt, K.; Fjærvik, E.; Terekhova, L.P.; Zotchev, S.B. Rare actinomycete bacteria from the shallow water sediments of the Trondheim Fjord, Norway: Isolation, diversity and biological activity. *Environ. Microbiol.* **2007**, *9*, 2756–2764. [[CrossRef](#)]

17. Fang, B.-Z.; Salam, N.; Han, M.-X.; Jiao, J.-Y.; Cheng, J.; Wei, D.-Q.; Xiao, M.; Li, W.-J. Insights on the effects of heat pretreatment, pH, and calcium salts on isolation of rare actinobacteria from karstic caves. *Front. Microbiol.* **2017**, *8*, 1535. [CrossRef] [PubMed]
18. Goodfellow, M.; Nouioui, I.; Sanderson, R.; Xie, F.; Bull, A.T. Rare taxa and dark microbial matter: Novel bioactive actinobacteria abundant in Atacama Desert soils. *Anton. Leeuw.* **2018**, *111*, 1315–1332. [CrossRef]
19. Benhadj, M.; Gacemi-Kirane, D.; Menasria, T.; Guebla, K.; Ahmane, Z. Screening of rare actinomycetes isolated from natural wetland ecosystem (Fetzara Lake, northeastern Algeria) for hydrolytic enzymes and antimicrobial activities. *J. King Saud Univ. Sci.* **2019**, *31*, 706–712. [CrossRef]
20. Zamora-Quintero, A.Y.; Torres-Beltrán, M.; Guillén Matus, D.G.; Oroz-Parra, I.; Millán-Aguiñaga, N. Rare actinobacteria isolated from the hypersaline Ojo de Liebre Lagoon as a source of novel bioactive compounds with biotechnological potential. *Microbiology* **2022**, *168*, 001144. [CrossRef]
21. Tiwari, K.; Upadhyay, D.J.; Mösker, E.; Süßmuth, R.; Gupta, R.K. Culturable bioactive actinomycetes from the Great Indian Thar Desert. *Ann. Microbiol.* **2015**, *65*, 1901–1914. [CrossRef]
22. Mohammadipanah, F.; Wink, J. Actinobacteria from arid and desert habitats: Diversity and biological activity. *Front. Microbiol.* **2016**, *6*, 1541. [CrossRef]
23. Gacem, M.A.; Ould-El-Hadj-Kheli, A.; Abd-Elsalam, K.A.; Wink, J. Actinobacteria in the Algerian Sahara: Diversity, adaptation mechanism and special unexploited biotopes for the isolation of novel rare taxa. *Biologia* **2001**, *76*, 3787–3799. [CrossRef]
24. Hui, M.L.-Y.; Tan, L.T.-H.; Letchumanan, V.; He, Y.-W.; Fang, C.-M.; Chan, K.-G.; Law, J.W.-F.; Lee, L.-H. The extremophilic Actinobacteria: From microbes to medicine. *Antibiotics* **2021**, *10*, 682. [CrossRef] [PubMed]
25. Gonzalez-Pimentel, J.L.; Martin-Pozas, T.; Jurado, V.; Miller, A.Z.; Caldeira, A.T.; Fernandez-Lorenzo, O.; Sanchez-Moral, S.; Saiz-Jimenez, C. Prokaryotic communities from a lava tube cave in La Palma Island (Spain) are involved in the biogeochemical cycle of major elements. *PeerJ* **2021**, *9*, e11386. [CrossRef] [PubMed]
26. Martin-Pozas, T.; Cuezva, S.; Fernandez-Cortes, A.; Cañaveras, J.C.; Benavente, D.; Jurado, V.; Saiz-Jimenez, C.; Janssens, I.; Seijas, N.; Sanchez-Moral, S. Role of subterranean microbiota in the carbon cycle and greenhouse gas dynamics. *Sci. Total Environ.* **2022**, *831*, 154921. [CrossRef]
27. Cuezva, S.; Martin-Pozas, T.; Fernandez-Cortes, A.; Cañaveras, J.C.; Janssens, I.; Sanchez-Moral, S. On the role of cave-soil in the carbon cycle. A first approach. *EGU Gen. Assem.* **2020**. Available online: https://presentations.copernicus.org/EGU2020/EGU2020-21793_presentation.pdf. (accessed on 22 April 2022).
28. Martin-Pozas, T.; Fernandez-Cortes, A.; Cuezva, S.; Cañaveras, J.C.; Benavente, D.; Duarte, E.; Saiz-Jimenez, C.; Sanchez-Moral, S. New insights into the structure, microbial diversity and ecology of yellow biofilms in a Paleolithic rock art cave (Pindal Cave, Asturias, Spain). *Sci. Total Environ.* **2023**, *882*. *in press*.
29. González-Pimentel, J.L. Microorganismos de las Cuevas Volcánicas de La Palma (Islas Canarias). Diversidad y Potencial Uso Biotecnológico. Ph.D. Thesis, Universidad Pablo Olavide, Sevilla, Spain, 2019.
30. Jurado, V.; del Rosal, Y.; Gonzalez-Pimentel, J.L.; Hermosin, B.; Saiz-Jimenez, C. Biological control of phototrophic biofilms in a show cave: The case of Nerja Cave. *Appl. Sci.* **2020**, *10*, 3448. [CrossRef]
31. Martin-Pozas, T. Papel de los Microorganismos en Procesos de Captación y Emisión de Gases de Efecto Invernadero en Ambientes Subterráneos. Ph.D. Thesis, Universidad Complutense de Madrid, Madrid, Spain, 2023.
32. Sánchez-Moral, S.; Martín-Pozas, T.; Seijas Morales, N.; Fernández-Cortés, A.; Benavente García, D.; Cañaveras Jiménez, J.C.; Cuezva, S. *Instalación de Sensores en Sótano Arqueológico del Museo Carmen Thyssen de Málaga Para la Toma de Datos, el Análisis y Adopción de Medidas Correctoras del Deterioro Del Recinto*; Unpublished Report; MNCN: Madrid, Spain, 2021.
33. Stomeo, F.; Portillo, M.C.; Gonzalez, J.M.; Laiz, L.; Saiz-Jimenez, C. *Pseudonocardia* in white colonizations in two caves with Paleolithic paintings. *Int. Biodeter. Biodegr.* **2008**, *62*, 483–486. [CrossRef]
34. Portillo, M.C.; Gonzalez, J.M. Microbial community diversity and the complexity of preserving cultural heritage. In *Biocolonization of Stone: Control and Preventive Methods*; Charola, A.E., McNamara, C., Koestler, R.J., Eds.; Smithsonian Institution, Scholarly Press: Washington, DC, USA, 2011; pp. 19–28.
