Competition-cooperation in the chemoautotrophic ecosystem of Movile Cave: first metagenomic approach on sediments

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Abstract

**Background:** Movile Cave (SE Romania) is a chemoautotrophically-based ecosystem fed by hydrogen sulfide-rich groundwater serving as a primary energy source analogous to the deep-sea hydrothermal ecosystems. Our current understanding of Movile Cave microbiology has been confined to the sulfidic water and its proximity, as most studies focused on the water-floating microbial mat and planktonic accumulations likely acting as the primary production powerhouse of this unique subterranean ecosystem. By employing comprehensive genomic-resolved metagenomics, we questioned the spatial variation, chemoautotrophic abilities, ecological interactions and trophic roles of Movile Cave’s microbiome thriving beyond the sulfidic-rich water.

**Results:** A customized bioinformatics pipeline led to the recovery of 106 high-quality metagenome-assembled genomes from 7 cave sediment metagenomes. Assemblies’ taxonomy spanned 19 bacterial and three archaeal phyla with **Acidobacteriota**, **Chloroflexota**, **Proteobacteria**, **Planctomycetota**, Ca. **Patescibacteria**, **Thermoproteota**, **Methylo**-**mirabilota**, and Ca. **Zixibacteria** as prevalent phyla. Functional gene analyses predicted the presence of CO2 fixation, methanotrophy, sulfur and ammonia oxidation in the explored sediments. Species Metabolic Coupling Analysis of metagenome-scale metabolic models revealed the highest competition-cooperation interactions in the sediments collected away from the water. Simulated metabolic interactions indicated autotrophs and methanotrophs as major donors of metabolites in the sediment communities. Cross-feeding dependencies were assumed only towards ‘currency’ molecules and inorganic compounds (O2, PO4 3−, H+, Fe2+, Cu2+) in the water proximity sediment, whereas hydrogen sulfide and methanol were assumedly traded exclusively among distant gallery communities.

**Conclusions:** These findings suggest that the primary production potential of Movile Cave expands way beyond its hydrothermal waters, enhancing our understanding of the functioning and ecological interactions within chemo-lithoautotrophically-based subterranean ecosystems.

**Keywords:** Chemoautotrophic, Genome-scale metabolic models, Competition-cooperation interactions, Cross-feeding dependencies, Sulfidic cave, Romania

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**Background**

The most studied chemoautotrophically-based ecosystems are deep-sea hydrothermal vents and cold seeps [1–4]. But carbon fixation via chemosynthesis also plays a crucial role in reduced sulfur-rich water and sediments of circumneutral saline and soda lakes [5–7] and sulfidic caves [8–10]. In contrast to deep-sea chemoautotrophic...
systems, their subterranean counterparts, namely chem-

oautotrophic caves, have been largely underexplored. To
date, only a few cave ecosystems that rely totally or par-
tially on chemosynthesis have been explored, including
Ayyalon Cave (Israel), Movile Cave (Romania), Frasassi
Cave (Italy), Lower Kane Cave and Cesspool Cave (USA),
and Villa Luz Cave (Mexico) [9, 11–16]. In these caves,
microorganisms produce organic matter in situ, start-
ing from inorganic compounds as nutrient and energy

sources.

The Movile Cave (SE Romania) was the first to be
mentioned as defying the conventional view of subter-
raneean ecosystems as supported by aboveground phos-
tosynthesis. Movile Cave is a small-surfaced, closed
chemoautotrophic system [8] driven by in-house sulfur
and methane oxidation and CO₂ fixation as primary
production processes. The cave, located in south-east-
ern Romania (Dobrogea region), developed in oolitic
and fossil-rich limestone of the Sarmatian age (Late
Miocene) and was sealed off during the Quaternary by
a thick and impermeable layer of clays and loess [17].
Movile Cave has a complex geological evolution with an
ongoing speleogenesis driven by two main processes: the
sulfuric acid corrosion in the partially submerged lower
cave level; and the condensation-corrosion processes
active in the upper level of the cave [18]. The upper gal-

lery (approx. 200 m long) is dry, whereas the lower gal-

lery (approx. 40 m long) is partially flooded by sulfidic
hydrothermal waters (T ≈ 20.9 °C). The two cave levels
converge in the so-called Lake Room (Fig. 1). Air pockets
(Air Bells) are present in the submerged gallery (Fig. 1).
Here, an active redox interface is created on both the
water’s surface and cave walls, colonized by floating
microbial mats and biofilms. Most of our knowledge of
the fauna is abundant in the Lake Room [15, 19], par-
ticularly at the water surface in the Air-Bells [23], where
the redox potential is high.

Except for a snapshot investigation of the rock’s surface
collected at about 2 m away from the water [24]—which
revealed the presence of sulfur oxidizers and methyl-

otrophic bacteria—Movile Cave has not yet been explored
for the microbial life associated with sediments distant
from the sulfidic waters. Also, no metagenome-assem-
bled genomes (MAGs) reconstruction studies have been
carried out, and the genomic information available in
databases about this unique environment is limited to
a Ca. Methylomonas sp. LWB [19] and a Thiovulum sp.
[22] genome assemblies from the microbial mat.

Considering the unique features of Movile Cave as a
model chemoautotrophic subterranean ecosystem and its
overlooked microbial communities away from the sulfidic
water, we hypothesized that the scarcity of high-energy
organic substrates beyond the primary energy source of
sulfidic water would strengthen the ecological interac-
tions among community members to optimize the flow
of nutrients and ultimately, the energy gain. To address
this hypothesis, genome-resolved metagenomics was
employed to infer the diversity and abundance of spatially
distinct sediment-associated microbiomes and to pre-
dict their metabolic abilities, ecological interactions and
roles within the cave’s ecosystem. Our genome resolved
metagenomic study adds 106 higher-quality MAGs to the
Movile Cave microbial genomes. The results broaden our
understanding of sediment microbial communities’ role
within the complex food web of Movile Cave, which sup-
ports 52 endemic invertebrate species [15].

Materials and methods
Study site and sample collection
Sediment samples were collected from seven sites located
in the cave’s upper and lower levels (galleries) (Fig. 1)
in December 2019. Sampling sites were selected based
on their physical characteristics (detailed in Table 1 and
Additional file 1: Fig. S1) and positions related to the
Lake Room. Three sampling sites were near the water,
in the Lake Room (PMV1, PMV3, PMV4), and the other
two (PMV2, PMV6, PMV7, PMV8) in the upper, dry gal-
leries. The PMV5 sample consisted of sulfidic water and
was not the subject of this study. Stable environmental
conditions typical to a subterranean habitat combined
with hydrothermal activity drive a constant temperature
of the water and air at ≈ 20.9 °C within Movile Cave.
Aseptically collected top sediments (up to 50 g) were
kept at 4 °C after sampling and while transporting, then
at −20 °C until processing.

