

1 **Assessment of the Potential Role of *Streptomyces* in Cave Moonmilk**

2 **Formation**

3 Marta Maciejewska¹, Delphine Adam¹, Aymeric Naômé¹, Loïc Martinet¹, Elodie Tenconi¹,
4 Magdalena Całusińska², Philippe Delfosse², Marc Hanikenne^{3,4}, Denis Baurain^{4,5}, Philippe
5 Compère⁶, Monique Carnol⁷, Hazel Barton⁸, and Sébastien Rigali^{1*}

6
7 ¹InBioS - Centre for Protein Engineering, Institut de Chimie B6a, University of Liège, B-4000,
8 Liège, Belgium

9 ²Environmental Research and Innovation Department, Luxembourg Institute of Science and
10 Technology, Rue du Brill 41, Belvaux, L-4422, Luxembourg

11 ³InBioS - Functional Genomics and Plant Molecular Imaging, University of Liège, B-4000 Liège,
12 Belgium

13 ⁴PhytoSYSTEMS, University of Liège, B-4000 Liège, Belgium

14 ⁵InBioS – Eukaryotic Phylogenomics, University of Liège, B-4000, Liège, Belgium

15 ⁶Department of Biology, Ecology and Evolution & Centre of Aid for Research and Education in
16 Microscopy (CAREm-ULg), Institute of Chemistry B6a University of Liège, B-4000, Liège,
17 Belgium

18 ⁷InBioS - Plant and Microbial Ecology, Botany B22, University of Liège, B-4000, Liège, Belgium

19 ⁸Department of Biology, University of Akron, Akron, Ohio, United States of America

20 *Corresponding author. E-mail: srigali@ulg.ac.be; Tel: +32 4 366 98 30; Fax: +32 4 366 33 64

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23 **Abstract**

24 Moonmilk is a karstic speleothem mainly composed of fine calcium carbonate crystals (CaCO_3)
25 with different textures ranging from pasty to hard, in which the contribution of biotic rock-building
26 processes is presumed to involve indigenous microorganisms. The real bacterial input in the genesis
27 of moonmilk is difficult to assess leading to controversial hypotheses explaining the origins and
28 the mechanisms (biotic versus abiotic) involved. In this work we undertook a comprehensive
29 approach in order to assess the potential role of filamentous bacteria, particularly a collection of
30 moonmilk-originating *Streptomyces*, in the genesis of this speleothem. Scanning electron
31 microscopy (SEM) confirmed that indigenous filamentous bacteria could indeed participate in
32 moonmilk development by serving as nucleation sites for CaCO_3 deposition. The metabolic
33 activities involved in CaCO_3 transformation were furthermore assessed *in vitro* among the
34 collection of moonmilk *Streptomyces*, which revealed that peptides/amino acids ammonification,
35 and to a lesser extent ureolysis, could be privileged metabolic pathways participating in carbonate
36 precipitation by increasing the pH of the bacterial environment. Additionally, *in silico* search for
37 the genes involved in biomineralization processes including ureolysis, dissimilatory nitrate
38 reduction to ammonia, active calcium ion transport, and reversible hydration of CO_2 allowed to
39 identify genetic predispositions for carbonate precipitation in *Streptomyces*. Finally, their
40 biomineralization abilities were confirmed by environmental SEM, which allowed to visualize the
41 formation of abundant mineral deposits under laboratory conditions. Overall, our study provides
42 novel evidences that filamentous Actinobacteria could be key protagonists in the genesis of
43 moonmilk through a wide spectrum of biomineralization processes.

44

45 **Introduction**

46 The hypogean environment, although highly deprived of nutrients, sustains a diverse
47 microbial life. This subterranean microbiome plays an important ecological role in caves, with
48 secondary effects on mineralogy, including host rock dissolution or mineral precipitation, leading
49 to the formation of various secondary mineral deposits termed speleothems (Barton and Northup
50 2007; Jones 2010; Cuezva et al. 2012). A biogenic origin has been hypothesized for a number of
51 speleothems, including coralloids (Banks et al. 2010), pool fingers (Melim et al. 2001),
52 ferromanganese deposits (Northup et al. 2003; Spilde et al. 2005), helictites (Tisato et al. 2015),
53 and moonmilk (Cañaveras et al. 2006). Unlike typical mineral deposits, moonmilk is present as a
54 soft and pasty precipitate on cave surfaces and within pools (Richter et al. 2008; Cacchio et al.
55 2014). The origin of moonmilk has been controversial for many years due to the complex
56 mineralogy, the atypical crystalline morphology, and also the size of its crystals (Verrecchia and
57 Verrecchia 1994; Cañaveras et al. 1999; Cañaveras et al. 2006; Bindschedler et al. 2010;
58 Bindschedler et al. 2014). Notably, moonmilk deposits are characterized by several crystal habits
59 including nano-fibers, and micro-meter sized needle-fiber crystals in a form of monocrystalline
60 rods and polycrystalline chains (Cañaveras et al. 1999; Cañaveras et al. 2006; Bindschedler et al.
61 2010; Bindschedler et al. 2014). While initially postulated as a speleothem of abiotic origin
62 (Harmon et al. 1983; Borsato et al. 2000), recent studies attributed the genesis of moonmilk to
63 indigenous microbial population (Cañaveras et al. 2006; Cailleau et al. 2009; Baskar et al. 2011;
64 Braissant et al. 2012).

65 Microbial carbonate precipitation (MCP) is a broad spectrum phenomenon either mediated
66 by autotrophic pathways, such as photosynthesis and methanogenesis that lead to depletion of local

67 CO₂, or heterotrophic pathways that alter local conditions to promote CaCO₃ precipitation
68 (Castanier et al. 2000; Banks et al. 2010). Caves are devoid of sunlight, ruling out photosynthesis,
69 while methanogenesis has been documented rarely in these systems. Heterotrophic processes may
70 therefore play an important role (Banks et al. 2010). Active calcite precipitation by heterotrophs in
71 calcium-rich environments has been hypothesized to be the consequence of a detoxification
72 process, wherein the acidification of the local environment induced by passive influx of Ca requires
73 growing cells that would actively export the excess of this metal to maintain cellular calcium
74 homeostasis (Banks et al. 2010). Such metal detoxification strategies have also been linked to the
75 formation of the unusual speleothems known as helictites (Tisato et al. 2015). Heterotrophic growth
76 can also increase the environmental pH, which can in turn increase the saturation index of CaCO₃
77 and drive precipitation. Calcite precipitation through nitrogen metabolism is thought to operate by
78 different metabolic pathways, including ureolysis, ammonification through amino acid and peptide
79 catabolism, and dissimilatory nitrate reduction to ammonia (DNRA), all of which increase the local
80 pH (Fig. 1) (Castanier et al. 2000).

81 Moonmilk was reported to host wide spectrum of microbiota, including Archaea, Bacteria,
82 and Fungi (Rooney et al. 2010; Portillo and Gonzalez 2011; Engel et al. 2013; Reitschuler et al.
83 2014; Reitschuler et al. 2015; Axenov-Gibanov et al. 2016; Maciejewska et al. 2016; Reitschuler
84 et al. 2016). Among this microbiome, Fungi and filamentous microorganisms, particularly
85 members of Actinobacteria phylum were reported to be possibly involved in the moonmilk genesis
86 (Cañaveras et al. 2006; Bindschedler et al. 2010; Bindschedler et al. 2014). Bindschedler et al.
87 (2010, 2014) suggested that the presence of nano-fibers within the crystalline structure of
88 moonmilk was associated with biomineralized fungal hyphae. The authors suggest that organized
89 networks of nano-fibers, often observed in moonmilk, could represent fibrous fungal cell wall
90 polymers, such as chitin and β -(1→3)glucans (Bindschedler et al. 2010). On the other hand, the

91 observation of unstructured aggregates of unconsolidated microcrystalline fibers with calcified
92 Actinobacteria-like filaments led Cañaveras et al. (2006) to propose a model of moonmilk
93 formation wherein Actinobacteria promoted calcium carbonate precipitation by creating locally
94 favorable conditions, with the bacterial cell walls serving as nucleation zones (Cañaveras et al.
95 2006). The presence of metabolically active microorganisms in moonmilk was demonstrated using
96 isothermal microcalorimetry (Braissant et al. 2012), although the progressive accumulation of
97 CaCO₃ (and presumably entombment) ultimately leads to a decrease of the microbial activity
98 (Cañaveras et al. 2006; Sanchez-Moral et al. 2012). As a result, microorganisms would play a
99 significant role in the initiation of moonmilk formation, which ultimately would be overtaken by
100 abiotic processes leading to the growth of the deposit, which can reach up to 1 m in thickness
101 (Sanchez-Moral et al. 2012).

102 In all of these studies, there has been no clear distinction as to whether the increase or
103 decrease in local pH is ultimately leading to the precipitation of moonmilk by the dominant
104 actinobacterial species observed. In this work we use a combination of microscopy, cultivation and
105 genomic approaches to provide an *in vitro* and *in silico* assessment of the actinobacterial metabolic
106 activities that could promote CaCO₃ precipitation. Our data suggest that the *Streptomyces* species
107 would play an important role in nitrogen metabolism, which could locally raise pH and contribute
108 to moonmilk formation.

109

110 **Materials and methods**

111 **Moonmilk sampling and *Streptomyces* strains used in this study**

112 Samples for microscopy and cultivation were taken from moonmilk deposits originating from three
113 sampling points (collection points COL1, COL3, COL4, supplementary Fig. 1 from Maciejewska

114 et al. 2016) in the upper Viséan limestone cave ‘Grotte des Collembolés’ (Springtails’ Cave),
115 Comblain-au-Pont, Belgium (more detailed cave description in supplementary Fig. 1).
116 Moonmilk samples for strains isolation were brought to the laboratory on ice and stored at 4°C
117 prior to lyophilization. Extensive attempts at the cultivation of Actinobacteria led to the isolation
118 of 31 phylogenetically distinct *Streptomyces* strains representing phylogenetically distinct
119 phylotypes (as previously described in Maciejewska et al. 2016 and supplementary Fig. 2).
120 Moonmilk samples for scanning electron microscopy (SEM) were preserved in two separate
121 fixative solutions, 2.5% glutaraldehyde in 0.1 M Na-acetate buffer (pH 7.4), and 100% ethanol,
122 and stored at 4°C until analysis. To exclude the effect of fixatives on the crystalline structure of
123 moonmilk, the lyophilized samples were also observed under the microscope as controls (data not
124 shown).