35. Yun, Y.; Wang, H.; Man, B.; Xiang, X.; Zhou, J.; Qiu, X.; Duan, Y.; Engel, A.S. The relationship between pH and bacterial communities in a single karst ecosystem and its implication for soil acidification. *Front. Microbiol.* **2016**, *7*, 1955. [CrossRef] [PubMed]
36. Lepinay, C.; Mihajlovski, A.; Seyer, D.; Tournon, S.; Bousta, F.; Di Martino, P. Biofilm communities survey at the areas of salt crystallization on the walls of a decorated shelter listed at UNESCO World cultural Heritage. *Int. Biodeter. Biodegr.* **2017**, *122*, 116–127. [CrossRef]
37. Lepinay, C.; Mihajlovski, A.; Tournon, S.; Seyer, D.; Bousta, F.; Di Martino, P. Bacterial diversity associated with saline efflorescences damaging the walls of a French decorated prehistoric cave registered as a World Cultural Heritage Site. *Int. Biodeter. Biodegr.* **2018**, *130*, 55–64. [CrossRef]
38. Alonso, L.; Pommier, T.; Kaufmann, B.; Dubost, A.; Chapulliot, D.; Doré, J.; Douady, C.J.; Moëgne-Loccoz, Y. Anthropization level of Lascaux Cave microbiome shown by regional-scale comparisons of pristine and anthropized caves. *Mol. Ecol.* **2019**, *28*, 3383–3394. [CrossRef] [PubMed]
39. Li, M.; Fang, C.; Kawasaki, S.; Huang, M.; Achal, V. Bio-consolidation of cracks in masonry cement mortars by *Acinetobacter* sp. SC4 isolated from a karst cave. *Int. Biodeter. Biodegr.* **2019**, *141*, 94–100. [CrossRef]

40. Long, Y.; Jiang, J.; Hu, X.; Zhou, J.; Hu, J.; Zhou, S. Actinobacterial community in Shuanghe Cave using culture-dependent and -independent approaches. *World J. Microbiol. Biotechnol.* **2019**, *35*, 153. [CrossRef]
41. Wischart, A.; Mhuantong, W.; Tangphatsornruang, S.; Chantasingh, D.; Pootanakit, K. Shotgun metagenomic sequencing from Manao-Pee cave, Thailand, reveals insight into the microbial community structure and its metabolic potential. *BMC Microbiol.* **2019**, *19*, 144. [CrossRef] [PubMed]
42. Frazier, V.E. Carbon Metabolism in Cave Subaerial Biofilms. Master's Thesis, University of Tennessee, Knoxville, TN, USA, 2020.
43. He, D.; Wu, F.; Ma, W.; Zhang, Y.; Gu, J.-D.; Duan, Y.; Xu, R.; Feng, H.; Wang, W.; Li, S.-W. Insights into the bacterial and fungal communities and microbiome that causes a microbe outbreak on ancient wall paintings in the Maijishan Grottoes. *Int. Biodeter. Biodegr.* **2021**, *163*, 105250. [CrossRef]
44. Ma, L.; Huang, X.; Wang, H.; Yun, Y.; Cheng, X.; Liu, D.; Lu, X.; Qiu, X. Microbial interactions drive distinct taxonomic and potential metabolic responses to habitats in karst cave ecosystem. *Microbiol. Spect.* **2021**, *9*, e01152-21. [CrossRef]
45. Zada, S.; Xie, J.; Yang, M.; Yang, X.; Sajjad, W.; Rafiq, M.; Hasan, F.; Hu, Z.; Wang, H. Composition and functional profiles of microbial communities in two geochemically and mineralogically different caves. *Appl. Microbiol. Biotechnol.* **2021**, *105*, 8921–8936. [CrossRef]
46. Ai, J.; Guo, J.; Li, Y.; Zhong, X.; Lv, Y.; Li, J.; Yang, A. The diversity of microbes and prediction of their functions in karst caves under the influence of human tourism activities—A case study of Zhijin Cave in Southwest China. *Environ. Sci. Pollut. Res.* **2022**, *29*, 25858–25868. [CrossRef]
47. Buresova-Faitova, A.; Kopecky, J.; Sagova-Mareckova, M.; Alonso, L.; Vautrin, F.; Moëne-Loccoz, Y.; Rodriguez-Nava, V. Comparison of Actinobacteria communities from human-impacted and pristine karst caves. *MicrobiologyOpen* **2022**, *11*, e1276. [CrossRef]
48. Djebaili, R.; Mignini, A.; Vaccarelli, I.; Pellegrini, M.; Spera, D.M.; Del Gallo, M.; D'Alessandro, A.M. Polyhydroxybutyrate-producing cyanobacteria from lampenflora: The case study of the “Stiffe” caves in Italy. *Front. Microbiol.* **2022**, *13*, 933398. [CrossRef]
49. Cheng, X.; Xiang, X.; Yun, Y.; Wang, W.; Wang, H.; Bodelier, P.L.E. Archaea and their interactions with bacteria in a karst ecosystem. *Front. Microbiol.* **2023**, *14*, 1068595. [CrossRef] [PubMed]
50. Dimkic, I.; Copic, M.; Petrovic, M.; Stupar, M.; Savkovic, Ž.; Knežević, A.; Simic, G.S.; Grbic, M.L.; Unkovic, N. Bacteriobiota of the cave church of Sts. Peter and Paul in Serbia—Culturable and non-culturable communities' assessment in the bioconservation potential of a peculiar fresco painting. *Int. J. Mol. Sci.* **2023**, *24*, 1016. [CrossRef]
51. Riquelme, C.; Rigal, F.; Hathaway, J.J.M.; Northup, D.E.; Spilde, M.N.; Borges, P.A.V.; Gabriel, R.; Amorin, I.R.; Dapkevicius, M.L.N.E. Cave microbial community composition in oceanic islands: Disentangling the effect of different colored mats in diversity patterns of Azorean lava caves. *FEMS Microbiol. Ecol.* **2015**, *91*, fiv141. [CrossRef] [PubMed]
52. Spilde, M.N.; Northup, D.E.; Caimi, N.A.; Boston, P.J.; Stone, F.D.; Smith, S. Microbial mat communities in Hawaiian lava caves. *Int. Symp. Vulcanospeleol.* **2016**. Available online: <https://www.cavepics.com/IVS17/SPILDE.pdf>. (accessed on 29 October 2022).