Mineralogy and geochemistry measurements
Powdered X-ray diffraction analyses were performed on
sediments in order to establish their mineralogy. Samples
were analyzed with a Rigaku Ultima IV diffractometer in
parallel beam geometry equipped with CuKα radiation
(wavelength 1.5406 Å). The XRD patterns were collected in 2Θ range between 5 to 80 with a speed of 2°/min and a
step size of 0.02°. PDXL software from Rigaku, connected
to the ICDD database was used for phase identification.
The quantitative determination was made using the RIR
(Reference Intensity Ratio) methodology.

The pH and electric conductivity were measured in
1:5 solid to water extract using a Seven Excellence (Met-
tler Toledo) multimeter. The N, C and H were measured
on freeze-dried samples using a Flash 2000 (Thermo
Scientific, Thermo Fisher Scientific, Waltham, MA, United States) analyzer. For measurement of metals, samples were digested using a 1:3 mixture of 65% HNO₃ and 37% HCl at reflux conditions. Major elements (Na, K, Ca, Mg, Al, Fe, S, P) in the digested samples were determined by inductively coupled plasma optical emission spectrometry (ICP-OES) using a 5300 Optima DV spectrometer (Perkin Elmer, Shelton, CT, United States), while trace metals and metalloids by inductively coupled plasma mass spectrometry (ICP-MS) using an ELAN DRC II spectrometer (Perkin Elmer, Waltham, MA, United States). Additional measurements were done for the aqueous fraction of the PMV4 sample. Total nitrogen (TN) was measured in unfiltered water, while dissolved nitrogen (DN) was measured in water samples filtered through 0.45 µm pore size PTFE syringe filters by catalytic combustion and chemiluminescence detection using a Multi N/C 2100 (Analytik Jena, Jena, Germany) analyzer. Total carbon (TC) and total inorganic carbon (TIC) were measured from unfiltered samples, while dissolved

**Fig. 1** Schematic representations of the Movile Cave map (B), profile (C) and its localization in Romania and Europe (A). The sampling sites from this study are PMV1-PMV8 (modified from Sarbu et al. [25]).
AMPure XP system was used for PCR product purification. Sequencing indexes were added to each sample. The PCR randomly fragmented the DNA to a size of around 350 bp. used starting from 200 ng DNA. Sonication was used to break up the DNA with the NEBNext Ultra DNA Library Prep Kit (New England BioLabs, Ipswich, MA, United States) was used to break up the DNA into smaller fragments. Agilent 2100 Bioanalyzer was used to analyze the size distribution of the DNA library, and qPCR was performed to quantify DNA according to conventional Illumina library quantification protocol. The samples were sequenced and paired-end reads were generated (PE150) on the Illumina NovaSeq 6000 platform.

**Reads assembly and annotation**

Metagenomic raw reads (fastq) were adapter-trimmed using Trimmomatic v0.39 [26] and, their quality was evaluated using FastQC v0.11.9 [27]. The resulting sequences were assembled into contigs using MEGAHIT v1.2.9 [28], with the following parameters: **no-mercy, k-min = 31, k-max = 101, k-step = 10.** The assembly of reads was done separately, for each metagenome (sample). Assembled contigs (> 1 kb) were binned using two binners: MaxBin v2.0 [29] and MetaBAT2 v2.12.1 [30]. DAS Tool (v1.1.2) was applied to integrate the bins generated from the two methods [31]. Only bins with over 70% completion and less than 10% contamination based on the results of CheckM v1.1.3 [32] were analyzed. Protein-coding sequences (CDS) of selected metagenome-assembled genomes (MAGs) were predicted and annotated with Prodigal v2.6.1 [33] and DIAMOND v2.0.5 [34] against Uniprot databases. Furthermore, the functional annotation of CDS and the prediction of metabolic pathways related to sulfur, nitrogen, carbon, and methane metabolism was carried out using the KEGG’s Ghost Koala tool [35]. For confirmation, CDS of interest were identified by blastp against NCBI nr database. In addition to the results obtained by functional annotation, the shotgun preprocessed reads were mapped to a set of reference sequences of nitrogen and carbon fixation hallmark genes with Minimap2 v2.21 with the short reads settings (-sr option).

**Taxonomic assignment and abundance of MAGs**

Taxonomic classification of MAGs was assessed using Genome Taxonomy Database Toolkit (GTDB-Tk v1.5.0,
reference data for GTDB R06-RS202) [36] based on 120 bacterial and 122 archaeal marker genes. For phylogenetic analysis, closely related MAGs, reference genomes, or type strains genomes were selected from GTDB (July 2021). The marker genes alignment was concatenated and then imported into R using the readAA Multiple Alignment function from the package Biostrings. Phylogenetic distances were calculated using the function dist.alignment from the package seqinr, and a phylogenetic tree was built using the neighbor-joining tree estimation as implemented in the function nj in the R package ape. The tree was visualized using the online iTOL tool [37].

Finally, for MAGs coverage, the filtered shotgun reads were mapped back to contigs belonging to each MAG with Minimap2 v2.21 [38], and the coverage was summarized with the coverage command from SAMtools v1.11 [39]. The relative abundance of each MAG in each metagenome was given by the number of reads mapped per Kb of MAG divided by Gb of corresponding metagenome (RPKG) [40].

### Genome-scale metabolic reconstruction and interaction models

Genome-scale metabolic models derived from MAGs (metaGEMs) were reconstructed using CarveMe v1.5.1 [41], with the default CPLEX solver (v12.8.0.0) (IBM, 2019). Two sets of metaGEMs were reconstructed: one set without gap-filling for any particular medium, based only on genetic evidence; and another set gap-filled for a custom minimal medium that would guarantee the models’ growth in a nutrient-poor environment as in Movile Cave. MEMOTE tests suite [42] was applied to the gap-fill models initialized for the minimal medium to ensure that the metaGEMs could generate biomass and reproduce growth in a scarce environment. The custom minimal medium composition is detailed in Additional file 2: Tables S2, S3.

For the simulations, the samples were divided into two groups based on their distance from the sulfidic water: samples from the lower gallery in the Lake Room (PMV2, PMV3, PMV4 and PMV6) electrical conductivity ranging from 60.6 to 1738.8 µS cm⁻¹ (Table 2). The physicochemical characteristics of the sediment samples are shown in Table 2. Total carbon (TOC) and total nitrogen (TN) content, measured for the aqueous fraction of the sample collected from the water edge (PMV4) were low (TOC = 14.9 mg L⁻¹, TN = 3.7 mg L⁻¹) with a TOC/TN of ~ 4 mg L⁻¹ (Additional file 3: Table S4).