125
126 **Environmental scanning electron microscopy (ESEM) and elemental X-ray energy dispersive**
127 **microanalysis (EDS)**

128 Glutaraldehyde-fixed moonmilk samples were post-fixed in 1% osmium tetroxide (OsO₄) in
129 distilled water, rinsed and dehydrated through a graded ethanol series (30-100%). Glutaraldehyde-
130 fixed samples and ethanol-preserved samples were then processed by critical point drying, prior to
131 mounting on the glass slides covered by double-side carbon tape together with lyophilized samples.
132 Parts of each sample were mounted to expose the outer surface, a vertical section or fracture made
133 with a scalpel blade. Dry samples were subsequently sputter coated with platinum on Balzers
134 sputtering Unit SCD 030 (Balzers, Lichtenstein).

135 The production of mineral deposits by isolates MM24 and MM99 following growth in two different
136 culture conditions - calcite precipitation agar (CPA) and modified B-4 medium (more details in
137 CaCO₃ precipitation section) was detected from the living bacterial colonies after being air-dried.

138 Morphological observations were performed by light microscopy (reflected, transmitted and
139 polarized light) using an Olympus Provis AX-70 microscope fitted with a Visicam 5.0 videocamera
140 for image capture. SEM observations were performed in an environmental scanning electron
141 microscope FEI XL30 ESEM-FEG (Eindhoven, The Netherlands). Platinum-coated samples were
142 observed under high vacuum (HV) conditions with the ET-secondary electron (SE) detector at 10
143 mm working distance and 15 kV accelerating voltage. Air-dried cultures, were observed under low
144 vacuum (LV) conditions (0.4 Torr) with the large field gaseous secondary electron (GSE) detector
145 and the backscattered electron (BSE) detector at 10 mm working distance and 10 and 20 kV
146 accelerating voltage, respectively. As a result of applying two types of detection – GSE and BSE,
147 the contrast of the images due to the surface morphology or due to the atomic number of the
148 elements and the density of minerals could be obtained. Elemental X-ray microanalysis and
149 mapping was carried out using a Bruker silicon drift energy dispersive detector (SDD Quantax 129
150 eV, Billerica, MA, USA) at 10-20 kV accelerating voltage with the Esprit 1.9 software. Semi-
151 quantitative analyses of the elemental composition were done using the standard-less ZAF method
152 with automatic background subtraction.

153

154 **Genomic analysis of moonmilk-derived isolates**

155 The genes of interest (see Fig. 1) including those coding for i) the ureolytic system (*ure*), ii) the
156 $\text{Ca}^{2+}/2\text{H}^{+}$ antiporter system (*chaA*), iii) the nitrate/nitrite reductases (*nar/nas/nir*) with the
157 corresponding transporters (*narK*), and iv) the carbonic anhydrase (CA) together with sulfate
158 transporter in cluster with CA (*sulP*) (Felce and Saier 2005), were retrieved from the genomes of
159 moonmilk *Streptomyces* sequenced at the Luxembourg Institute of Science and Technology, as
160 previously described (Maciejewska et al. 2016). These genes were first identified within the

161 chromosome of the model *Streptomyces* species – *Streptomyces coelicolor* (Bentley et al. 2002).
162 The designations of the selected genes are listed in supplementary Table 1. Subsequently, genes
163 sequences encoding the corresponding proteins were identified within the genomes of additional
164 54 reference *Streptomyces* strains (supplementary Table 2) for which completely assembled
165 genomes are available in NCBI FTP server (data retrieved on January 8th 2016).
166 A total of 407,461 protein sequences were organized in clusters of orthologous groups (COGs)
167 using Proteinortho v 5.12 (Lechner et al. 2010) with the PoFF extension to further discriminate
168 similar sequences based on synteny. Created COGs were used as models to screen moonmilk
169 *Streptomyces* genomes. For every *S. coelicolor* gene, the collection of protein sequences in the
170 corresponding COG was used to build a hidden Markov model (HMM) profile (Eddy 1998). As an
171 example, the gamma sub-unit of the urease metallo-protein of *S. coelicolor* (UreA, SCO1236)
172 clusters in a COG with 52 sequences from other *Streptomyces* (supplementary Table 1). This COG
173 is used to construct a HMM profile representing the UreA protein that is used to search a database
174 of translated predicted coding sequences of the moonmilk *Streptomyces*. Partial coding sequences
175 resulting from the fragmented nature of the moonmilk *Streptomyces* genomes were also considered
176 in the screening. The moonmilk *Streptomyces* coding sequences were predicted with Prodigal
177 v2.6.2 (Hyatt et al. 2010). HMM profile building and HMM search were carried out using the
178 HMMER3 software package (v3.1b2, <http://hmmer.org/>). The accession numbers of genes
179 recovered from moonmilk *Streptomyces* are compiled in the supplementary Table 3.

180

181 **Metabolic assays**

182 **Ammonification**

183 The ability of isolates to decompose organic nitrogen into ammonia was tested on nutrient agar
184 containing: peptone, 5 g/l; beef extract, 3 g/l; NaCl, 5 g/l; phenol red, 0.012 g/l; agar, 15 g/l; pH

185 7.0 (Food and Agriculture Organization of the United Nations 1983). Each representative
186 moonmilk *Streptomyces* isolate was spot-inoculated on an individual Petri dish and incubated for
187 7 days at 28°C. *Citrobacter freundii* ATCC 43864 was used as a positive control strain, while
188 uninoculated media was used as a negative control. The development of a pink color, indicating a
189 pH increase due to the formation of ammonia following peptides/amino acids degradation was
190 monitored every day during the incubation.

191

192 **Ureolysis**

193 Rapid screening of urease activity was performed on Christensen's Urea Agar Base (UAB) solid
194 media as described previously (Hammad et al. 2013). The UAB medium was prepared as follows:
195 urea, 20.0 g/l; NaCl, 5.0 g/l; peptone, 1.0 g/l; glucose, 1.0 g/l; KH₂PO₄, 2.0 g/l; phenol red, 0.012
196 g/l and agar, 15.0 g/l; pH 6.5. All components of the media were autoclaved except urea which was
197 filter-sterilized and added after autoclaving. The UAB medium without urea was used as a negative
198 control. Both types of media were inoculated with representative of each phylotype together with
199 urease negative control strain (*Escherichia coli* ATCC 25922) and urease positive control strain
200 (*Klebsiella pneumoniae* ATCC 13883) and incubated at 28°C. Plates were examined continually
201 to record development of the pink color indicating a pH increase as a result of urease enzyme
202 activity, leading to generation of ammonia through urea degradation, according to the following
203 reaction: $(\text{NH}_2)_2\text{CO} + \text{H}_2\text{O} \rightarrow 2\text{NH}_3 + \text{CO}_2$.

204

205 **Nitrate and nitrite reduction**

206 The assessment of nitrate and nitrite reduction was performed as described by Li et al. (2016), with
207 small modifications. Briefly, the phylotypes were inoculated in nitrate or nitrite agar slants

208 (potassium nitrate / sodium nitrite, 1g/l; peptone, 5 g/l; beef extract, 3 g/l; agar, 12 g/l; pH 7.0) and
209 nitrate / nitrite broth tubes (potassium nitrate / sodium nitrite, 1g/l; peptone, 5 g/l; beef extract, 3
210 g/l; pH 7.0) equipped with the Durham tubes. *Escherichia coli* ATCC 25922 was used as a control
211 strain for exclusive reduction of nitrate to nitrite, while *Pseudomonas aeruginosa* ATCC 27853 as
212 a complete reducer of nitrate into the nitrogen gas, collected in the Durham tube. Uninoculated
213 media were used as an additional control. Inoculated test tubes were incubated at 28°C for 9 days
214 in static conditions, to reduce amount of dissolved oxygen. After incubation time few drops of
215 sulfanilic acid and alpha-naphthylamine were added to each test tube, which together react with
216 nitrite generating red/pink color. Reduction of nitrate (NO_3^-) is indicated by appearance of red color
217 in nitrate broth, while red color disappearance in nitrite broth indicates nitrite (NO_2^-) reduction.

218

219 **Oxidative glucose breakdown**

220 The glucose oxidative test was carried out according to Hugh and Leifson (1953). Briefly, each
221 representative of the phylotypes was spot-inoculated on Hugh and Leifson's OF basal medium,
222 prepared as follows: peptone, 2.0 g/l; NaCl, 5.0 g/l; bromothymol blue, 0.03 g/l; K_2HPO_4 , 0.3 g/l;
223 agar, 3.0 g/l; pH 7.1. Filter-sterilized glucose was added after autoclaving to a final concentration
224 of 1%. The OF medium not supplemented with glucose was used as a negative control, and
225 oxidative *Pseudomonas aeruginosa* ATCC 27853 strain as a positive control. The inoculated plates
226 were incubated at 28°C during 7 days and monitored continually to observe development of yellow
227 color indicating on the acid production due to glucose metabolism.

228

229 **CaCO₃ precipitation**

230 The screening for isolates able to precipitate calcium carbonate through ureolysis was performed
231 using calcite precipitation agar (CPA) as previously described (Stocks-Fischer et al. 1999). The

232 CPA medium was prepared as follows: (g/l); nutrient broth, 3.0 g/l; urea, 20.0 g/l; $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$,
233 28.5 g/l; NaHCO_3 , 2.12 g/l; NH_4Cl , 10.0 g/l; Agar, 15.0 g/l. All components were autoclaved apart
234 from urea, which was added filter-sterilized. The same medium, but without urea, was used as an
235 additional control. Alternatively, precipitation of CaCO_3 was tested on modified B-4 medium (pH
236 7.0) composed of: yeast extract, 4 g/l; calcium acetate, 2.5 g/l; agar, 15 g/l. The plates inoculated
237 with MM24 and MM99, following incubation at 28°C, were examined under ESEM after 2 months
238 of incubation for CPA media, and 1 month of incubation for B-4.