53. Lavoie, K.H.; Winter, A.S.; Read, K.J.H.; Hughes, E.M.; Spilde, M.N.; Northup, D.E. Comparison of bacterial communities from lava cave microbial mats to overlying surface soils from Lava Beds National Monument, USA. *PLoS ONE* **2017**, *12*, e0169339. [CrossRef] [PubMed]
54. Weng, M.M.; Zaikova, E.; Millan, M.; Williams, A.J.; McAdam, A.C.; Knudson, C.A.; Fuqua, S.R.; Wagner, N.Y.; Craft, K.; Nawotniak, S.K.; et al. Life underground: Investigating microbial communities and their biomarkers in Mars-analog lava tubes at Craters of the Moon National Monument and Preserve. *J. Geophys. Res. Planets* **2022**, *127*, e2022JE007268. [CrossRef]
55. Nicolosi, G.; Gonzalez-Pimentel, J.L.; Piano, E.; Isaia, M.; Miller, A.Z. First insights into the bacterial diversity of Mount Etna volcanic caves. *Microb. Ecol.* **2023**, *85*, in press. [CrossRef] [PubMed]
56. Barton, H.A.; Taylor, N.M.; Krete, M.P.; Springer, A.C.; Oehrle, S.A.; Bertog, J.L. The impact of host rock geochemistry on bacterial community structure in oligotrophic cave environments. *Int. J. Speleol.* **2007**, *36*, 93–104. [CrossRef]
57. Ghezzi, D.; Sauro, F.; Columbu, A.; Carbone, C.; Hong, P.-Y.; Vergara, F.; De Waele, J.; Cappelletti, M. Transition from unclassified *Ktedonobacterales* to *Actinobacteria* during amorphous silica precipitation in a quartzite cave environment. *Sci. Rep.* **2021**, *11*, 3921. [CrossRef]
58. Weber, C.F. Reduced vertical stratification of soil bacterial community structure and composition is associated with *Bromus tectorum* invasion of sagebrush steppe. *J. Arid Environ.* **2015**, *115*, 90–99. [CrossRef]
59. Osman, J.R.; Fernandes, G.; Regeard, C.; Jaubert, C.; DuBow, M.S. Examination of the bacterial biodiversity of coastal eroded surface soils from the Padza de Dapani (Mayotte Island). *Geomicrobiol. J.* **2018**, *35*, 355–365. [CrossRef]
60. Lambrechts, S.; Willems, A.; Tahon, G. Uncovering the uncultivated majority in Antarctic soils: Toward a synergistic approach. *Front. Microbiol.* **2019**, *10*, 242. [CrossRef]
61. Li, J.; Wu, Z.; Yuan, J. Impact of agro-farming activities on microbial diversity of acidic red soils in a *Camellia Oleifera* Forest. *Rev. Bras. Cien. Solo* **2019**, *43*, e0190044. [CrossRef]
62. Zhenqing, Z.; Binglin, Z.; Wei, Z.; Guangxiu, L.; Tuo, C.; Yang, L.; Jingwei, C.; Mao, T. Distribution characteristics and anti-radiation activity of culturable bacteria in black gobi ecosystem of the Hexi Corridor. *J. Desert Res.* **2020**, *40*, 52–62.
63. Bossolani, J.; Crusciol, C.A.C.; Leite, M.F.A.; Merloti, L.F.; Moretti, L.G.; Pascoaloto, I.M.; Kuramae, E.E. Modulation of the soil microbiome by long-term Ca-based soil amendments boosts soil organic carbon and physicochemical quality in a tropical no-till crop rotation system. *Soil Biol. Biochem.* **2021**, *156*, 108188. [CrossRef]

64. Chen, B.; Jiao, S.; Luo, S.; Ma, B.; Qi, W.; Cao, C.; Zhao, Z.; Du, G.; Ma, X. High soil pH enhances the network interactions among bacterial and archaeal microbiota in alpine grasslands of the Tibetan Plateau. *Environ. Microbiol.* **2021**, *23*, 464–477. [[CrossRef](#)]
65. Liu, X.; Liu, Y.; Zhang, L.; Yin, R.; Wu, G.-L. Bacterial contributions of bio-crusts and litter crusts to nutrient cycling in the Mu Us Sandy Land. *Catena* **2021**, *199*, 105090. [[CrossRef](#)]
66. Liu, Z.; Yang, Y.; Ji, S.; Dong, D.; Li, Y.; Wang, M.; Han, L.; Chen, X. Effects of elevation and distance from highway on the abundance and community structure of bacteria in soil along Qinghai-Tibet highway. *Int. J. Environ. Res. Public Health* **2021**, *18*, 13137. [[CrossRef](#)]
67. Schulze-Makuch, D.; Lipus, D.; Arens, F.L.; Baqué, M.; Bornemann, T.L.V.; de Vera, J.-P.; Flury, M.; Frösler, J.; Heinz, J.; Hwang, Y.; et al. Microbial hotspots in lithic microhabitats inferred from DNA fractionation and metagenomics in the Atacama Desert. *Microorganisms* **2021**, *9*, 1038. [[CrossRef](#)]
68. Xie, J.; Wu, Z.; Zhang, X.; Peng, T.; Yang, C.; Zhang, J.; Liang, J. Diversity and structural characteristics of soil microbial communities in different habitats of wild *Lilium regale* Wilson in Wenchuan area. *Bioengineered* **2021**, *12*, 10457–10469. [[CrossRef](#)] [[PubMed](#)]
69. Benaud, N.; Chelliah, D.S.; Wong, S.Y.; Ferrari, B.C. Soil substrate culturing approaches recover diverse members of *Actinomycetota* from desert soils of Herring Island, East Antarctica. *Extremophiles* **2022**, *26*, 24. [[CrossRef](#)] [[PubMed](#)]
70. Guerra, V.A.; Beule, L.; Mackowiak, C.L.; Dubeux, J.C.B., Jr.; Blount, A.R.S.; Wang, X.-B.; Rowland, D.L.; Liao, H.-L. Soil bacterial community response to rhizoma peanut incorporation into Florida pastures. *J. Environ. Qual.* **2022**, *51*, 55–65. [[CrossRef](#)] [[PubMed](#)]
71. Ke, M.; Xu, N.; Zhang, Z.; Qiu, D.; Kang, J.; Lu, T.; Wang, T.; Peijnenburg, W.J.G.M.; Sun, L.; Hu, B.; et al. Development of a machine-learning model to identify the impacts of pesticides characteristics on soil microbial communities from high-throughput sequencing data. *Environ. Microbiol.* **2022**, *24*, 5561–5573. [[CrossRef](#)]
72. Sun, H.; Zhang, H. Alien species invasion of deep-sea bacteria into terrestrial soil. *J. Clean. Product.* **2022**, *371*, 133662. [[CrossRef](#)]
73. Sun, H.; Peng, Q.; Guo, J.; Zhang, H.; Bai, J.; Mao, H. Effects of short-term soil exposure of different doses of ZnO nanoparticles on the soil environment and the growth and nitrogen fixation of alfalfa. *Environ. Pollut.* **2022**, *309*, 119817. [[CrossRef](#)]
74. Topalovic, O.; Santos, S.S.; Heuer, H.; Nesme, J.; Kanfra, X.; Hallmann, J.; Sørensen, S.J.; Vestergård, M. Deciphering bacteria associated with a pre-parasitic stage of the root-knot nematode *Meloidogyne hapla* in nemato-suppressive and nemato-conductive soils. *Appl. Soil Ecol.* **2022**, *172*, 104344. [[CrossRef](#)]
75. Wang, L.; Peng, C.; Gong, B.; Yang, Z.; Song, J.; Li, L.; Xu, L.; Yue, T.; Wang, X.; Yang, M.; et al. Actinobacteria community and their antibacterial and cytotoxic activity on the Weizhou and Xieyang volcanic islands in the Beibu Gulf of China. *Front. Microbiol.* **2022**, *13*, 911408. [[CrossRef](#)]
76. Feng, Z.; Sun, H.; Qin, Y.; Zhou, Y.; Zhu, H.; Yao, Q. A synthetic community of siderophore-producing bacteria increases soil selenium bioavailability and plant uptake through regulation of the soil microbiome. *Sci. Total Environ.* **2023**, *871*, 162076. [[CrossRef](#)]
77. Conte, A. Phylogenetic Diversity and Metabolic Potential of Prokaryotic Communities in Permafrost and Brine Pockets of Perennially Frozen Antarctic Lakes (Northern Victoria Land). Ph.D. Thesis, Università Degli Studi di Messina, Messina, Italy, 2017.