In the upper cave gallery, the identified minerals are calcite, dolomite, aragonite, quartz, muscovite, gypsum,
and in small amounts, goethite. Near the Lake, in the lower gallery, the association is dominated by dolomite and calcite, followed by quartz, gypsum and muscovite (Table 2). Carbonates are represented mainly by calcite derived from the limestone bedrock, dolomite and aragonite. Dolomite is present in substantial amounts in both levels of the cave. The bedrock mineralogy reveals the presence of magnesium-rich carbonate, which could be the explanation for the occurrence of aragonite, a signature of PMV8 mineralogy. Samples mineralogy is shown in Table 2 and Additional file 3: Table S5.

MAGs recovery and phylogeny
A total of 106 medium- to high-quality MAGs (>70% complete and <10% contamination) [48] were recovered from the sediment metagenomes of Movile Cave. The taxonomic assignment performed using GTDB-tk indicated that the recovered MAGs span 19 bacterial and three archaeal phyla. Out of those, 4 were candidate phyla Ca. Patescibacteria, KSB1, Krumholzibacteriota and Zixibacteria. The percentages of reads mapped to MAGs varied among samples from ca. 80% to 13% for MAG recovery efficiency (summarized in Additional file 4: Table S6). The low binning efficiency in some of the samples points toward a very diverse community (feature specific to sediment samples) where the low abundance species were unable to be assembled into MAGs as a consequence of low or partial coverage.

Table 2  Physicochemical and mineralogical composition of the sediment samples in Movile Cave

| Parameter (unit)/Sample | PMV1 | PMV2 | PMV3 | PMV4 | PMV6 | PMV7 | PMV8 |
|-------------------------|------|------|------|------|------|------|------|
| pH                      | 8.5  | 8.3  | 7.9  | 8.3  | 8.1  | 8.9  | 9.2  |
| Electrical conductivity (µS cm⁻¹) | 270  | 751  | 955  | 1 237 | 1 739 | 1 19 | 60.6 |
| N (%SU)                 | 0.21 | <0.01 | <0.01 | 1.37 | <0.01 | <0.01 | <0.01 |
| C (%SU)                 | 9.1  | 4.8  | 3.9  | 8.8  | 8    | 6.6  | 4.1  |
| H (%SU)                 | 0.4  | 0.4  | 0.8  | 0.3  | 0.4  | 0.4  | 0.6  |
| Ca (mg kg⁻¹)            | 172 900 | 125 000 | 119 100 | 255 100 | 159 500 | 136 900 | 92 300 |
| Al (mg kg⁻¹)            | 21 450 | 25 950 | 19 520 | 12 635 | 11 630 | 29 540 | 38 490 |
| Mg (mg kg⁻¹)            | 42 960 | 29 860 | 6 834  | 27 590 | 51 980 | 36 320 | 28 120 |
| Fe (mg kg⁻¹)            | 10 160 | 10 540 | 21 470 | 10 030 | 5 545 | 10 140 | 12 780 |
| K (mg kg⁻¹)             | 5 103 | 4 279 | 4 983  | 2 415 | 2 140 | 5 816 | 6 185 |
| Na (mg kg⁻¹)            | 415  | 289  | 126   | 336  | 564  | 374  | 240  |
| S (mg kg⁻¹)             | 902  | 3 003 | 13 270 | 5 730 | 30 480 | 1 610 | 136  |
| P (mg kg⁻¹)             | 162  | 239  | 357   | 110  | 163  | 186  | 124  |
| Mn (mg kg⁻¹)            | 278  | 216  | 138   | 38.5 | 99.1 | 184  | 343  |
| Ba (mg kg⁻¹)            | 86.5 | 135  | 60.3  | 429  | 87.3 | 183  | 110  |
| Ti (mg kg⁻¹)            | 202  | 246  | 127   | 230  | 149  | 196  | 87.8 |
| Sr (mg kg⁻¹)            | 75.4 | 106  | 52.2  | 1060 | 270  | 91.6 | 48.2 |
| V (mg kg⁻¹)             | 29.6 | 26.9 | 261   | 15.5 | 16.4 | 24.2 | 33.6 |
| As (mg kg⁻¹)            | 39.1 | 24.7 | 322.5 | 20.6 | 24.8 | 26.4 | 19.5 |
| Zn (mg kg⁻¹)            | 9.9  | 14.9 | 19.4  | 4288 | 5.7  | 10.8 | 17.7 |
| Cr (mg kg⁻¹)            | 14.9 | 104  | 101   | 8    | 4.7  | 11.9 | 11.1 |
| Mineralogy (> 5%)       | dolomite, calcite | quartz, calcite | calcite, muscovite | dolomite, calcite | dolomite, gyspum, quartz | dolomite, calcite, muscovite | dolomite, muscovite, aragonite |
Based on the relative abundance of MAGs in the sample (expressed as RPKG), the most abundant phyla were Acidobacteriota, Chloroflexota, Proteobacteria and Planctomycetota (>20 RPKGs in any of the samples) (Fig. 3A). In the lower gallery, Chloroflexota was abundant in PMV1 and PMV3, while Proteobacteria (class Gammaproteobacteria) dominated PMV4. In the upper, dry gallery, Acidobacteriota was the most abundant phylum for PMV8 and PMV7. For the phyla with a lower relative abundance (<20 RPKGs), Ca. Patescibacteria was the signature phylum for PMV2, Thermoproteota for PMV3, Methyloirribiota for PMV7 and Ca. Zixibacteria for PMV8 (Fig. 3B).

Out of the 106 MAGs, 25 were classified as high-quality (>90% complete and <5% contamination) (Fig. 3C.), but only two were assigned to species level (PMV3.39 and PMV4.117 affiliated to Chromohalobacter marismortui) with available genomes in the NCBI database (gANI>95%). One-third of the MAGs (32 of 106) was classified by Relative Evolutionary Divergence (RED) as new species of established GTDB taxa [49]. Given the taxonomic novelty of recovered MAGs, RefSeq type material genomes (GCF) and representatives MAGs from GeneBank (GCA) were incorporated into the phylogenetic tree construction for a better representation (Fig. 3C.)

MAGs attributes, extended taxonomy and abundance are summarized in Additional file 4: Tables S7–S9.