239
240 **CaCO_3 solubilization**
241 Isolates were tested for their ability to solubilize calcium carbonate on two different media
242 including i) minimal medium (MM) (Kieser et al. 2000) containing CaCO_3 (2 g/l), supplemented
243 or not with glucose (5 g/l), and ii) 1:100 diluted nutrient agar (Portillo et al. 2009), containing
244 CaCO_3 (2.5 g/l), supplemented or not with glucose (2 g/l). The spot-inoculated plates were
245 incubated for 4 weeks at 28°C and the capability of calcium carbonate solubilization was confirmed
246 by observation of the clear halo around a colony.

247 248 **Results and Discussion**

249 **Microscopic evaluation of indigenous moonmilk filamentous bacteria as nucleation sites for** 250 **carbonate precipitation**

251 Filamentous bacteria, particularly Actinobacteria, have been proposed to participate in the
252 genesis of moonmilk deposits by serving as nucleation sites for carbonate deposition (Cañaveras
253 et al. 2006). Regardless the fixation procedure (glutaraldehyde, ethanol, and freeze-drying),

254 classical SEM observations revealed the same crystal morphologies that have also been described
255 in the literature (data not shown) (Cañaveras et al. 1999; Cañaveras et al. 2006; Bindschedler et al.
256 2010; Bindschedler et al. 2014). The surface of moonmilk samples revealed the presence of dense,
257 unstructured meshes of micrometer-size filaments known as needle-fiber calcite (Fig. 2a), which,
258 based on EDS analysis, were shown to be mainly composed of calcium, carbon and oxygen
259 (supplementary Fig. 3a). The structure of moonmilk deposits was characterized by the presence of
260 abundant, randomly oriented, monocrystalline rods and polycrystalline fibers composed of stacked
261 rhombohedra (Fig. 2a). Those crystals showed variable dimensions, ranging from 0.5 – 1 μm width
262 and 30 - 100 μm length for monocrystals, and 2 - 20 μm width, 10 - 100 μm length for polycrystals,
263 as previously reported (Cañaveras et al. 1999). Interestingly, we observed within the moonmilk
264 microscopic composition, abundant networks of filaments with nano-sized width (50 - 150 nm),
265 which either formed compacted pellets (Fig. 2b) or mats (Fig. 2c). The organized networks of nano-
266 fibers, similar to the one observed in Fig. 2c, were previously reported from moonmilk and
267 associated with fungal wall polymers (Bindschedler et al. 2010; Bindschedler et al. 2014).
268 However, randomly-oriented, compacted pellets of nano-fibers as presented on Fig. 2b, were highly
269 comparable to Actinobacteria, but characterized by a much smaller cell size which could be a result
270 of the oligotrophic nature of the cave environment. It has been demonstrated that the cell size is
271 largely dependent on the nutritional status of the environment, with resource-poor ecosystems
272 stimulating dwarfism (Young 2006; Portillo et al. 2013). In this work, the observed size of the
273 putative bacterial nano-filaments, ranging from 0.05 to 0.15 μm , could also be a consequence of
274 the oligotrophic nature of the moonmilk niche as cell elongation/filamentation has been shown to
275 be the result of nutritional stress in some bacteria (Steinberger et al. 2002), including Actinobacteria
276 (Pine and Boone 1967; Wills and Chan 1978; Deutch and Perera 1992). However, even in nutrient-
277 rich soils the majority of bacteria can display a diameter less than 0.2 μm (Hahn 2004). In addition,

278 the imprints of nano-sized microorganisms were already reported from other geological formations,
279 such as sedimentary rocks (Folk and Chafetz 2000; Folk 1993). Finally, recent findings of ultra-
280 small marine Actinobacteria with an average diameter of about 0.3 μm , provides an additional
281 evidence for the existence of nano-bacteria in oligotrophic ecosystems (Ghai et al. 2013). Unlike
282 crystal fibers, the tiny filaments observed in glutaraldehyde- and ethanol-fixed samples, were not
283 completely straight and regular in their shape but rather displayed plasticity and were often curved,
284 either without preferential orientation (Fig. 2b) or in the same direction (Fig. 2d/e). The tiny, curved
285 filaments were not observed - probably not preserved - in freeze-dried samples that suffered of ice
286 crystal growth (data not shown). One-directional growth is not a typical behavior of growing
287 actinobacterial filaments that are commonly branching in diverse directions in order to form a
288 complex mycelial network. This rigid and unidirectional growth might suggest that they represent
289 calcified filaments potentially still actively growing at their tip, which remains curved (Fig. 2d).
290 Elemental analysis performed with EDS revealed that the observed nano-size filaments contained
291 higher content of carbon and oxygen in comparison to the surrounding crystals, suggesting a
292 possible biological origin (supplementary Fig. 3b). However, these EDS analyses should be viewed
293 with great prudence as the difference in the elemental compositions between filaments and crystals
294 could simply be a consequence of the structure and not the nature (organic vs mineral) of the
295 analyzed areas. Additionally, along (Fig. 2f) or on the tip (Fig. 2g) of some filaments, a possible
296 initiation of calcium carbonate deposition was observed. Besides nano-sized filaments, reticulated
297 filaments were sporadically observed within moonmilk crystals (Fig. 2h). Those particular
298 filamentous forms, with the size of about 0.5 μm width and up to 75 μm length, are often found in
299 subsurface environment, including limestone or lava caves, and possess higher carbon content than
300 the one typically observed for calcite minerals, suggesting their biogenic origin. However, the
301 associated microorganisms are not yet identified (Melim et al. 2008; Northup et al. 2011; Miller et

302 al. 2012; Melim et al. 2015). Overall, these observations tend to confirm the hypothesis of
303 filamentous microorganisms (bacteria and fungi) serving as a nucleation sites for moonmilk
304 mineral deposition (Cañaveras et al. 2006; Bindschedler et al. 2010; Bindschedler et al. 2014).

305

306 **Potential role of cultivable moonmilk-derived *Streptomyces* in carbonate precipitation**

307 A nucleation site itself is not sufficient to promote CaCO₃ precipitation, as dead bacterial
308 cells lose the ability to precipitate minerals (Banks et al. 2010). The dominant role of bacteria in
309 calcification is attributed to metabolic activities which increase the pH of the environment (above
310 pH 8) and therefore favor a shift of the CO₂ – HCO₃⁻ – CO₃²⁻ equilibrium towards carbonate ions
311 which precipitate with Ca²⁺ ions. We screened 31 representative *Streptomyces* strains isolated from
312 moonmilk (see supplementary Fig. 2 retrieved from Maciejewska et al. 2016) for their metabolic
313 activities that could lead to a raise in pH, including ureolysis, peptides/amino acids ammonification,
314 and dissimilatory nitrate/nitrite reduction to ammonia (Fig. 1). Although these assays were
315 performed under laboratory conditions, a qualitative assessment of these processes allowed ranking
316 the tested phylotype representatives according to their metabolic performance, and therefore their
317 potential to drive biomineralization through an increase in the extracellular pH. The results are
318 shown in Fig. 3, along with a compilation of activities and phylogenetic relationships (Fig. 4). The
319 results of each metabolic activity assay for all the tested strains are presented in supplementary Fig.
320 4.

321

322 **Ureolysis**

323 Among the 31 isolates tested, 15 showed an ability to increase the pH by hydrolysis of urea
324 (Fig. 4). MM99 and MM122 were the strongest ureolytic strains, with comparable metabolic
325 performance to the positive control strain - *Klebsiella pneumoniae* ATCC 13883 (Fig. 3a and
326 supplementary Fig. 4a). The majority of urease-positive moonmilk isolates displayed weak and
327 moderate activities, which were observed either within 3 days of incubation (5 strains) or after
328 extended time (more than 1 week) (6 strains) (Fig. 3a and supplementary Fig. 4a).

329 In order to know if a relation could be established between the assessed *in vitro* activity and
330 the genetic predispositions for ureolysis, we examined the genomes of the phylotype
331 representatives for the presence of urease genes. We used HMM profiles constructed from Clusters
332 of Orthologous Groups (COGs) of proteins of the urease structural subunits
333 (UreA/UreB/Ure(AB)/UreC), as well as the accessory proteins (UreF/UreG/UreD). The
334 corresponding genes originate from functional clusters of three types *i.e.*, *ureABCFGD*, *ure(AB)C*,
335 and *ure(AB)CFGD*, which are all present in the urease-positive species. The large majority of
336 moonmilk strains (90%) was found to encode all the urease genes, in some cases present in several
337 copies (Table 1), suggesting that even the strains displaying urease-negative phenotypes are
338 capable of urease activity. This suggests that in urease-negative strains urease activity is not
339 expressed under the conditions tested, or that they harbor mutations that prevent expression or
340 activity. Nonetheless, urea transport appears to be functional in all urease-negative isolates as urea
341 exerted a toxic effect in the growth media of these strains (an effect that could be reversed by
342 growth in the same medium lacking urea; data not shown).

343 Urease activity has been recently linked to an activity of the zinc-containing enzyme –
344 carbonic anhydrase (CA) (Achal and Pan 2011). While urease maintains an alkaline environment
345 by generating ammonia, carbonic anhydrase would provide carbon dioxide for biomineralization

346 through dehydration of carbonic acid (H_2CO_3) also produced during ureolysis (Fig. 1). It was
347 recently demonstrated that the activities of CA and urease were correlated along the bacterial
348 growth and corresponded to maximum calcite production (Banks et al. 2010; Achal and Pan 2011),
349 while inhibition of carbonic anhydrase activity decreased the rate of calcification, with calcite
350 precipitation occurring more efficiently with the synergistic action of both enzymes – CA and
351 urease (Dhami et al. 2014).