78. Perez-Mon, C.; Stierli, B.; Plötze, M.; Frey, B. Fast and persistent responses of alpine permafrost microbial communities to in situ warming. *Sci. Total Environ.* **2022**, *807*, 150720. [[CrossRef](#)]
79. Narendrula, R. Biochemical and Molecular Characterization of Microbial Communities from a Metal Contaminated and Reclaimed Region. Ph.D. Thesis, Laurentian University, Sudbury, ON, Canada, 2017.
80. Lin, J.; He, F.; Su, B.; Sun, M.; Owens, G.; Chen, Z. The stabilizing mechanism of cadmium in contaminated soil using green synthesized iron oxide nanoparticles under long-term incubation. *J. Hazard. Mater.* **2019**, *379*, 120832. [[CrossRef](#)]
81. Dong, S.; Liu, S.; Cui, S.; Zhou, X.; Gao, Q. Responses of soil properties and bacterial community to the application of sulfur fertilizers in black and sandy soils. *Pol. J. Environ. Stud.* **2022**, *31*, 35–47. [[CrossRef](#)] [[PubMed](#)]
82. Pu, C.; Liu, H.; Ding, G.; Sun, Y.; Yu, X.; Chen, J.; Ren, J.; Gong, X. Impact of direct application of biogas slurry and residue in fields: In situ analysis of antibiotic resistance genes from pig manure to fields. *J. Hazard. Mater.* **2018**, *344*, 441–449. [[CrossRef](#)] [[PubMed](#)]
83. Deng, J.; Zhang, Y.; Yin, Y.; Zhu, X.; Zhu, W.; Zhou, Y. Comparison of soil bacterial community and functional characteristics following afforestation in the semi-arid areas. *PeerJ* **2019**, *7*, e7141. [[CrossRef](#)]
84. Deng, J.; Zhou, Y.; Zhu, W.; Yin, Y. Effects of afforestation with *Pinus sylvestris* var. *mongolica* plantations combined with enclosure management on soil microbial community. *PeerJ* **2020**, *8*, e8857. [[PubMed](#)]
85. Liu, K.; Ding, X.; Wang, J. Soil metabolome correlates with bacterial diversity and co-occurrence patterns in root-associated soils on the Tibetan Plateau. *Sci. Total Environ.* **2020**, *735*, 139572. [[CrossRef](#)]
86. Jiang, H.; Chen, Y.; Hu, Y.; Wang, Z.; Lu, X. Soil bacterial communities and diversity in alpine grasslands on the Tibetan Plateau based on 16S rRNA gene sequencing. *Front. Ecol. Evol.* **2021**, *9*, 630722. [[CrossRef](#)]
87. Solon, A.J.; Mastrangelo, C.; Vimercati, L.; Sommers, P.; Darcy, J.L.; Gendron, E.M.S.; Porazinska, D.L.; Schmidt, S.K. Gullies and moraines are islands of biodiversity in an arid, mountain landscape, Asgard Range, Antarctica. *Front. Microbiol.* **2021**, *12*, 654135. [[CrossRef](#)]

88. Rodríguez-Berbel, N.; Ortega, R.; Lucas-Borja, M.E.; Solé-Benet, A.; Miralles, I. Long-term effects of two organic amendments on bacterial communities of calcareous mediterranean soils degraded by mining. *J. Environ. Manag.* **2020**, *271*, 110920. [CrossRef]
89. Chuvochina, M.S.; Alekhina, I.A.; Normand, P.; Petit, J.-R.; Bulat, S.A. Three events of Saharan dust deposition on the Mont Blanc glacier associated with different snow-colonizing bacterial phylotypes. *Microbiology* **2011**, *80*, 125–131. [CrossRef]
90. Hui, N.; Sun, N.; Du, H.; Umair, M.; Kang, H.; Liu, X.; Romantschuk, M.; Liu, C. Karst rocky desertification does not erode ectomycorrhizal fungal species richness but alters microbial community structure. *Plant Soil* **2019**, *445*, 383–396. [CrossRef]
91. Reverdy, A.; Hathaway, D.; Jha, J.; Michaels, G.; Sullivan, J.; Diaz Mac-Adoo, D.; Riquelme, C.; Chai, Y.; Godoy, V.G. Insights into the diversity and survival strategies of soil bacterial isolates from the Atacama Desert. *bioRxiv* **2020**. [CrossRef]
92. Biderre-Petit, C.; Hochart, C.; Gardon, H.; Dugat-Bony, E.; Terrat, S.; Jouan-Dufournel, I.; Paris, R. Analysis of bacterial and archaeal communities associated with Fogo volcanic soils of different ages. *FEMS Microbiol. Ecol.* **2020**, *96*, fiae104. [CrossRef] [PubMed]
93. Zhang, X.; Du, W.; Xu, Y.; Wang, Y.L. Soil bacterial diversity and function in semi-arid forest parks in Baotou City. *Biodivers. Sci.* **2022**, *30*, 22245. [CrossRef]
94. Li, Y.; Gao, W.; Wang, C.; Gao, M. Distinct distribution patterns and functional potentials of rare and abundant microorganisms between plastisphere and soils. *Sci. Total Environ.* **2023**, *873*, 162413. [CrossRef]
95. Zhang, S.; Pei, L.; Zhao, Y.; Shan, J.; Zheng, X.; Xu, G.; Sun, Y.; Wang, F. Effects of microplastics and nitrogen deposition on soil multifunctionality, particularly C and N cycling. *J. Hazard. Mater.* **2023**, *451*, 131152. [CrossRef]
96. Lin, Y.; Yang, L.; Chen, Z.; Gao, Y.; Kong, J.; He, Q.; Su, Y.; Li, J.; Qiu, Q. Seasonal variations of soil bacterial and fungal communities in a subtropical *Eucalyptus* plantation and their responses to throughfall reduction. *Front. Microbiol.* **2023**, *14*, 1113616. [CrossRef]
97. De Tender, C.; Haegeman, A.; Vandecasteele, B.; Clement, L.; Cremelie, P.; Dawyndt, P.; Maes, M.; Debode, J. Dynamics in the strawberry rhizosphere microbiome in response to biochar and *Botrytis cinerea* leaf infection. *Front. Microbiol.* **2016**, *7*, 2062. [CrossRef]
98. Echeverría Molinar, A. Efecto de Factores Abióticos y Bióticos Sobre la Estructura de la Comunidad Microbiana del Suelo en un Ambiente Oligotrófico. Master's Thesis, Instituto Potosino de Investigación Científica y Tecnológica, San Luis Potosí, México, 2017.