**Potential for biogeochemical cycling of S and N, CH4 oxidation and CO2 fixation**

**Sulfur metabolism**

Microbial sulfur cycling has been proposed as a driving force for bacterial proliferation in microbial mats of Movile Cave [24] but not investigated in the cave’s sediments. Here, we examined the presence of the marker genes for sulfur cycle in the metagenomes of Movile Cave’s sediments. For sulfur oxidation (Fig. 4), the complete canonical pathway for thiosulfate (S2O3−2) to sulfate (SO4−2) conversion (sosAX, BYZ, (CD)) was annotated in the water edge dataset PMV4; and partially annotated in the upper gallery datasets PMV2 (sosZ), PMV6 (sos(CD), Y) and PMV7 (sos(YZ)). In the PMV4 dataset, Sox-complex was encoded in MAGs affiliated to order Thiohalomonadales (class Gammaproteobacteria) (PMV4.23) and family Arcobacteraceae (class Campylobacteria) (PMV4_maxbin.013). The Thiohalomonadales-affiliated MAG encoded an incomplete thiosulfate-oxidation pathway lacking Sox(CD) and carrying multiple copies of SoxB. For the sulfide (HS−) oxidation, the MAG encoded both the pathway to elemental sulfur (S0) via flavocytochrome c sulfide dehydrogenase (fccAB), and to sulfate (SO4−2) via the reverse-operating dissimilatory sulfate reductase pathway (dsrAB + aprAB + sat). The complete path for sulfite (SO3−2) oxidation to sulfate (SO4−2) (soeABC) was also annotated here. This Thiohalomonadales MAG also encoded (hydBD) the production of HS− from polysulfides by sulfhydrogenase complex (hyd(G,B),(A,D)).

In the rest of the datasets, Sox(YZ) subunits were encoded in Proteobacteria MAGs and Sox(CD) in a Gemmatimonadota MAG (PMV6_maxbin.020). Thiosulfate oxidation with tetrathionate (S4O6−2) formation was partially encoded (doxD) in all datasets except for PMV8, and mostly in bins affiliated to Chloroflexota. Sulfide:quinone reductase (sqr) for the oxidation of HS− with the zero-valent sulfur S0 formation was encoded in all datasets. The oxidation of sulfide via SQR was predicted as a widespread trait encoded in 27 MAGs. The pathway for sulfite (SO3−2) oxidation to sulfate (SO4−2) was also partially encoded (soeB) in PMV6 and PMV8 datasets. Sulfur respiration, dissimilatory reduction of oxidized sulfur compounds (SO4−2, SO3−2, S2O3−2, S0) coupled with sulfide (HS−) production, were also detected. Sulfate (SO4−2) to sulfite (SO3−2) reduction (sat + aprAB) was present in the PMV4 dataset, in a MAG affiliated to order Thromodesulfovibrioales (phylum Nitrospirina) (PMV4_maxbin.018). An NCBI blast (blastx against RefSeq Select database) showed the AprAB sequences similarities to
Fig. 3 The abundance and phylogeny of MAGs recovered from sediments of Movile Cave. A. Most abundant phyla (relative abundance > 20 RPKGs). B. Less abundant phyla (relative abundance < 20 RPKGs). C. Phylogenetic tree of MAGs from Movile Cave sediments, including their closely related MAGs from GTDB (GCA) and NCBI type material genomes (GCF) (type strain and/or reference genomes). The neighbor-joining phylogenetic tree was constructed based on the GTDB marker genes. The MAGs detected in this study are shown in blue or red for medium- or high-quality MAGs, respectively.
Fig. 4 Overview of pathways and genes involved in sulfur, nitrogen cycling, methane oxidation and CO₂ fixation encoded by MAGs recovered from Movile Cave sediments. The color scheme gives the presence/absence of functional genes: presence is indicated in red, absence in grey. The involvement of each gene in specific pathways is indicated in the diagrams. Red arrows indicate oxidation, and the blue arrows show the reduction of compounds. Full arrows indicate the enzymatic reactions for which the coding genes were found in the datasets based on the analyzed MAGs. The dotted arrows show enzymatic reactions absent in the datasets.
**Deltaproteobacteria** (≈73% to 80%), placing them in the direct-operating dissimilatory pathway.

Thiosulfate/elemental sulfur (S₂O₃⁻⁻/S⁰) disproportionation and tetrahydroionate respiration were partially encoded (phsA, phsC; ttrA/B) in different phylogenetic groups, but a Planctomycetae-affiliated MAG (PMV1.61) that might encode both as ttrB and phsA were present in the bin. The production of hydrogen sulfide from polysulfides by sulfhydrogenase complex (hyd(G,B),(A,D)) was partially encoded, especially by MAGs affiliated to Acidobacteriota, Chloroflexota and Planctomycetae.

**Nitrogen metabolism**

Analogous to sulfur, we addressed the potential for biogeochemical N cycling across sediments of Movile Cave. Primary producers capable of obtaining energy for autotrophy by nitrogen oxidation (nitrification) were questioned. The first step of nitrification, the ammonia NH₃⁺ to nitrite NO₂⁻ oxidation, was suggested in Movile Cave sediments as ammonia monooxygenase AMO (amoABC) was encoded in PMV1 to PMV3 datasets. All three subunits of AMO’s were encoded in an order Methyllococcales-affiliated MAG (PMV2.70_sub). However, the amoABC sequences were homologous (>65% similarity) to the sequence encoding particulate methane monooxygenase pMMO in the genus Methylothericola. The methanotrophs can oxidize both substrates (NH₃ and CH₄) but grow only on their characteristic substrate [50]. Interestingly, AmoA-like subunit was annotated in an archaeon MAG affiliated to Nitrososphaera genus (phylum Thermoproteota) (PMV3_maxbin.65_sub). For the second step of nitrification, the oxidation of NO₂⁻ to NO₃⁻ of none of the bins encoded the nitrite oxidoreductase (nxxAB) found in known nitrite-oxidizing genera.

Also, no marker genes (hzoA and hzo) for the anaerobic ammonium oxidation (anammox) (NH₃ to N₂H₄ and then to N₂) were annotated in the Movile datasets.

In the chemoaotrophic cave environment, the nitrogen demand can be met by converting inorganic nitrogen to a biologically useful form by nitrogen reduction. The conversion involves microbial dinitrogen fixation or nitrate assimilation. Surprisingly, the N₂ fixation pathway was not detected in any sediment datasets, as no nitrogenase genes (nif) for the reduction of atmospheric molecular nitrogen (N₂) to ammonia (NH₃⁺) were annotated in MAGs. This result was reinforced by mapping the metagenomics reads against a set of nif reference sequences (listed in Additional file 5: Table S10) as no nifH/D were found in the PMV datasets except PMV4 (Additional file 5: Fig. S2). The assimilatory process (NO₃⁻, NO₂⁻ conversion to NH₃⁺), catalyzed by nitrate and nitrite reductases (nasA/B, narB; nirA), was fully encoded in PMV3, PMV6, and PMV8 datasets. The bins that encoded the nitrate-assimilatory enzymes were taxonomically diverse as the ability is however widely distributed among bacteria.