352 The presence of this highly efficient enzyme in cave settings was previously confirmed
353 through metagenomic study of a speleothem in Tjuv-Ante's Cave (Sweden) (Mendoza et al. 2016),
354 and highly acidic cave biofilms, known as 'snottites' (Jones et al. 2011). However, it has never
355 been directly associated to a specific taxonomic group through genome-based approach. The only
356 link was suggested by Cuezva et al. (2012), who proposed CA to be responsible for CO_2
357 sequestration by grey spot colonization found on the walls of Altamira cave, which were dominated
358 by Actinobacteria.

359 Evaluation of the genomes of moonmilk phylotypes for the presence of β -CA (Smith and
360 Ferry 2000), together with the sulfate transporter family protein in cluster with CA (SulP-type
361 permease) revealed that all the investigated strains encode at least one copy of carbonic anhydrase
362 (100% strains encoded β -CA (1) and 87% β -CA (2)) and 90% of them possessing sulfate
363 transporter (Table 1). High copy number of this intracellular zinc metalloenzyme, reaching up to 7
364 copies in MM17, revealed their ubiquitous distribution among karstic bacteria, and suggests their
365 applications in multiple and essential cellular processes beyond their presumed role in carbonate
366 precipitation. Interestingly, a high representation of sulfate permeases of SulP family was also
367 characteristic for the studied population. These broad specificity inorganic anion transporters were
368 suggested to assist bicarbonate (HCO_3^-) transport (Felce and Saier 2005), which was

369 experimentally confirmed in marine cyanobacteria (Price et al. 2004). While in cyanobacteria SulP
370 transporter mediates $\text{HCO}_3^-/\text{Na}^{2+}$ symport, the substrate specificity in the case of *Streptomyces* is
371 highly speculative. Nevertheless, fusion of this protein with carbonic anhydrases indeed strongly
372 suggests its participation in HCO_3^- transport. However, whether it is an importer or exporter
373 remains an open question. It could be possible that HCO_3^- uptake through SulP increases the
374 intracellular pool of this inorganic carbon species, which potentially might be efficiently
375 transformed into carbon dioxide by carbonic anhydrases, and be exported outside the cell, unless
376 required for cellular metabolism. Alternatively, SulP-dependent export of intracellularly formed
377 HCO_3^- through CA-mediated hydration of carbon dioxide, would be assisted with import of other
378 ions (Fig. 1). Altogether, these findings reveal abundant distribution of genes involved in the
379 inorganic ionic transport and metabolism, which might be related to the biomineralization
380 phenomenon.

381

382 **Ammonification**

383 Moonmilk *Streptomyces* were also evaluated for their ability to raise the pH through peptide/amino
384 acid mineralization. 94 % of tested strains efficiently decomposed nitrogenous compounds into
385 ammonia (Fig. 1, Fig. 3b, Fig. 4 and supplementary Fig. 4b). The majority displayed a strong
386 metabolic phenotype (Fig. 5), which is unsurprising given that *Streptomyces* are well known
387 ammonifying bacteria in soils, where they actively participate in the decomposition of organic
388 matter (Prakash et al. 2012). In the isolated cave environment, with limited organic matter input
389 from the surface, the source of such macromolecules is unclear, although peptides and amino acids
390 might be entering the cave through water that has percolated through the soil, making such

391 molecules more readily available than urea (Northup and Lavoie 2001). Amino acid/peptide
392 ammonification was found to be more widespread among the moonmilk isolates than ureolysis,
393 supporting this hypothesis.

394

395 **Dissimilatory nitrate reduction to ammonium**

396 Dissimilatory nitrate reduction to ammonium (DNRA) is another nitrogen cycle-related process
397 considered to be involved in calcification (Castanier et al. 2000) (Fig. 1). This pathway operates in
398 oxygen-limited environments, which could be encountered in the inner layers of the moonmilk
399 deposits. Moreover, moonmilk develops alongside dripping water and its often pasty structure can
400 become fluid, based on its water content, which can drastically reduce oxygen availability.
401 Although *Streptomyces* are obligate aerobes, they are genetically capable of survival under oxygen-
402 limited conditions, encoding genes related to anaerobic respiration, the so-called “anaerobic
403 paradox” (Borodina et al. 2005). Indeed, the model species *Streptomyces coelicolor* was reported
404 to anaerobically respire nitrate (Fischer et al. 2010; Fischer et al. 2014). Though nitrite, the product
405 of this process, was not reduced to ammonia, but detoxified through extrusion via $\text{NO}_3^-/\text{NO}_2^-$
406 antiporter system (Fischer et al. 2010; Fischer et al. 2012). In *S. coelicolor* the NirBD reductase
407 was demonstrated to participate in nitrogen assimilation; however a *nirBD* null-mutant grown in
408 the presence of nitrite and excess ammonium was still able to reduce nitrite suggesting the activity
409 of an alternative and yet unknown enzyme (Fischer et al. 2012). We therefore questioned whether
410 moonmilk isolates would be able to mediate DNRA and reduce nitrate and nitrite under oxygen-
411 limited conditions. For this purpose, we incubated each strain in static (without agitation) liquid
412 culture conditions to limit oxygen availability. Overall, 68% and 77% of strains revealed a capacity

413 to reduce either nitrate (NO_3^-) or nitrite (NO_2^-), respectively, with 52% able to reduce both nitrate
414 and nitrite (Fig. 3c/d, Fig. 4 and Fig. 5). No N_2 gas production was observed, excluding
415 denitrification, which has been only rarely reported for *Streptomyces* (Albrecht et al. 1997; Shoun
416 et al. 1998; Kumon et al. 2002). The lack of N_2 generation would suggest a complete reduction of
417 nitrate/nitrite to ammonia via dissimilatory nitrate reduction. Ammonia produced by this pathway,
418 unless not incorporated by other bacteria or oxidized to other nitrogenous compounds, might
419 alkalize the extracellular environment and thus stimulate CaCO_3 precipitation (Fig. 1). In order
420 to evaluate the presence of a DNRA pathway in moonmilk isolates we screened their genomes for
421 the presence of genes coding for respiratory nitrate reductases (*narGHJI*) and their associated
422 NarK-type nitrate/nitrite transporter - NarK2 (Fig. 1). While 40% of moonmilk strains encoded
423 NarK2 transporter, 30% of them possessed the respiratory nitrate reductases genes (*narGHJI*), with
424 isolates MM7, MM10, MM48, MM106, MM109, MM111, encoding a complete *nar* cluster (Table
425 1). Most of those strains were found to be among the strongest nitrate reducers under oxygen-
426 limited conditions (Fig. 4). The fact that only a minority of the moonmilk *Streptomyces* possessed
427 the genetic material to perform the first step of DNRA, while a majority (68%) was able to reduce
428 nitrate, suggests that another nitrate reduction pathway was operating under the condition tested.
429 This alternative pathway is most likely the NO_3^- and NO_2^- assimilatory process that uses nitrate
430 and nitrite as nutrient sources through assimilatory *nasA* (nitrate reductase) and *nirBD* (nitrite
431 reductase) genes, with the assistance of additional NarK-type NO_3^- transporter (Tiffert et al. 2008;
432 Amin et al. 2012; Fischer et al. 2012). Assimilatory reduction of nitrate and nitrite to ammonium
433 is highly plausible as 93% of moonmilk strains possess *nasA*, *nirBD*, and *narK* NO_3^- importer genes
434 (Table 1). When monitored on solid medium and thus without oxygen limitation, 68% and 77% of
435 the tested strains were able to reduce nitrate and nitrite, respectively (supplementary Fig. 4c/d),
436 which confirmed the high potential of moonmilk *Streptomyces* to use nitrate and nitrite as a

437 nitrogen source, as previously reported for terrestrial *Streptomyces* (Pullan et al. 2011; Fischer et
438 al. 2012). Altogether, although moonmilk *Streptomyces* possess metabolic ability to reduce nitrate
439 and nitrite, without production of gas, pointing on ammonia as a final product, we cannot at this
440 point conclude whether this process represents assimilatory or dissimilatory pathway and whether
441 DNRA is fully functional.

442

443 **Active calcium transport**

444 In addition to processes passively influencing carbonate precipitation, bacteria can also
445 actively impact this phenomenon, through an active transport of calcium ions. Banks et al. (2010)
446 suggested that the calcium-toxicity driven removal of this ion outside the bacterial cell is a factor
447 driving calcification phenotype. Therefore, we have also retrieved through an *in silico* search
448 ChaA, the $\text{Ca}^{2+}/2\text{H}^{+}$ antiporter system suggested to be involved in CaCO_3 deposition (Hammes and
449 Verstraete 2002; Banks et al. 2010) (Fig. 1). The presence of the *chaA* gene was confirmed for 50%
450 of moonmilk cultivable phylotypes (Table 1), extending in those strains the calcium-detoxification
451 system to their spectrum of biomineralization-related processes.