99. Visioli, G.; Sanangelantoni, A.M.; Vamerali, T.; Dal Cortivo, C.; Blandino, M. 16S rDNA profiling to reveal the influence of seed-applied biostimulants on the rhizosphere of young maize plants. *Molecules* **2018**, *23*, 1461. [CrossRef]
100. Gao, X.; Wu, Z.; Liu, R.; Wu, J.; Zeng, Q.; Qi, Y. Rhizosphere bacterial community characteristics over different years of sugarcane ratooning in consecutive monoculture. *BioMed Res. Int.* **2019**, *2019*, 4943150. [CrossRef]
101. Chen, Y.; Tian, W.; Shao, Y.; Li, Y.-J.; Lin, L.-A.; Zhang, Y.-J.; Han, H.; Chen, Z.-J. *Miscanthus* cultivation shapes rhizosphere microbial community structure and function as assessed by Illumina MiSeq sequencing combined with PICRUSt and FUNGUild analyses. *Arch. Microbiol.* **2020**, *202*, 1157–1171. [CrossRef] [PubMed]
102. López-Lozano, N.E.; Echeverría Molinar, A.; Ortiz Durán, E.A.; Hernández Rosales, M.; Souza, V. Bacterial diversity and interaction networks of *Agave lechuguilla* rhizosphere differ significantly from bulk soil in the oligotrophic basin of Cuatro Ciénegas. *Front. Plant Sci.* **2020**, *11*, 1028. [CrossRef] [PubMed]
103. Monteiro, L.C.P. Comunidades Microbianas Rizosféricas de Plantas em Coexistência Sob Diferentes Condições Edáficas. Ph.D. Thesis, Universidade Federal de Viçosa, Viçosa, Brasil, 2020.
104. Bettermann, A.; Zethof, J.H.T.; Babin, D.; Cammeraat, L.H.; Solé-Benet, A.; Lázaro, R.; Luna, L.; Nesme, J.; Sorensen, S.J.; Kalbitz, K.; et al. Importance of microbial communities at the root-soil interface for extracellular polymeric substances and soil aggregation in semiarid grasslands. *Soil Biol. Biochem.* **2021**, *159*, 108301. [CrossRef]
105. Deng, Q.; Zhang, T.; Xie, D.; Yang, Y. Rhizosphere microbial communities are significantly affected by optimized phosphorus management in a slope farming system. *Front. Microbiol.* **2021**, *12*, 739844. [CrossRef]
106. Engelbrecht, G.; Claassens, S.; Mienie, C.M.S.; Fourie, H. Screening of rhizosphere bacteria and nematode populations associated with soybean roots in the Mpumalanga Highveld of South Africa. *Microorganisms* **2021**, *9*, 1813. [CrossRef]
107. Li, C.; Chen, G.; Zhang, J.; Zhu, P.; Bai, X.; Hou, Y.; Zhang, X. The comprehensive changes in soil properties are continuous cropping obstacles associated with American ginseng (*Panax quinquefolius*) cultivation. *Sci. Rep.* **2021**, *11*, 5068. [CrossRef]
108. Ye, F.; Wang, X.; Wang, Y.; Wu, S.; Wu, J.; Hong, Y. Different pioneer plant species have similar rhizosphere microbial communities. *Plant Soil* **2021**, *464*, 165–181. [CrossRef]
109. Zuo, J.; Zu, M.; Liu, L.; Song, X.; Yuan, Y. Composition and diversity of bacterial communities in the rhizosphere of the Chinese medicinal herb *Dendrobium*. *BMC Plant Biol.* **2021**, *21*, 127. [CrossRef]
110. Gu, Y.-Y.; Zhang, H.-Y.; Liang, X.-Y.; Fu, R.; Li, M.; Chen, C.-J. Impact of biochar and bioorganic fertilizer on rhizosphere bacteria in saline-alkali soil. *Microorganisms* **2022**, *10*, 2310. [CrossRef]
111. He, C.; Wang, R.; Ding, W.; Li, Y. Effects of cultivation soils and ages on microbiome in the rhizosphere soil of *Panax ginseng*. *Appl. Soil Ecol.* **2022**, *174*, 104397. [CrossRef]
112. Jara-Servin, A.; Silva, A.; Barajas, H.; Cruz-Ortega, R.; Tinoco-Ojanguren, C.; Alcaraz, L.D. The Allelopathic Buffelgrass and Its Rhizosphere Microbiome. Available online: https://papers.ssrn.com/sol3/papers.cfm?abstract_id=4263505 (accessed on 28 February 2023).
113. Kushwaha, P.; Neilson, J.W.; Maier, R.M.; Babst-Kostecka, A. Soil microbial community and abiotic soil properties influence Zn and Cd hyperaccumulation differently in *Arabidopsis halleri*. *Sci. Total Environ.* **2022**, *803*, 150006. [CrossRef] [PubMed]

114. Lin, Y.; Zhang, Y.; Liang, X.; Duan, R.; Yang, L.; Du, Y.; Wu, L.; Huang, J.; Xiang, G.; Bai, J.; et al. Assessment of rhizosphere bacterial diversity and composition in a metal hyperaccumulator (*Boehmeria nivea*) and a nonaccumulator (*Artemisia annua*) in an antimony mine. *J. Appl. Microbiol.* **2022**, *132*, 3432–3443. [CrossRef] [PubMed]
115. Lizano-Bastardín, A.L.; Villadas, P.J.; Pulido-Suárez, L.; Fernández-López, M.; León-Barrios, M. The Rhizosphere Microbiome Associated with the Legume *Spartocytisus supranubius* in the High Mountain Ecosystem of Teide N.P. First Spanish-Portuguese Congress on Beneficial Plant-Microbe Interactions, Poster S1-P-03. Available online: https://events.iniav.pt/bemiplant/images/book-abstracts_15-10-2022.pdf (accessed on 9 February 2023).
116. Ren, H.; Islam, M.S.; Wang, H.; Guo, H.; Wang, Z.; Qi, X.; Zhang, S.; Guo, J.; Wang, Q.; Li, B. Effect of humic acid on soil physical and chemical properties, microbial community structure, and metabolites of decline diseased bayberry. *Int. J. Mol. Sci.* **2022**, *23*, 14707. [CrossRef] [PubMed]
117. Taniguchi, T.; Isobe, K.; Imada, S.; Eltayeb, M.; Akaji, Y.; Nakayama, M.; Allen, M.F.; Aronson, E. Root endophytic bacterial and fungal communities in a natural hot desert are differentially regulated in dry and wet seasons by stochastic processes and functional traits. Available online: <https://ssrn.com/abstract=4363629> (accessed on 25 February 2023).