The first step in the dissimilatory nitrate reduction to ammonium (DNRA) and denitrification, NO₃⁻ to NO₂⁻ reduction, was fully encoded as the cytoplasmic nitrate reductases (narGHI) (PMV1, PMV6) or as the periplasmic nitrate reductases (napAB) (PMV3, PMV8). The NO₂⁻ to NH₄⁺ step of DNRA was encoded in all datasets as the cytoplasmic nitrate reductase (nirBD) or the periplasmic nitrite reductase complex (nrfAH). MAGs that encoded at least partially both steps of the DNRA pathway were affiliated to Acidobacteriota (PMV1.51 (Nap-Nir); PMV2.75 (Nar-Nrf); PMV7.11 (Nar-Nrf), Planctomycetota (PMV8.19_sub (Nap-Nrf); PMV8.5 (Nar-Nrf)) and Gammaproteobacteria (PMV6.23 (Nar-Nir)). Nitrite reductase (nirK), the hallmark enzyme of denitrification (NO₃⁻ to (NO) conversion) was encoded in all datasets except PMV7, in bins taxonomically unrelated with common denitrifiers, including Ca. Zixibacteria (PMV8.32) and Ca. Methylomirabilis (PMV4.88). The conversion of NO to nitrous oxide (N₂O) was fully encoded as nitric oxide reductase (noriC) in PMV4 in the sulfur oxidizing Thiohalomonadales MAG (PMV4.23). The last step of denitrification, conversion of N₂O to N₂, carried out by an oxygen-sensitive enzyme, the nitrous-oxide reductase (nosZ), was annotated in all data sets and across taxonomically diverse bins.

**Methane metabolism**

Via methane oxidation, methanotrophs can metabolize methane as their source of carbon and energy. In the oxidation pathway, methane (CH₄) is oxidized to methanol (CH₃OH) and then to formaldehyde (CH₂O) which is incorporated into organic compounds via the serine or the ribulose monophosphate (RuMP) pathway. As previously mentioned, all subunits of the particulate methane monooxygenase pMMO (pmmABC) were predicted in the order Methyllococcales MAG (PMV2.70_sub). Separated subunits of pMMO were also annotated in MAGs affiliated to Methyllococcales order (PMV1.33) and Methyllocella genus (PMV3.41). No soluble methane monoxygenase (sMMO) was annotated across investigated metagenomes. The methanol oxidation to formaldehyde appeared encoded as Ln³⁺-dependent methanol dehydrogenases (soxF) and heterotetrameric methanol dehydrogenase (mxaFI) in the Methyllococcales-affiliated MAG PMV2.70_sub. Only XoxF methanol dehydrogenase was encoded in MAGs affiliated to the classes Gammaproteobacteria (PMV6.23), Alphaproteobacteria (order Dongiales) (PMV8.34_sub) and Acidobacteria (PMV1.51, PMV3.11).
**Methanogenesis** potential was absent in the Movile sediment datasets as suggested by the absence of methyl coenzyme-M reductase (mcrA) marker gene across investigated MAGs.

**CO₂ fixation**
The CO₂ fixation is presumably critical in a chemotrophic ecosystem such as Movile Cave. To verify the autotrophic potential of the sediment communities, the presence of genes for the key enzymes of CO₂ fixation pathways, namely the Calvin–Benson–Bassham (CBB) cycle (key enzyme: ribulose 1,5-bisphosphate carboxylase/oxygenase, genes *cbbL* and *cbbS*), the reverse tricarboxylic acid (rTCA) cycle (key enzyme: ATP citrate lyase, genes *aclA* and *aclB*) and the reductive acetyl-CoA, or Wood-Ljungdahl (WL) pathway (key enzyme: CO dehydrogenase/acytel-CoA synthase (CODH/ACS complex), genes *acsA* and *acsB*) was investigated.

No carbon fixation key enzyme was encoded by MAGs from PMV6 and PMV7 datasets. RuBisCO large subunit (*cbbL*) (CBB cycle) was predicted in all other datasets in MAGs affiliated to *Ca.* KSB1 (PMV1_maxbin.001), *Chloroflexota* (PMV2.24), *Micrarchaeota* (PMV4.13) phyla and classes *Alphaproteobacteria* (genus *Methyllocella* (PMV3.41) and order *Dongiales* (PMV8.34_sub)) and *Gammaproteobacteria* (order *Thiohalomonadales*) (PMV4.23). The *Thiohalomonadales* (PMV4.23) and the *Dongiales* (PMV8.34_sub) MAGs encoded both RuBisCO subunits (*cbbL/S*). Most of the enzymes of the rTCA cycle are shared with the TCA cycle, except for the ATP citrate lyase (ACL) used by autotrophic prokaryotes for the conversion of citrate to acetyl-CoA. The rTCA cycle hallmark enzyme subunits were annotated in MAGs affiliated with phyla *Campylobacterota* (PMV4_maxbin.013) and *Nitrospirota* (PMV8.22).

For the anaerobic carbon fixation via WL pathway, the marker genes of CODH/ACS complex, *acsAB*, were found only in PMV4 dataset. The Western branch (carbonyl) was encoded by MAGs affiliated to phyla *Nitrospirota*, (order *Thernodesulfivibrionales*) (PMV4. maxbin.018) (AcsA (β), AcsB (α), AcsD (δ), AcsC (γ)) and *Ca.* KSB1 (PMV4.37) (AcsA (β), AcsB (α), AcsC (γ)). The Eastern branch (methyl), for CO₂ conversion to 5-methyltetrahydrofolate, was also encoded in the *Nitrospirota*-affiliated MAG. The *Ca.* KSB1-affiliated MAG encoded for methylenetetrahydrofolate dehydrogenase (*folD*) of WL pathway Eastern branch as well as the acetyl-CoA to acetate enzymes: acetate kinase (*ackA*), phosphate acetyltransferase (*pta*) and a putative phosphotransacetylase. This suggests that the *Ca.* KSB1 MAG could be unable to gain ATP from acetyl-CoA degradation. Enzymes for the Eastern branch (methyl) of WL pathway were encoded in all sediment datasets.