452

453 **Production of CaCO_3 deposits by moonmilk *Streptomyces***

454 In order to confirm whether the moonmilk cultivable *Streptomyces* could indeed produce
455 mineral deposits, we selected two phylotype representatives to be first investigated by polarized
456 light microscopy then by ESEM in low vacuum mode for the presence of calcium carbonate
457 precipitates. The selection of strains was based on their predispositions for CaCO_3 precipitation as
458 judged by the sum of metabolic performance observed for ureolysis and peptide/amino acid

459 ammonification – the two most significant activities observed for moonmilk *Streptomyces* (Fig. 4).
460 Strains MM24 and MM99, amongst one of the best isolates based on the metabolic ranking (Fig.
461 4), were simultaneously cultivated on urea-containing CPA medium for two months, as well as for
462 one month on the modified B-4 medium commonly used for CaCO₃ precipitation assays. Combined
463 microscopic observations of bacterial colonies surfaces with BSE and GSE detectors revealed
464 highly abundant calcite deposits produced by both strains in both media tested (Fig. 6 and Fig. 7).
465 Ureolysis-mediated mineral precipitation was confirmed by the lack of any calcite in urea-deficient
466 CPA medium for both isolates (data not shown). All the produced mineral deposits appeared bright
467 under polarized light (data not shown). The morphology of the calcite polymorphs was comparable
468 between the isolates, however differed between the two culture conditions. On BSE-images,
469 bacterial colonies grown in CPA medium showed a rocky surface with discoidal- or oval-shaped
470 structures of variable diameter that were almost completely encrusting microbial colonies (Fig.
471 6a/c). The mineral nature of the deposits was confirmed through their high (white) contrast on
472 BSE-images compared to the surrounding dark organic matter of the colonies (Fig. 6a/c). In
473 addition, their CaCO₃ mineral composition was confirmed by the elemental X-ray analyses
474 (supplementary Fig. 5) and elemental mapping (Fig. 6b/d). Calcium, carbon and oxygen were
475 present roughly in stoichiometric proportion of CaCO₃ in the spectra (supplementary Fig. 5), and
476 the distribution of those elements was clearly visualized on the mapping (Fig. 6b/d). The presence
477 of calcium was associated with CaCO₃ minerals, while higher proportion of carbon was associated
478 with organic colony biomass (Fig. 6b/d). Interestingly, just on the mineral surface, dense webs of
479 nano-sized filaments were observed (Fig. 7a-e). On high resolution BSE-images, they appeared
480 either as dark curved filaments at the mineral surface or in the middle of mineralized wrinkles
481 suggesting that bacteria produced minerals in which they got progressively entombed (Fig. 7a-d).
482 The filaments free of mineral were also clearly seen interconnecting together and connecting

483 adjacent mineral deposits (Fig. 7e). While on the CPA medium both strains prolifically produced
484 relatively small-sized calcite polymorphs (up to 100 μm) (Fig. 6a/c), on the B-4 medium the
485 observed precipitates although being more scarce, were much larger (up to 400 μm) (Fig. 6e/g).
486 The inorganic nature of the larger CaCO_3 deposits (Fig. 6e/g) were confirmed by X-ray elemental
487 spectra (supplementary Fig. 5) and elemental mapping (Fig. 6f/h), which clearly distinguished
488 CaCO_3 minerals from the surrounding bacterial biomass rich in carbon and oxygen. On BSE-image
489 (Fig. 7f) and under polarized light (data not shown), tiny CaCO_3 deposits were also detected along
490 randomly distributed bacterial filaments. Additionally, unlike in CPA medium where the mineral
491 surface was rather irregular and unstructured, mineral produced by both strains in B-4 showed
492 morphologically distinct areas, either with a smooth, radiating texture (Fig. 7h), with visible
493 filamentous imprints (Fig. 7j) or wrinkles (Fig. 7g), that presumably corresponded to bacterial
494 nano-sized filaments.

495 **Potential role of cultivable moonmilk-derived *Streptomyces* in carbonate dissolution**

496 In addition to constructive processes, bacteria are also believed to induce cave bedrock
497 dissolution. As oppose to precipitation, a dissolution phenomenon is related to the acidification of
498 the bacterial microenvironment, most likely as a result of organic acid production, which are the
499 by-products of microbial carbon metabolism. The presence of detectable levels of organic acids in
500 cave environment was previously demonstrated by *in situ* analysis via ATR-FTIR spectroscopy
501 (Bullen et al. 2008). Released organic acids are able to bind cations such as Ca^{2+} and liberate
502 carbonates, which can be subsequently re-precipitated to form cave secondary deposits or be used
503 by bacteria. Therefore, we have tested the 31 phylotypes for their ability to decrease the pH of the
504 medium through oxidative degradation of glucose based on the standardized
505 oxidative/fermentative test (Hugh and Leifson 1953). Over 68% of isolates were found to induce

506 media acidification by this pathway, which was observed as yellow color to transparent halo
507 development around the inoculum (Fig. 8a and Fig. 9). Among them, 52% of the *Streptomyces*
508 strains exhibited either good or strong oxidative glucose respiration abilities, strongly reducing the
509 extracellular pH (Fig. 5, Fig. 9 and supplementary Fig. 6).

510 We have further tested solubilization abilities related to carbon metabolism by cultivating
511 the phlotypes in calcium carbonate containing media – either in minimal medium or in diluted
512 nutrient agar - supplemented or not with glucose. The clear effect of glucose breakdown was
513 observed in diluted nutrient agar in which the supplementation with the carbohydrate induced
514 CaCO₃ dissolution in 26% of the isolates, while none of the phlotypes promoted dissolution in
515 the non-supplemented medium (Fig. 8b and Fig. 9). In the non-supplemented nutrient agar, rich in
516 organic nitrogen source, the cellular energy comes from amino acid utilization, releasing ammonia
517 as the by-product (Fig. 1), which increases the pH of the medium and thus promotes precipitation
518 rather than dissolution. The addition of glucose clearly induces the opposite effect but only in a
519 minority of the isolates which suggests the preference towards amino acids as carbon source over
520 glucose in the large majority of the studied strains (Fig. 8b and Fig. 9). On the contrary, when
521 assays were performed in the minimal medium, CaCO₃ dissolution was instead rather inhibited by
522 the exogenous supply of glucose, as only 29% of isolates showed ability to solubilize CaCO₃ under
523 this condition, while in minimal media without glucose supply the dissolution phenotype was
524 characteristic for 81% of isolates (Fig. 8c and Fig. 9). This might be probably related to the fact
525 that in minimal medium not supplemented with glucose the only carbon source constitutes the
526 carbonate/bicarbonate from CaCO₃, which is probably efficiently scavenged by cave-dwelling
527 bacteria for autotrophic growth resulting in the high dissolution rate observed under this condition.
528 Although *Streptomyces* are mainly heterotrophic microorganisms, autotrophic growth using CO or

529 CO₂ as a sole carbon source within members of this genus has already been reported (Kim et al.
530 1998; Gadkari et al. 1990). The identification of a high number of carbonic anhydrases together
531 with SulP transporters among moonmilk *Streptomyces* (Table 1) could propose a mechanism via
532 which extracellular bicarbonate would be incorporated into the cell and subsequently converted to
533 CO₂ (Figure 1). In the moonmilk niche that is deprived of organic carbon, the uptake of inorganic
534 carbon could thus be a possible scenario, which would primarily promote CaCO₃ precipitation, and
535 in a second step would lead to CaCO₃ dissolution, as a result of organic acids excretion. The
536 availability of glucose also induces a dissolution phenotype via release of organic acids from
537 glucose breakdown, however only in 3 out of the 31 strains tested. This indicates that, although
538 carbohydrate metabolism might somehow play a role in rock weathering, it is probably not the only
539 operating system leading to this phenomenon, particularly in carbon-limited cave environment,
540 where the source of carbon might be the rock itself.

541 Discussion 542 Conclusions

542 If Actinobacteria really participate in the genesis of moonmilk deposits which metabolic
543 activities would potentially be involved? This was the main question addressed in our study which
544 used a collection of *Streptomyces* strains isolated from moonmilk in order to provide metabolic and
545 genetic evidences of their presumed role in mediating the formation of these speleothems.
546 Metabolic profiling revealed that all of the isolated *Streptomyces* possessed the capacity to promote
547 calcification through at least one pathway involved in biomineralization. Ammonification of
548 peptides/amino acids was found to be the most widespread and the strongest activity. This could
549 be in agreement with the fact that peptides and amino acids can constitute self-sustainable sources
550 of carbon and nitrogen for bacteria and thus support growth of microbial populations irrespectively
551 of allochthonous nutrient input. Interestingly, genome mining extended the possible spectrum of
552 metabolic capacities as it revealed the presence of additional pathways in each phylotype involved
553 in biomineralization processes, either related to CO₂ hydration or active transport of calcium ions.
554 These findings, supported by microscopy observations of bacteria-like filaments in moonmilk
555 deposits and crystals produced by individual moonmilk-originating bacteria, confirm its biogenic
556 origin and the importance of filamentous Actinobacteria in its genesis. However, the metabolic
557 activities evaluated *in vitro* were not always directly related to the genetic predisposition of
558 individual strains as some isolates with great genetic potential remained metabolically silent. This
559 may suggest that they were grown under conditions too different from those encountered in their
560 original niche to trigger the investigated activity or that specific environmental cues are required
561 for their activation. Consequently, whether those processes are indeed active *in situ* also remains
562 an open question. Additionally, our collection of moonmilk Actinobacteria, though being the most
563 significant population from these speleothems generated so far, does not include the large majority

564 of endemic representatives which are viable but not cultivable A metaproteomic analysis of
565 proteins extracted from moonmilk deposits is most likely the only approach that would accurately
566 identify the strains that importantly participate in carbonatogenesis and the metabolic pathways
567 involved. This approach is currently under investigation.