118. Zhou, Y.; Pang, Z.; Jia, H.; Yuan, Z.; Ming, R. Responses of roots and rhizosphere of female papaya to the exogenous application of GA₃. *BMC Plant Biol.* **2023**, *23*, 35. [CrossRef] [PubMed]
119. Obieze, C.C.; George, P.B.L.; Boyle, B.; Khasa, D.P. Black pepper rhizomicrobiome: Spectrum of plant health indicators, critical environmental factors and community compartmentation in Vietnam. *Appl. Soil Ecol.* **2023**, *187*, 104857. [CrossRef]
120. Deng, J.; Yin, Y.; Zhu, W.; Zhou, Y. Response of soil environment factors and microbial communities to phytoremediation with *Robinia pseudoacacia* in an open-cut magnesite mine. *Land Degrad. Dev.* **2020**, *31*, 2340–2355. [CrossRef]
121. Ezeokoli, O.T.; Bezuidenhout, C.C.; Maboeta, M.S.; Khasa, D.P.; Adeleke, R.A. Structural and functional differentiation of bacterial communities in post-coal mining reclamation soils of South Africa: Bioindicators of soil ecosystem restoration. *Sci. Rep.* **2020**, *10*, 1759. [CrossRef]
122. Thompson, E.; Erickson, M.; Malik, N.; Mettler, R.; Reman, B.; Ren, Y.; Bergmann, D. Culture-independent characterization of “cave silver” biofilms from the 1470 m level of the Sanford Underground Research Facility, Lead, SD. *Proc. South Dak. Acad. Sci.* **2020**, *99*, 29–55.
123. Arif, S.; Nacke, H.; Schliekmann, E.; Reimer, A.; Arp, G.; Hoppert, M. Composition and niche-specific characteristics of microbial consortia colonizing Marsberg copper mine in the Rhenish Massif. *Biogeosciences* **2021**, *19*, 4883–4902. [CrossRef]
124. Shi, A.; Hu, Y.; Zhang, X.; Zhou, D.; Xu, J.; Rensing, C.; Zhang, L.; Xing, S.; Ni, W.; Yang, W. Biochar loaded with bacteria enhanced Cd/Zn phytoextraction by facilitating plant growth and shaping rhizospheric microbial community. *Environ. Pollut.* **2023**, *327*, 121559. [CrossRef]
125. Diaz-Herrera, M.; Jurado, V.; Cuezva, S.; Laiz, L.; Pallecchi, P.; Tiano, P.; Sanchez-Moral, S.; Saiz-Jimenez, C. Deterioration of an Etruscan tomb by bacteria from the order *Rhizobiales*. *Sci. Rep.* **2014**, *4*, 3610. [CrossRef] [PubMed]
126. Zacharenka, F. Study of the Bacterial Diversity on Ancient Mural Paintings from Kalliroi’s Fountain and Pana’s Sanctuary. Master’s Thesis, University of Thessaly, Volos, Greece, 2014.
127. Duan, Y.; Wu, F.; Wang, W.; He, D.; Gu, J.-D.; Feng, H.; Chen, T.; Liu, G.; An, L. The microbial community characteristics of ancient painted sculptures in Maijishan Grottoes, China. *PLoS ONE* **2017**, *12*, e0179718.
128. Li, Q.; Zhang, B.; Wang, L.; Ge, Q. Distribution and diversity of bacteria and fungi colonizing ancient Buddhist statues analyzed by high-throughput sequencing. *Int. Biodeter. Biodegr.* **2017**, *117*, 245–254. [CrossRef]
129. Li, Q.; Zhang, B.; Yang, X.; Ge, Q. Deterioration-associated microbiome of stone monuments: Structure, variation, and assembly. *Appl. Environ. Microbiol.* **2018**, *84*, e02680-17. [CrossRef] [PubMed]
130. Zhang, X.; Ge, Q.; Zhu, Z.; Deng, Y.; Gu, J.-D. Microbiological community of the Royal Palace in Angkor Thom and Beng Mealea of Cambodia by Illumina sequencing based on 16S rRNA gene. *Int. Biodeter. Biodegr.* **2018**, *134*, 127–135. [CrossRef]
131. Dyda, M.; Pyzik, A.; Wilkojc, E.; Kwiatkowska-Kopka, B.; Sklodowska, A. Bacterial and fungal diversity inside the medieval building constructed with sandstone plates and lime mortar as an example of the microbial colonization of a nutrient-limited extreme environment (Wawel Royal Castle, Krakow, Poland). *Microorganisms* **2019**, *7*, 416. [CrossRef]
132. Jroundi, F.; Elert, K.; Ruiz-Agudo, E.; Gonzalez-Muñoz, M.T.; Rodriguez-Navarro, C. Bacterial diversity evolution in Maya plaster and stone following a bio-conservation treatment. *Front. Microbiol.* **2020**, *11*, 599144. [CrossRef]
133. Louati, M.; Ennis, N.J.; Ghodhbane-Gtari, F.; Hezbri, K.; Sevigny, J.L.; Fahnstock, M.F.; Cherif-Silini, H.; Bryce, J.G.; Tisa, L.S.; Gtari, M. Elucidating the ecological networks in stone-dwelling microbiomes. *Environ. Microbiol.* **2020**, *22*, 1467–1480. [CrossRef]
134. Schröer, L.; De Kock, T.; Cnudde, V.; Boon, N. Differential colonization of microbial communities inhabiting Lede stone in the urban and rural environment. *Sci. Total Environ.* **2020**, *733*, 139339. [CrossRef]
135. Yang, S.; Wu, L.; Wu, B.; Zhang, Y.; Wang, H.; Tan, X. Diversity and structure of soil microbiota of the Jinsha earthen relic. *PLoS ONE* **2020**, *15*, e0236165. [CrossRef]
136. Coelho, C.; Mesquita, N.; Costa, I.; Soares, F.; Trovão, J.; Freitas, H.; Portugal, A.; Tiago, I. Bacterial and archaeal structural diversity in several biodeterioration patterns on the limestone walls of the Old Cathedral of Coimbra. *Microorganisms* **2021**, *9*, 709. [CrossRef] [PubMed]
137. İpekci, E. Evaluation of Stone Deterioration Problems of Anavarza Archaeological Site for the Purpose of Conservation. Ph.D. Thesis, İzmir Institute of Technology, Urla, Turkey, 2021.

138. Sansupa, C.; Suphaphimol, N.; Nonthijun, P.; Ronsuek, T.; Yimklan, S.; Semakul, N.; Khrueraya, T.; Suwannarach, N.; Purahong, W.; Disayathanoowat, T. The microbiome of a 13th century Lan Na mural painting: Diversity, taxonomic distribution and their biodeterioration potentials. *Microorganisms* **2023**, *11*. [in press](#).
139. Chen, P.; Zhang, L.; Guo, X.; Dai, X.; Liu, L.; Xi, L.; Wang, J.; Song, L.; Wang, Y.; Zhu, Y.; et al. Diversity, biogeography, and biodegradation potential of actinobacteria in the deep-sea sediments along the Southwest Indian Ridge. *Front. Microbiol.* **2016**, *7*, 1340. [\[CrossRef\]](#) [\[PubMed\]](#)
140. Pietrzak, K.; Otlewska, A.; Dybka, K.; Danielewicz, D.; Pangallo, D.; Demnerová, K.; Ďurovič, M.; Kraková, L.; Scholtz, V.; Bučková, M.; et al. A modern approach to biodeterioration assessment and disinfection of historical book. In *A Modern Approach to Biodeterioration Assessment and the Disinfection of Historical Book Collections*; Gutarowska, B., Ed.; Institute of Fermentation Technology and Microbiology, Łódź University of Technology: Łódź, Poland, 2016; pp. 81–125.