In addition to MAG analysis, mapping the metagenomics reads against a set of reference CO₂ fixation gene sequences (listed in Additional file 5: Table S10) highlighted the CBB cycle key genes as present in all datasets, including PMV6 and PMV7, and the WL pathway marker genes as hallmark genes for only PMV4 dataset (Additional file 5: Fig. S2).

Interestingly, none of the genes of interest for biogeochemical cycling of S and N, CH₄ oxidation and CO₂ fixation were annotated in MAGs assigned to *Ca.* Patescibacteria or *Myxococccota* phyla.

All the functional genes implicated in the sulfur and nitrogen cycling, methane oxidation and CO₂ fixation annotated in MAGs from Movile Cave sediment are listed in Additional file 6: Tables S11–S14 and an overview of the genes, encoding MAGs and pathways are shown in Fig. 4.

**Potential metabolic interactions and dependencies within the communities**

To gain a deeper insight into the microbial metabolic webs in Movile Cave sediments, we used the MAGs to construct metagenome-scale metabolic models (metaGEMs) for simulation and prediction of potential metabolic interactions and dependencies within the communities. Noteworthy, no metabolic models could be constructed for three MAGs belonging to *Ca.* Patescibacteria (PMV2.56, 2.61 and 2.72) thus were excluded from the analysis. The inability to construct metabolic models for MAGs belonging to *Ca.* Patescibacteria can be a consequence of the size of their reduced genome (usually < 1 Mb). The rest of the metaGEMs could generate biomass and reproduce growth in the simulation conditions, as evidenced by MEMOTE tests results included in the Additional file 7: Table S15. The competition–cooperation potential predicted by SMETANA (Fig. 5A.; Additional file 7: Table S16) was highest in the communities associated with the upper gallery (e.g. PMV7). This was evident, especially in the case of the necessary resources overlap (competition). The pattern persisted regardless of metaGEMs reconstruction or community simulation parameters. When community simulation assumed minimum nutrient availability, as presumed for the Movile Cave environment, the community members of the upper gallery (samples PMV6 to PMV8) exhibited the highest similarities of metabolic requirements (competition) and highest potential for community self-sufficiency (cooperation) (Fig. 5A.b.).

For an insightful analysis of the microbial metabolic webs in the Movile Cave sediments, we grouped the samples based on distance, namely samples from the lower,
Fig. 5 Competition-cooperation landscape of each sample and cross-feeding interactions across wet and dry galleries. A. The competition (MRO) and cooperation (MIP) scores (divided by the numbers of MAGs in the community) are shown for different reconstruction and simulation parameters: a. metaGEMs reconstructed only on genetic evidence and community simulation on complete medium (unconstrained environment); b. metaGEMs reconstructed by gap-filling for minimal media and community simulation on minimal media (constrained environment). B and C. Alluvial diagrams showing compounds exchanged (SMETANA score = 1) in each condition (lower/wet and upper/dry gallery) between the donor (left) and receiver (right) phyla. The colors are used only to distinguish distinct components of the alluvial diagrams.
'wet' gallery (PMV1, PMV3, PMV4) and samples from the upper, 'dry' gallery (PMV2, PMV6, PMV7, PMV8). We examined the cross-feeding interactions and key-stone phyla across those two conditions ('wet' and 'dry').

Our simulation results (SMETANA score = 1) suggested that only 'currency' molecules and inorganic ions (O$_2$, PO$_4^{3-}$, H$^+$, Fe$_{2+}$, Cu$^{2+}$) were exchanged in the lower gallery. Here, the donor MAGs belonged to archaea Ca. Thermoplasmatota (PMV4.75), bacteria candidate division NC10 (Methylomirabilota) (PMV4.88) and the bacteria genus Methylocella (PMV1.12) (Fig. 5B.). In the upper gallery, besides inorganic ions (Fe$_{2+}$, NO$_3^-$), hydrogen sulfide (H$_2$S) and methanol (CH$_3$OH) were also exchanged. Here, the essential donors were affiliated to the Alphaproteobacteria within order Dongiales (PMV8.34_sub) and Planctomycetota within order Phycozystetes (PMV2.11) (Fig. 5C.). For both conditions, the taxonomic affiliation of receiver MAGs was diverse, represented by MAGs belonging to 8 and 17 phyla. The MAGs that interact in each simulation condition and their role as donors or recipients of exchanged metabolites are listed in Additional file 7: Tables S17 and S18.

Out of the predicted essential compounds (SMETANA score = 1) that are readily exchanged among MAGs, H$_2$S, NO$_3^-$, methanol, and H$^+$ exchanges were significantly different (Wilcoxon rank-sum test, BH adjusted p-values < 0.001) across upper and lower galleries (Additional file 7: Table S19).

**Discussions**

Our current understanding of microbial life within the Movile Cave ecosystem was limited to the hydrothermal waters, as only microbial mats, water samples and lake sediments were previously investigated [18, 19]. Our study gives a first insight into the cave's chemosynthetic and primary production potential beyond the hydrothermal waters, namely the cave's sediments.

Based on physicochemical and mineralogical characterization, sampled sediments showed a very different chemical composition, even if located just meters away from one another. PMV6 and PMV8 differed the most from the other samples, followed by PMV3 and PMV4. Mineralogy partially supports such chemical discrepancies, but some of the best-represented elements are of different, unknown origins, probably linked to the history of the region where the cave is located and the input of the underground sediments from the Miocene to the more recent climatic events.

The taxonomic novelty of recovered MAGs was high, with over 60% unaffiliated to a genus and 30% classified by RED as new species of established GTDB taxa. The community was diverse with 22 microbial phyla, mainly Acidobacteriota, Chloroflexota, Proteobacteria, Planctomycetota, Ca. Patescibacteria, Thermoproteota, Methylomirabilota, and Ca. Zixibacteria based on the relative abundance of MAGs in samples. Despite the high novelty at lower taxonomic levels, the overall phyla diversity of sediment MAGs was typical of sulfidic and nonsulfidic cave microbiology [51–53]. Something worth noticing is the lack of Betaproteobacteria among recovered MAGs, since it was previously demonstrated for the Movile Cave ecosystem [16, 21].