568

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581 **Conflict of interest**

582 The authors declare that they have no conflict of interest.

583 **Figure captions**

584 **Fig. 1 Heterotrophic pathways associated with carbonatogenesis presumed to occur in**
585 ***Streptomyces* species.** Microbially mediated carbonate precipitation might be either linked to
586 active transport of calcium ions across cellular membrane through $\text{Ca}^{2+}/2\text{H}^{+}$ antiporter system –
587 ChaA, or to nitrogen cycle-related pathways – ureolysis, ammonification and dissimilatory
588 reduction of nitrate to ammonium/ammonia (DNRA). All those pathways lead to alkalization of
589 the bacterial environment through the generation of ammonium, shifting the equilibrium towards
590 carbonate/bicarbonate ions, which, upon the presence of calcium, precipitate as calcium carbonate
591 (CaCO_3). ChaA, apart from providing calcium ions for potential precipitation, locally increase pH
592 through simultaneous incorporation of protons. The urease activity seems to be linked with
593 cytoplasmic carbonic anhydrases (β -CA), which catalyze dehydration of carbonic acid produced
594 during ureolysis into carbon dioxide that can constitute an additional source of bicarbonate ions for
595 precipitation. The export or import of bicarbonate ions could be potentially mediated via the sulfate
596 transporter family protein in cluster with CA (SulP-type permease). Assimilation of organic
597 nitrogen from amino acids releases extracellular ammonia through deamination, once the metabolic
598 demand for nitrogen is fulfilled. The inorganic nitrogen source (NO_3^-), which is imported in
599 *Streptomyces* by Nark-type transporters, can participate into biomineralization exclusively through
600 dissimilatory reduction to ammonia mediated by respiratory nitrate reductases (Nar) together with
601 potential nitrite reductases (Nir), which would be functional under dissimilatory conditions.
602 Reduction of nitrite to ammonia in streptomycetes was found to operate through assimilatory
603 pathway catalyzed by NasA and NirBD reductases

604

605 **Fig. 2 SEM-images of nano-size filaments found in the crystal structure of moonmilk deposits**
606 **from the cave “Grotte des Collemboles” (Comblain-au-Pont, Belgium).** Among typical
607 moonmilk monocrystalline rods and polycrystalline fibers indicated by white arrows (**a**), dense
608 meshes of tiny filaments were observed, which were compacted into the stacked pellets (**b**) or dense
609 biofilms (**c**), mostly randomly orientated, but occasionally one-way directed (**d**, **e**). Along (**f**) or on
610 the tip (**g**) of some of those filaments, calcium carbonate deposition was identified, with some of
611 the filaments presenting reticulated morphology (**h**) as indicated by arrows

612 **Fig. 3 Precipitation-related metabolic activities of the moonmilk *Streptomyces*.** (**a**) Ureolysis.
613 (**b**) Ammonification. (**c**) Nitrate reduction. (**d**) Nitrite reduction. *Klebsiella pneumoniae* ATCC
614 13883 (KP), *Citrobacter freundii* ATCC 43864 (CF), *Escherichia coli* ATCC 25922 (EC) and
615 *Pseudomonas aeruginosa* ATCC 27853 (PA) were used as positive controls for ureolysis,
616 ammonification, nitrate and nitrite reduction tests, respectively. The observed activities are
617 visualized for representative strains demonstrating different metabolic performance for each
618 activity tested, designated through the symbols: (-) lack, (+/-) weak, (+) moderate, (++) good, and
619 (+++) strong

620
621 **Fig. 4 The global pattern of carbonate precipitation-associated metabolic activities of**
622 **moonmilk *Streptomyces*.** The heatmap plot representing metabolic performance of moonmilk
623 *Streptomyces* strains indicated by color scale, correlated with their MLSA-based phylogenetic
624 classification (Maciejewska et al. 2016). The total value represents the sum of metabolic
625 performance observed for ureolysis and amino acids ammonification, ranking the isolates
626 according to their metabolic predispositions for calcium carbonate precipitation for the tested
627 activities. The metabolic performance of nitrate/nitrite reduction test was not included into the final

628 ranking. Abbreviations: U, ureolysis; A, peptide/amino acid ammonification; T, total sum of
629 activities for ureolysis and amino acid ammonification; NO_3^- , nitrate reduction; NO_2^- , nitrite
630 reduction

631

632 **Fig. 5 Percentage of moonmilk *Streptomyces* displaying carbonatogenesis related activities *in***
633 ***vitro* within different metabolic categories.** (-) lack, (+/-) weak, (+) moderate, (++) good, and
634 (+++) strong

635

636 **Fig. 6 Low vacuum-SEM-BSE images (a, c, e, g) and X-ray elemental mappings (b, d, f, h) of**
637 **CaCO_3 deposits produced by MM24 (a-b, e-f) and MM99 (c-d, g-h) isolates.** Abundant mineral
638 deposits produced by isolates MM99 (a) and MM24 (c) in CPA medium, nearly encrusting the
639 whole microbial colony, were morphologically different from less abundant, but much bigger,
640 mineral polymorphs produced in modified B-4 agar by MM99 (e) and MM24 (g). The observed
641 precipitates were found to be CaCO_3 minerals as revealed by elemental spectra (supplementary Fig.
642 5) and mappings in both media and for both isolates (MM99 (b) and MM24 (d) in CPA, MM99 (f)
643 and MM24 (h) in modified B-4). The mappings for MM99 and MM24 in B-4 are marked with the
644 white squares. The mappings are combined images in which detected dominant elements, namely
645 carbon (C), oxygen (O), and calcium (Ca) are assigned to a defined color

646

647 **Fig. 7 Biogenic signatures within mineral deposits produced by moonmilk-originating**
648 ***Streptomyces* (LV-SEM-BSE images).** Along with the different morphologies of produced
649 mineral deposits specific to the culture conditions used, numerous bacterial imprints were
650 observed. *Streptomyces* filaments were completely incorporated into the produced minerals as
651 observed for MM99 (a/b), MM24 (c/d/e) in CPA medium, as well as for MM99 (g) and MM24

652 **(i/j)** in modified B-4 agar. Their mineralization also appeared as wrinkles each containing a
653 bacterial filament suggesting their progressive encrustation within the mineral **(b/e/g, arrows)**.
654 Alternatively, non-mineralized microbial filaments were seen interconnecting adjacent mineral
655 deposits, as detected for MM24 in CPA **(c/e, arrows)**, or possible compacted aggregates of
656 filaments were observed at the edges of the mineral produced by MM99 in B-4 **(h)**. Initial steps of
657 mineral deposition were detected along bacterial filaments in modified B-4 culture of isolate
658 MM99 **(f, arrows)**

659
660 **Fig. 8 Dissolution-related metabolic activities of the moonmilk *Streptomyces*.** Metabolic
661 performance observed for oxidative glucose degradation **(a)**, and calcium carbonate dissolution in
662 diluted nutrient agar **(b)** or minimal media **(c)**. *Pseudomonas aeruginosa* ATCC 27853 (PA) was
663 used as positive control in glucose oxidative assay. The metabolic performance is designated
664 through the symbols: (-) lack, (+/-) weak, (+) moderate, (++) good, and (+++) strong activity.
665 Media not supplemented with glucose are in the upper line in panel **b** and **c**, while media with
666 addition of glucose are displayed in the bottom line of the corresponding panels

667
668 **Fig. 9 The global pattern of carbonate dissolution-associated metabolic activities of moonmilk**
669 ***Streptomyces*.** The heatmap plot representing metabolic performance of moonmilk *Streptomyces*
670 strains indicated by color scale, correlated with their MLSA-based phylogenetic classification
671 (Maciejewska et al. 2016). Abbreviations: O, glucose oxidation; MM, minimal media with CaCO₃;
672 MMg, minimal media with CaCO₃ and glucose; NA, diluted nutrient agar with CaCO₃; NAg,
673 diluted nutrient agar with CaCO₃ and glucose

674 **Tables**

675 **Table 1.** *In silico* prediction of individual genes putatively involved in the moonmilk
676 biomineralization process retrieved from moonmilk-originating *Streptomyces* strains, including
677 genes related to ureolysis (*ure*), nitrate/nitrite transport (*narK*) and reduction (*nar/nas/nir*), carbon
678 dioxide (CO₂) hydration (carbonic anhydrase - CA), and active transport of calcium ions through
679 Ca²⁺/2H⁺ antiporter system (*chaA*).

strain	Ureolysis							NO ₃ ⁻ / NO ₂ ⁻ transport		Respiratory NO ₃ ⁻ reduction					Assimilatory NO ₃ ⁻ reduction	NO ₂ ⁻ reduction			CO ₂ hydration			Ca ²⁺ transport
	<i>ureA</i>	<i>ureB</i>	<i>ureAB</i>	<i>ureC</i>	<i>ureF</i>	<i>ureG</i>	<i>ureD</i>	<i>narK2</i>	<i>narK</i>	<i>narG</i>	<i>narH</i>	<i>narJ</i>	<i>narJ2</i>	<i>narI</i>	<i>nasA</i>	<i>nirB1</i>	<i>nirB2</i>	<i>nirD</i>	β-CA (1)	β-CA (2)	<i>sulP</i>	<i>chaA</i>
MM1	1	1	2	3	1	1	2	-	+	-	-	-	-	1	1	1	1	2	1	1	-	
MM3	1	1	2	3	2	2	3	-	+	-	-	-	-	1	1	1	1	2	1	1	-	
MM5	1	1	2	3	2	2	2	-	+	-	-	-	-	1	1	1	1	3	3	1	1	
MM6	1	1	1	3	1	1	1	-	+	-	-	-	-	1	1	2	2	4	-	1	1	
MM7	2	2	2	3	2	2	2	+	+	1	1	-	1	1	1	1	1	1	1	1	-	
MM10	1	1	1	2	2	2	2	+	+	3	2	1	1	2	1	1	1	2	1	1	-	
MM12	1	1	2	3	3	3	3	-	+	-	-	-	-	1	1	1	1	2	2	-	1	
MM13	1	1	1	2	2	2	2	+	+	1	-	-	-	1	1	1	1	2	1	1	1	
MM14	1	1	2	3	2	2	2	-	+	-	1	-	1	1	1	1	1	1	2	1	-	
MM17	1	1	3	3	2	2	2	-	+	1	-	-	-	1	1	1	1	6	1	1	1	
MM19	1	1	1	2	1	1	1	-	+	-	-	-	-	1	1	1	1	1	1	1	-	
MM21	1	1	2	3	2	2	2	-	+	-	-	-	-	1	1	1	1	2	1	1	-	
MM23	1	1	2	3	2	2	2	-	+	-	-	-	-	1	1	1	1	1	1	1	-	
MM24	2	2	2	5	2	2	4	+	+	-	-	-	-	1	1	1	1	2	2	1	1	
MM44	1	1	2	3	2	2	2	-	+	-	-	-	-	1	1	1	1	2	1	1	-	
MM48	2	2	2	4	2	2	2	-	+	1	1	-	1	1	1	2	1	5	1	1	1	
MM59	1	1	-	1	1	1	1	-	+	-	-	-	-	1	1	1	1	3	2	1	1	
MM68	1	1	1	2	3	2	2	-	+	-	-	-	-	1	1	1	1	2	2	1	1*	
MM99	3	3	1	4	3	3	3	+	-	-	-	-	-	1	-	-	-	1	1	1	-	
MM100	1	1	2	4	2	2	2	+	+	-	-	-	-	2	1	1	1	2	1	-	-	
MM104	1	1	1	1	1	1	1	-	+	-	-	-	-	-	1	1	1	2	3	1	1	
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MM106	2	2	-	2	2	2	2	+	+	2	2	-	2	2	1	1	1	1	-	1	1	
MM107	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-	3	2	1	1	
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MM109	1	1	2	3	2	2	2	+	+	2	1	-	1	2	1	1	1	2	-	1	-	
MM111	2	2	2	4	2	2	2	-	+	1	1	-	1	1	1	1	1	1	1	1	1	
MM117	1	1	1	2	1	1	1	+	+	-	-	-	-	2	1	1	1	1	1	1	-	
MM122	2	2	2	4	3	3	3	+	+	-	-	-	-	1	1	1	1	1	3	-	-	
MM128	1	1	1	2	1	1	1	-	+	-	-	-	-	1	1	1	1	2	2	1	1	