141. Gozari, M.; Bahador, N.; Jassbi, A.R.; Mortazavi, M.S.; Hamzehei, S.; Eftekhari, E. Isolation, distribution and evaluation of cytotoxic and antioxidant activity of cultivable actinobacteria from the Oman Sea sediments. *Acta Oceanol. Sin.* **2019**, *38*, 84–90. [\[CrossRef\]](#)
142. Van Assche, A. Characterization of the Bacterial Community Composition in Drinking Water Production and Distribution Systems, Emphasizing *Acinetobacter* species. Ph.D. Thesis, University of Leuven, Leuven, Belgium, 2019.
143. Argudo Fernández, M. Microbial Communities Responses in Fluvial Biofilms under Metal Stressed Scenarios. Ph.D. Thesis, Universitat de Girona, Girona, Spain, 2020.
144. Cao, W.; Xiong, Y.; Zhao, D.; Tan, H.; Qu, J. Bryophytes and the symbiotic microorganisms, the pioneers of vegetation restoration in karst rocky desertification areas in southwestern China. *Appl. Microbiol. Biotechnol.* **2020**, *104*, 873–891. [\[CrossRef\]](#) [\[PubMed\]](#)
145. Caffrey, P.; Hogan, M.; Song, Y. New glycosylated polyene macrolides: Refining the ore from genome mining. *Antibiotics* **2022**, *11*, 334. [\[CrossRef\]](#)
146. Yang, Y.; Qiu, J.; Wang, X. Exploring the dynamic of bacterial communities in Manila clam (*Ruditapes philippinarum*) during refrigerated storage. *Front. Microbiol.* **2022**, *13*, 882629. [\[CrossRef\]](#)
147. Boquet, E.; Boronat, A.; Ramos-Cormenzana, A. Production of calcite (calcium carbonate) crystals by soil bacteria is a general phenomenon. *Nature* **1973**, *246*, 527–528. [\[CrossRef\]](#)
148. Barton, H.A.; Northup, D.E. Geomicrobiology in cave environments: Past, current and future perspectives. *J. Cave Karst Stud.* **2007**, *69*, 163–178.
149. Banks, E.D.; Taylor, N.M.; Gulley, J.; Lubbers, B.R.; Giarrizzo, J.G.; Bullen, H.A.; Hoehler, T.M.; Barton, H.A. Bacterial calcium carbonate precipitation in cave environments: A function of calcium homeostasis. *Geomicrobiol. J.* **2010**, *27*, 444–454. [\[CrossRef\]](#)
150. Cañaveras, J.C.; Hoyos, M.; Sanchez-Moral, S.; Sanz-Rubio, E.; Bedoya, J.; Soler, V.; Groth, I.; Schumann, P.; Laiz, L.; Gonzalez, I.; et al. Microbial communities associated to hydromagnesite and needle fiber aragonite deposits in a karstic cave (Altamira, Northern Spain). *Geomicrobiol. J.* **1999**, *16*, 9–25.
151. Sanchez-Moral, S.; Cañaveras, J.C.; Laiz, L.; Saiz-Jimenez, C.; Bedoya, J.; Luque, L. Biomediated precipitation of calcium carbonate metastable phases in hypogean environments: A short review. *Geomicrobiol. J.* **2003**, *20*, 491–500. [\[CrossRef\]](#)
152. Cuezva, S.; Fernandez-Cortes, A.; Porca, E.; Pasic, L.; Jurado, V.; Hernandez-Marine, M.; Serrano-Ortiz, P.; Cañaveras, J.C.; Sanchez-Moral, S.; Saiz-Jimenez, C. The biogeochemical role of Actinobacteria in Altamira Cave, Spain. *FEMS Microbiol. Ecol.* **2012**, *81*, 281–290. [\[CrossRef\]](#) [\[PubMed\]](#)
153. Maciejewska, M.; Adam, D.; Naômé, A.; Martinet, L.; Tenconi, E.; Calusinska, M.; Delfosse, P.; Hanikenne, M.; Baurain, D.; Compère, P.; et al. Assessment of the potential role of *Streptomyces* in cave moonmilk formation. *Front. Microbiol.* **2017**, *8*, 1181. [\[CrossRef\]](#) [\[PubMed\]](#)
154. Hoffmann, T.D.; Reeksting, B.J.; Gebhard, S. Bacteria-induced mineral precipitation: A mechanistic review. *Microbiology* **2021**, *167*, 001049. [\[CrossRef\]](#)
155. Tomé, D. Yeast extracts: Nutritional and flavoring food ingredients. *ACS Food Sci. Technol.* **2021**, *1*, 487–494. [\[CrossRef\]](#)
156. Joubert, J.J.; van Rensburg, E.J.; Pitout, M.J. A plate method for demonstrating the breakdown of heparin and chondroitin sulphate by bacteria. *J. Microbiol. Methods* **1984**, *2*, 197–202. [\[CrossRef\]](#)
157. Sanchez-Moral, S.; Luque, L.; Cañaveras, J.C.; Laiz, L.; Jurado, V.; Saiz-Jimenez, C. Bioinduced barium precipitation in St. Callixtus and Domitilla catacombs. *Ann. Microbiol.* **2004**, *54*, 1–12.
158. Sanchez-Moral, S.; Bedoya, J.; Luque, L.; Cañaveras, J.C.; Jurado, V.; Laiz, L.; Saiz-Jimenez, C. Biomineralization of different crystalline phases by bacteria isolated from catacombs. In *Molecular Biology and Cultural Heritage*; Saiz-Jimenez, C., Ed.; Balkema: Lisse, The Netherlands, 2003; pp. 179–185.
159. Rivadeneyra, M.A.; Ramos-Cormenzana, A.; García-Cervigón, A. Bacterial formation of struvite. *Geomicrobiol. J.* **1983**, *3*, 151–163. [\[CrossRef\]](#)
160. Rivadeneyra, M.A.; Pérez-García, I.; Ramos-Cormenzana, A. Influence of ammonium ion on bacterial struvite production. *Geomicrobiol. J.* **1992**, *10*, 125–137. [\[CrossRef\]](#)
161. Manzoor, M.A.P.; Singh, B.; Agrawal, A.K.; Arun, A.B.; Mujeeburahman, M.; Rekha, P.-D. Morphological and micro-tomographic study on evolution of struvite in synthetic urine infected with bacteria and investigation of its pathological biomineralization. *PLoS ONE* **2018**, *13*, e0202306. [\[CrossRef\]](#) [\[PubMed\]](#)
162. Sánchez-Román, M.; Rivadeneyra, M.A.; Vasconcelos, C.; McKenzie, J.A. Biomineralization of carbonate and phosphate by moderately halophilic bacteria. *FEMS Microbiol. Ecol.* **2007**, *61*, 273–284. [\[CrossRef\]](#)

163. Cañaveras, J.C.; Cuezva, S.; Sanchez-Moral, S.; Lario, J.; Laiz, L.; Gonzalez, J.M.; Saiz-Jimenez, C. On the origin of fiber calcite crystals in moonmilk deposits. *Naturwissenschaften* **2006**, *93*, 27–32. [[CrossRef](#)] [[PubMed](#)]
164. Onac, B.P.; Ghergari, L. Moonmilk mineralogy in some Romanian and Norwegian Caves. *Cave Sci.* **1993**, *20*, 106–120.