Functional analyses suggested the presence of chemolithoautotrophic primary producers in the cave sediments from both galleries. As expected, sulfur oxidation, proposed as the ecosystem’s driving force, was mainly present in the lakeside dataset PMV4. The complete oxidation pathways (Sox and Dsr pathways), RuBisCO and partial nitrate/nitrite respiration and denitrification were encoded by the Thiohalomonadales-affiliated MAG (class Gammaproteobacteria). As Thiohalomonas members are obligate chemolithoautotrophic facultative anaerobic sulfur-oxidizing bacteria [54], this MAG might play a key role as a primary producer within the ecosystem. It uses reduced sulfur compounds as energy sources, nitrate as an electron acceptor, and assimilating CO$_2$ via the Calvin-Benson-Bassham cycle. Another primary producer inferred from the lake edge sample was an Arcobacteraceae-related MAG (phylum Campylobacterota/Epsilonproteobacteria) that encoded the capacity for sulfur oxidation (Sox) potentially coupled with nitrate-reduction (NapB) and CO$_2$ fixation via the reverse TCA cycle (aclAB). Those are typical metabolic features of Epsilonproteobacteria chemolithotrophic primary producers from the deep-sea hydrothermal vent [55]. Similar metabolic traits were found for the recently characterized Thiovulum sp. that dominates Movile Cave’s hypoxic Air Bells microbial mat [22]. Moreover, Arcobacteraceae family was found dominant in the white filaments from the thermal sulfidic spring of Fetida Cave, Italy [56]. Sulfur oxidation was not, however, limited to the lakeside sediments. Genes coding for Sox pathway (soxAB) were found in PMV2, 6 and 7 datasets of the upper, dry gallery across MAGs affiliated to Alpha-, Gammaproteobacteria and Gemmatimonadota phylum. The Gemmatimonadota role in the sulfur cycle is uncertain, but MAGs with similar attributes were identified in the Siberian soda lakes [6]. In the sediments from around the lake, sulfur respiration was also evident, which is less critical in self-sustaining ecosystems and a characteristic of heterotrophs. In addition to previous reports [16, 21] describing Deltaproteobacteria sulfate reducers in Movile Cave water and microbial mat samples, we assembled a hypothetical thermophilic sulfate reducer MAG affiliated to Nitrosopira (order Thermodesulfovibrionales) possessing DSR pathway genes (aprAB). These results might indicate that
sulfate reduction is important in and around the sulfidic water but not away from it.

Considering the relatively high (0.2–0.3 mM) ammonium concentrations in the cave waters [57], it was formerly implied that nitrogen oxidation might also be a driving force for the ecosystem [21]. A few Nitrosopriota-affiliated MAGs were identified in the upper and lower galleries, but none of the nitrite or ammonia-oxidation genes were annotated. No nitrifying bacteria were identified based on gene annotation, but an ammonia-oxidizing *Nitrososphaera* archaeon encoding for an AmoA-like subunit was assembled from the Lake Room PMV3 sediments. *Nitrososphaera* archaea are facultative chemolithoautotrophs with potential metabolic flexibility [58, 59]. Our metabolic annotation results suggest that the nitrogen cycle throughout the Movile Cave sediments is mostly driven by nitrate/nitrite respiration and denitrification. Those nitrogen reduction processes are linked to taxonomically diverse bacteria and spread among all investigated locations. Assimilatory and dissimilatory nitrate reduction to ammonium were predicted in all datasets, emphasizing the ability of the microbial communities to provide bioavailable N for the other trophic links in the Movile Cave ecosystem. Methanotrophs were also postulated as primary producers in the water and microbial mats [19–21, 24, 60] as 1–2% methane concentration was highlighted, especially in the Air-Bells [57]. In this study we were able to assemble methanotrophic MAGs from both lower and upper galleries. These were affiliated to the uncultured UBA1147 genus of Methylococcales (in PMV1, PMV2, PMV6) and Methy locella genus of Rhizobiales (in PMV1, PMV3, PMV6) and encoded for subunits of pMMO monooxygenase. Although no methane-oxidation gene could be annotated, *Methylomirabilales*-affiliated (candidate division NC10) MAGs were found in PMV2 (order *Rokubacteriales*), PMV4 and PMV7 (order *Methylomirabilales*) datasets. Interestingly *Methylomirabilales*-affiliated MAG was one of the most abundant MAGs in PMV7. The presence of Methylococcales (Methylococcus, Methylo monas, Meth ylocaldum) and Rhizobiales (Methylcystis/Methyl sinus, Methylocella) methanotrophs was previously postulated in the microbial mats based on pMMO-sequence clones from a CH₄-enriched culture [19, 20]. The genus *Methylocella* comprises facultative methanotrophs that utilize multicarbon compounds (acetate, pyruvate, succinate, malate, and ethanol) [61]. While the order *Rokubacteriales* might comprise non-methanotrophic bacteria [62], *Methylomirabilales* are known autotrophic (CO₂ fixing via CBB cycle), denitrifying methanotrophs that can oxidize methane anaerobically. The molecular oxygen needed for methane oxidation is generated by reducing nitrate to dinitrogen gas and O₂ and bypassing the nitrous oxide formation [63–65]. This is considered the fourth biological pathway known to produce oxygen besides photosynthesis, chlorate respiration, and the detoxification of reactive oxygen species [63].

The key enzymes for CO₂ fixation were found in 5 out of 7 sediment samples (except PMV6, PMV7), including PMV8 collected farthest from the lake. Noteworthy, in PMV8 MAGs both the CBB and rTCA enzymes were annotated. WL pathway of anaerobic CO₂ fixation was postulated only in the water edge dataset PMV4. A sulfur-respiring *(aprAB)* MAG affiliated to the order *Thermodesulfovibrio nales* (phylum *Nitrospira*) encoded for the WL pathway key enzymes (acsAB). However, the *Thermodesulfovibrio nales* order includes members (genus *Thermodesulfovibrio*) that are chemoorganotroph, fermentative and dissimilatory sulfate-reducing bacteria [66]. Therefore, the MAG encodes the WL pathway in reverse to break down acetate to CO₂ and H₂. Uncultured *Nitrospira* MAG from PMV8 dataset encoded key genes for rTCA cycle, confirming early evidence revealed by stable-isotope probing (SIP) of water and microbial mat samples that *Nitrospira* might be able of CO₂ fixation [21]. CBB cycle key enzymes were detected in most sediment samples, except for PMV6 and PMV7. The archaeal MAG encoding CBB capability found in the water’s edge sample (PMV4) pertains to *Ca*. Thermoplasmatota’s class EX4484-6 that includes MAGs retrieved from marine hydrothermal vent sediments (BioProject PRJNA362212). Thermoplasmata members were also identified in the snotties (thick snot-like biofilm) in the Frasassi caves and in the gyspum moonmilk of Feti da Cave, both in Italy [51, 67, 68]. The presence of RubisCO (cbbL) and sulfhydrogenase (hydBG) subunits in the genome may point toward an autotrophic organism that couples sulfur (S⁰, S₂) reduction to hydrogen oxidation. Among the bacteria encoding RubisCO, a MAG affiliated to the order *Dongiales* from the upper gallery PMV8 stands out. GTDB’s *Dongiales* order comprises the members of the formerly known family *Rhospirillaceae*. The RubisCO enzyme presence and the lack of genes for the photosynthetic reaction center (*psuLM*) are intriguing for *Rhospirillaceae*-like bacteria. *Rhospirillaceae* are known as photoautotrophic, photoheterotrophic, and chemoheterotrophic bacteria [69], but not as chemoa utotrophs. Since the sulfite dehydrogenase *(soeA)* subunit was also annotated, the *Dongiales*-affiliated MAG may be a chemolithoautotrophic bacterium that fix CO₂ and uses sulfur compounds as electron sources. Another interesting phylum encoding autotrophic features was *Ca*. KSBI phylum, which currently consists of a single class termed UBA2214. The two *Ca*. KSBI-related MAGs recovered in this study encode oxic- (CBB) and anoxic (WL) CO₂ fixation potential. Both MAGs also seem to carry nitrate
reduction by DNRA and denitrification, which can serve as a nitrogen retainer (DNRA) and a nitrogen remover (denitrification) in the environment.