680 Abbreviations: CA_sulf, sulfate transporter family protein in cluster with carbonic anhydrase; * pseudogene

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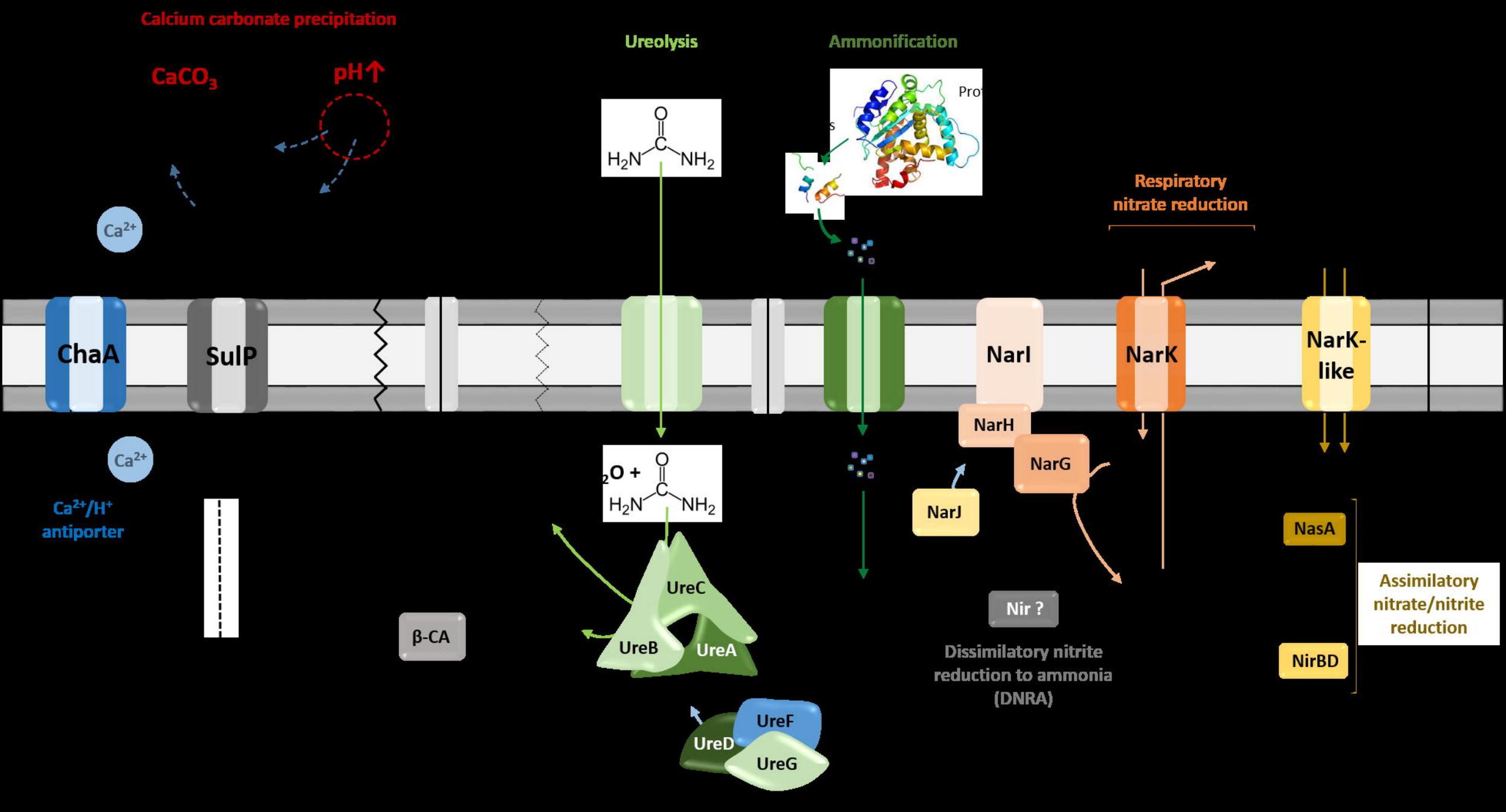
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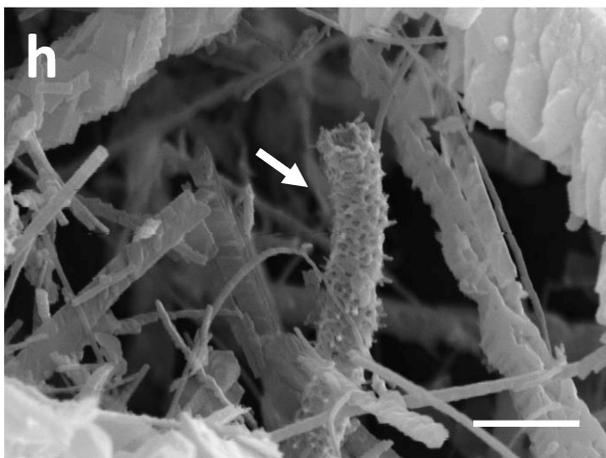
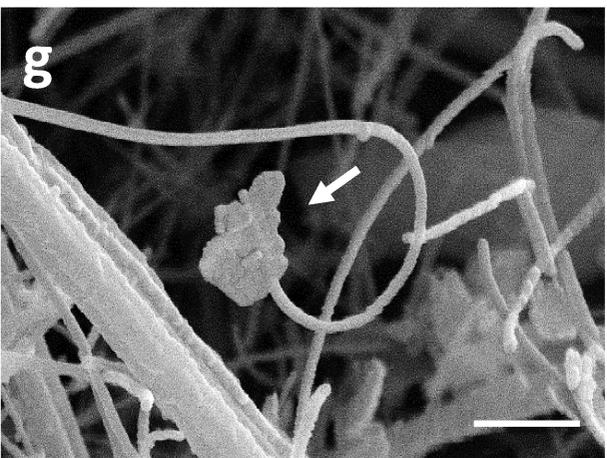
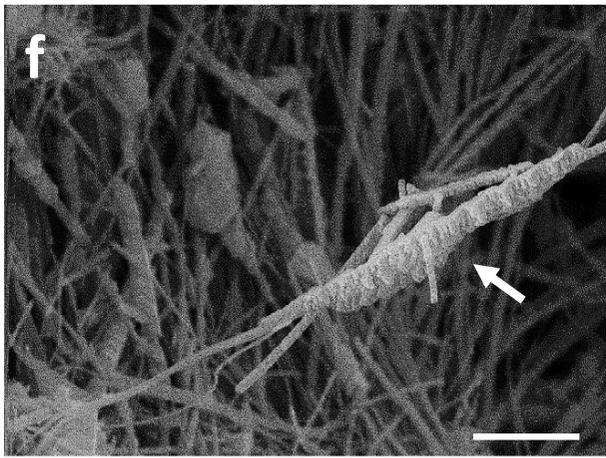
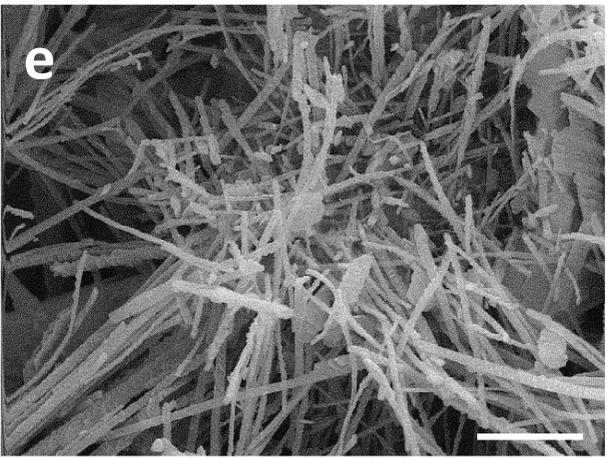
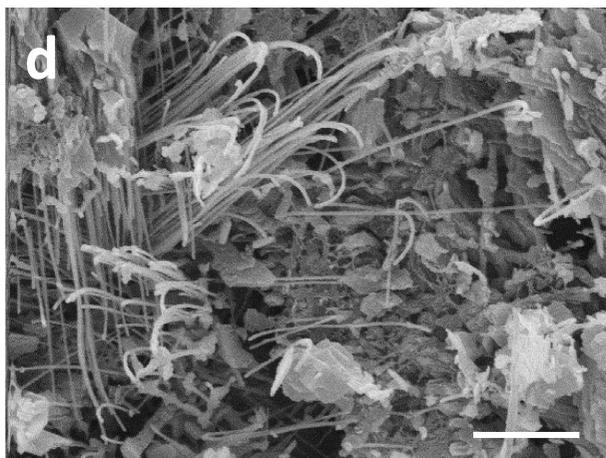
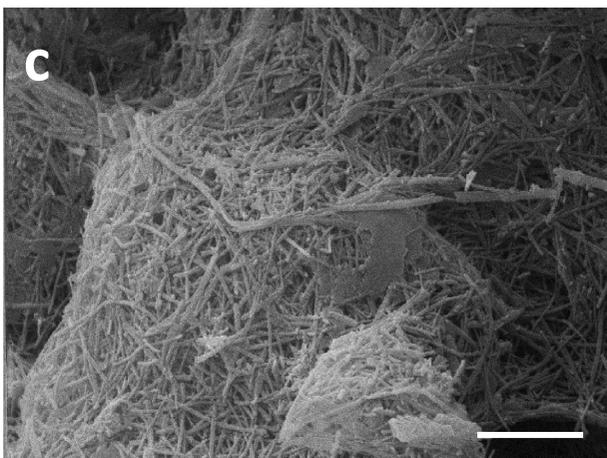