165. Cañaveras, J.C.; Sanchez-Moral, S.; Soler, V.; Saiz-Jimenez, C. Microorganisms and microbially induced fabrics in cave walls. *Geomicrobiol. J.* **2001**, *18*, 223–240.
166. Baskar, S.; Baskar, R.; Routh, J. Biogenic evidences of moonmilk deposition in the Mawmluh Cave, Meghalaya, India. *Geomicrobiol. J.* **2011**, *28*, 252–265.
167. Jones, B.; Peng, X. Abiogenic growth of needle-fiber calcite in spring towers at Shiqiang, Yunnan province, China. *J. Sediment. Res.* **2014**, *84*, 1021–1040. [[CrossRef](#)]
168. Cuezva, S.; Sanchez-Moral, S.; Saiz-Jimenez, C.; Cañaveras, J.C. Microbial communities and associated mineral fabrics in Altamira Cave, Spain. *Int. J. Speleol.* **2009**, *38*, 83–92.
169. Sanchez-Moral, S.; Portillo, M.C.; Janices, I.; Cuezva, S.; Fernández-Cortés, A.; Cañaveras, J.C.; Gonzalez, J.M. The role of microorganisms in the formation of calcitic moonmilk deposits and speleothems in Altamira Cave. *Geomorphology* **2012**, *139–140*, 285–292. [[CrossRef](#)]
170. Maciejewska, M.; Calusinska, M.; Cornet, L.; Adam, D.; Pessi, I.S.; Malchair, S.; Delfosse, P.; Baurain, D.; Barton, H.; Carnol, M.; et al. High-throughput sequencing analysis of the actinobacterial spatial diversity in moonmilk deposits. *Antibiotics* **2018**, *7*, 27. [[CrossRef](#)]
171. Groth, I.; Schumann, P.; Laiz, L.; Sanchez-Moral, S.; Cañaveras, J.C.; Saiz-Jimenez, C. Geomicrobiological study of the Grotta dei Cervi, Porto Badisco, Italy. *Geomicrobiol. J.* **2001**, *18*, 241–258. [[CrossRef](#)]
172. Park, S.; Cho, Y.-J.; Jung, D.; Jo, K.; Lee, E.-J.; Lee, J.-S. Microbial diversity in moonmilk of Baeg-nyong Cave, Korean CZO. *Front. Microbiol.* **2020**, *11*, 613. [[CrossRef](#)] [[PubMed](#)]
173. Cirigliano, A.; Tomassetti, M.C.; Di Pietro, M.; Mura, F.; Maneschi, M.L.; Gentili, M.D.; Cardazzo, B.; Arrighi, C.; Mazzoni, C.; Negri, R.; et al. Calcite moonmilk of microbial origin in the Etruscan Tomba degli Scudi in Tarquinia, Italy. *Sci. Rep.* **2018**, *8*, 15839. [[CrossRef](#)] [[PubMed](#)]
174. Maciejewska, M.; Pessi, I.S.; Arguelles-Arias, A.; Noirfalise, P.; Luis, G.; Ongena, M.; Barton, H.; Carnol, M.; Rigali, S. *Streptomyces lunaelactis* sp. nov., a novel ferroverdin A-producing *Streptomyces* species isolated from a moonmilk speleothem. *Anton. Leeuw.* **2015**, *107*, 519–531. [[CrossRef](#)] [[PubMed](#)]
175. Svec, P.; Kosina, M.; Zeman, M.; Holochová, P.; Králová, S.; Nemcová, E.; Micenková, L.; Urvashi, M.; Gupta, V.; Sood, U.; et al. *Pseudomonas karstica* sp. nov. and *Pseudomonas spelaei* sp. nov., isolated from calcite moonmilk deposits from caves. *Int. J. Syst. Evol. Microbiol.* **2020**, *70*, 5131–5140. [[CrossRef](#)]
176. Adam, D.; Maciejewska, M.; Naômé, A.; Martinet, L.; Coppieters, W.; Karim, L.; Baurain, D.; Rigali, S. Isolation, Characterization, and antibacterial activity of hard-to-culture Actinobacteria from cave moonmilk deposits. *Antibiotics* **2018**, *7*, 28. [[CrossRef](#)]
177. Jaroszewicz, W.; Bielanska, P.; Lubomska, D.; Kosznik-Kwasnicka, K.; Golec, P.; Grabowski, Ł.; Wiczerzak, E.; Drózd, W.; Gaffke, L.; Pierzynowska, K.; et al. Antibacterial, antifungal and anticancer activities of compounds produced by newly isolated *Streptomyces* strains from the Szczelina Chochołowska Cave (Tatra Mountains, Poland). *Antibiotics* **2021**, *10*, 1212. [[CrossRef](#)]
178. Jaroszewicz, W.; Bielanska, P.; Lubomska, D.; Kosznik-Kwasnicka, K.; Golec, P.; Grabowski, Ł.; Wiczerzak, E.; Drózd, W.; Gaffke, L.; Pierzynowska, K.; et al. Antimicrobial activities of compounds produced by newly isolated *Streptomyces* strains from Mountain Caves. *Med. Sci. Forum* **2022**, *12*, 7.
179. Maciejewska, M.; Adam, D.; Martinet, L.; Naômé, A.; Całusińska, M.; Delfosse, P.; Carnol, M.; Barton, H.A.; Hayette, M.-P.; Smargiasso, N.; et al. A Phenotypic and genotypic analysis of the antimicrobial potential of cultivable *Streptomyces* isolated from cave moonmilk deposits. *Front. Microbiol.* **2016**, *7*, 1455. [[CrossRef](#)]
180. Martinet, L.; Naômé, A.; Rezende, L.C.D.; Tellatin, D.; Pignon, B.; Docquier, J.-D.; Sannio, F.; Baiwir, D.; Mazzucchelli, G.; Frédérich, M.; et al. Lunaemycins, new cyclic hexapeptide antibiotics from the cave moonmilk-dweller *Streptomyces lunaelactis* MM109T. *Int. J. Mol. Sci.* **2023**, *24*, 1114. [[CrossRef](#)]
181. Martinet, L.; Naômé, A.; Baiwir, D.; De Pauw, E.; Mazzucchelli, G.; Rigali, S. On the risks of phylogeny-based strain prioritization for drug discovery: *Streptomyces lunaelactis* as a case study. *Biomolecules* **2020**, *10*, 1027. [[CrossRef](#)] [[PubMed](#)]

Disclaimer/Publisher’s Note: The statements, opinions and data contained in all publications are solely those of the individual author(s) and contributor(s) and not of MDPI and/or the editor(s). MDPI and/or the editor(s) disclaim responsibility for any injury to people or property resulting from any ideas, methods, instructions or products referred to in the content.