N$_2$ and CO$_2$ fixation prediction obtained by MAGs functional analysis was mostly reinforced by metagenomic read mapping on the marker genes (Additional file 5: Figs. S2, S3). This reinforcement could also be considered a validation of the obtained MAGs-based metabolic prediction even if a low binning efficiency (percentages of reads mapped to MAGs) was the case for some samples.

The metabolic interactions were investigated to extend our understanding of the metabolic potential in sediment-associated microbial communities. Microbial communities in the lower, wet and upper dry galleries were analyzed using MAG-based metabolic models (metaGEM). The community metabolic modeling approach using metaGEM reconstruction and in silico simulation is only recently applied in different fields [70–74]. The community MRO and MIP distribution patterns support the expectation of lower nutrient availability in the dry gallery vs. the wet one. In scant nutrient environments, the microbes compete over the available nutrients (high MRO), and its members might need to have complementary biosynthetic capabilities to decrease their dependency on the scarce external resources (high MIP). In caves, it is known that selfish competition for resources can be replaced by cooperative and mutualistic associations, such as the ones seen in biofilms [75], maintaining bacterial communities with diverse metabolic pathways, interdependent and cooperative [76].

On the other hand, the MRO/MIP distribution pattern supports the supposition of higher nutrient availability in the areas where invertebrates were present. Those communities (PMV1, PMV2, PMV3, PMV4) had lower MRO, and MIP than the communities where no invertebrates were identified (PMV6, PMV7, PMV8). The simulated cross-feeding interactions highlighted the key donor MAGs for each condition as *Methylomirabilales* and *Methylocella* methanotrophs and *Thermoplasmatota* autotrophic archaean for the lower, wet gallery; and the autotrophic *Dongiales* and a *Physicphaerales*-related MAG for the dry gallery. Little could be deduced for the *Physicphaerales*-affiliated donor MAG. None of the marker genes for sulfur, nitrogen, methane metabolism, or CO$_2$ fixation were assembled or annotated. This is not surprising since the phylum *Planctomycetes* has the highest values (35–65%) of protein sequences with unknown functions among bacterial phyla [77].

Moreover, *Physicphaerales* MAG is the second of its genus (SLJ01). The first was assembled from the surface sediments of a hypersaline soda lake in Siberia (GCA_007135295). As an observation, MAGs belonging to *Ca. Patescibacteria* could not be modeled or were on the receivers’ side of cross-feeding interactions. This is typical for *Ca. Patescibacteria* members with a reduced genomes size (usually < 1.5 Mb) that lack essential biosynthetic capacities have metabolic dependence and may have a parasitic or symbiotic lifestyle [78–80].

In the absence of light, the chemolithoautotrophic ecosystems are fueled by the oxidation of reduced compounds such as H$_2$S (HS$^-$), CH$_4$, NH$_3$ (NH$_4^+$), Fe$^{2+}$ and H$^+$. The metabolic modeling community simulations pointed to distinct metabolic dependencies of simple compounds in lower and upper galleries. We postulate that the compound accessibility influences the established microbial dependencies in the environment, as H$_2$S, NO$_3^-$ (a result of ammonia oxidation), and CH$_4$O (a result of methanotrophy) are more available in the lower gallery than in the upper one. Hence the organism’s dependencies on those compounds (i.e., a likelihood of species A growth depending on metabolite X from species B) are established in the upper gallery, where those compounds are lacking in the environment. Similarly, in the case of O$_2$, the dependencies appear in the lower gallery where O$_2$ concentration is reduced. Ferrous iron (Fe$^{2+}$) dependencies are characteristics of both conditions, probably because under oxidizing conditions, iron is found mainly in Fe(III) (oxyhydr) oxide minerals (i.e. goethite).

**Conclusions**

The present work addressed the diversity, biogeochemical potential and ecological interaction of sediment-associated microbiome located near and distant from the sulfidic hydrothermal waters feeding the chemolithoautotrophic-based Movile Cave. Metagenomic-based approaches have indicated that the diversity of the microbiomes detected in Movile Cave sediments spans a wide taxonomic range and is likely to have a high degree of novelty. This study pinpoints chemolithoautotrophy as an essential metabolic asset in an organic carbon-poor Movile Cave environment that is not confined to the high-redox potential hydrothermal water and nearby sediments but to as far as the most distant locations in the dry gallery. This assumption is supported by the recovery of autotrophic MAGs encoding CO$_2$ fixation ability via at least three different pathways (CBB, rTCA, WL). Sulfur oxidation was predicted for microorganisms detected nearby the sulfidic water, whereas ammonia-oxidation might be active in cave sediments in contrast with apparently absent nitrification.

Additionally, methanotrophy has been inferred across all sampled sediments. Therefore, it seems to play a key role in the primary production along the entire Movile Cave, not only in the water proximity. Despite simulation simplifications, our modeling approach postulates
that nutrient scarcity is the driving force of competition-cooperation patterns across Movile Cave. The metabolic annotation and simulations point towards the autotrophic and methanotrophic MAGs as key donors in the sediments. Cross-feeding interactions can reveal the limiting compounds in the environment and the notable differences between the lower and the upper galleries.

Our findings point to the potential ecological roles and interactions of the sediment-associated microbiome and add to the previous microbiological investigations focused on the sulfidic waters in Movile Cave, thus comprehensively expanding our understanding of the peculiar chemoaototrophically-based subterranean ecosystems. Nevertheless, prospective direct metabolic quantitative assessments adjoined by multi-omics and isolation and cultivating efforts are needed to further unveil the full microbiological picture of this intriguing cave ecosystem.

Supplementary Information

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