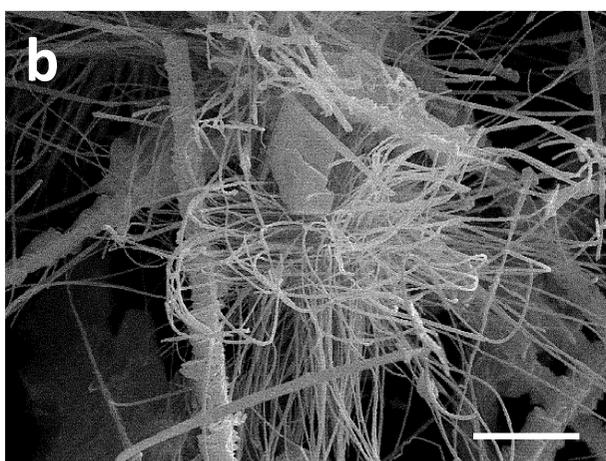
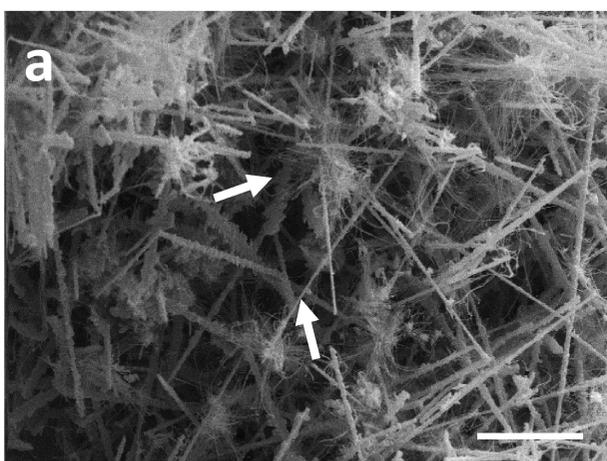
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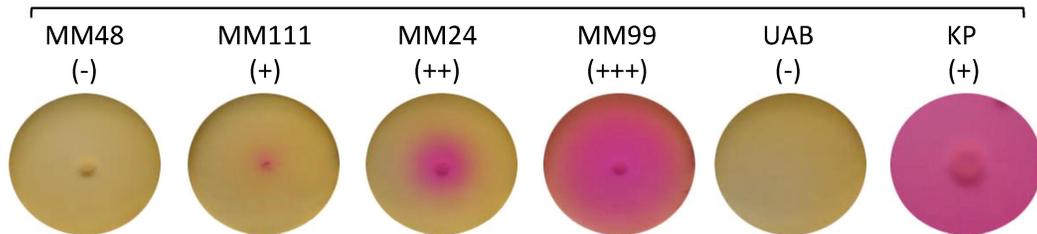
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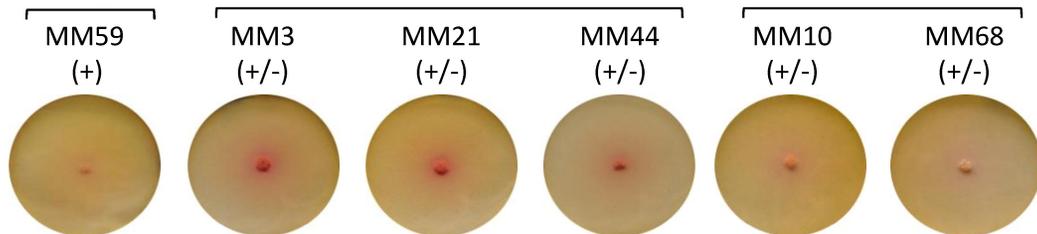
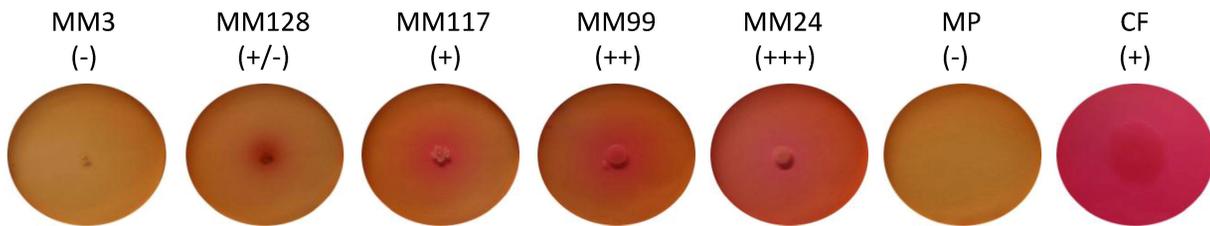
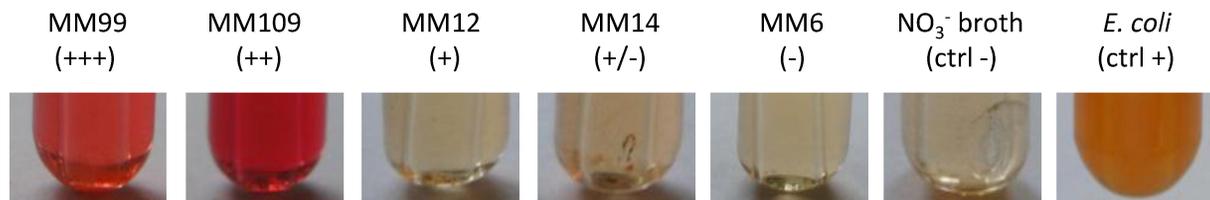
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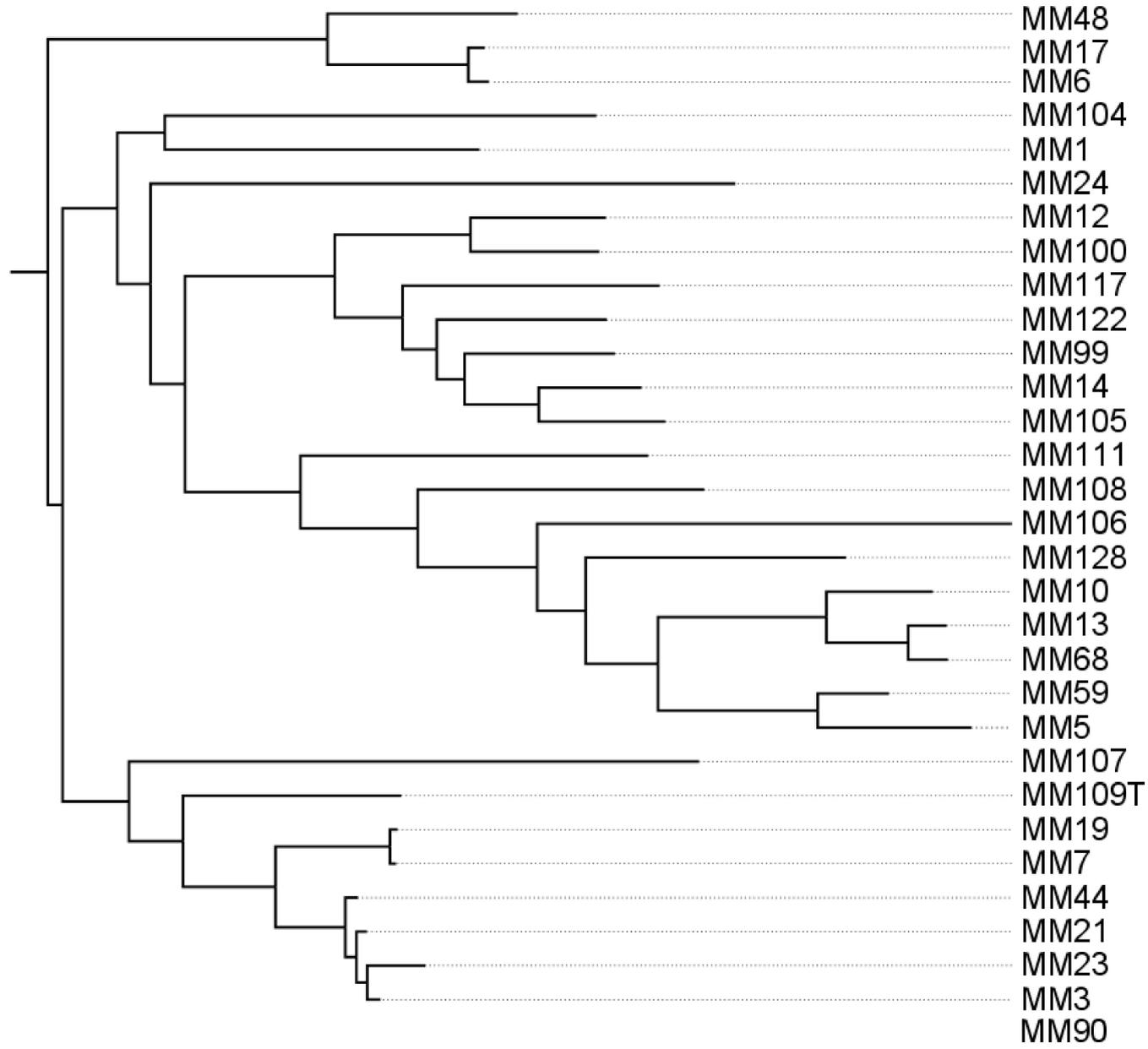


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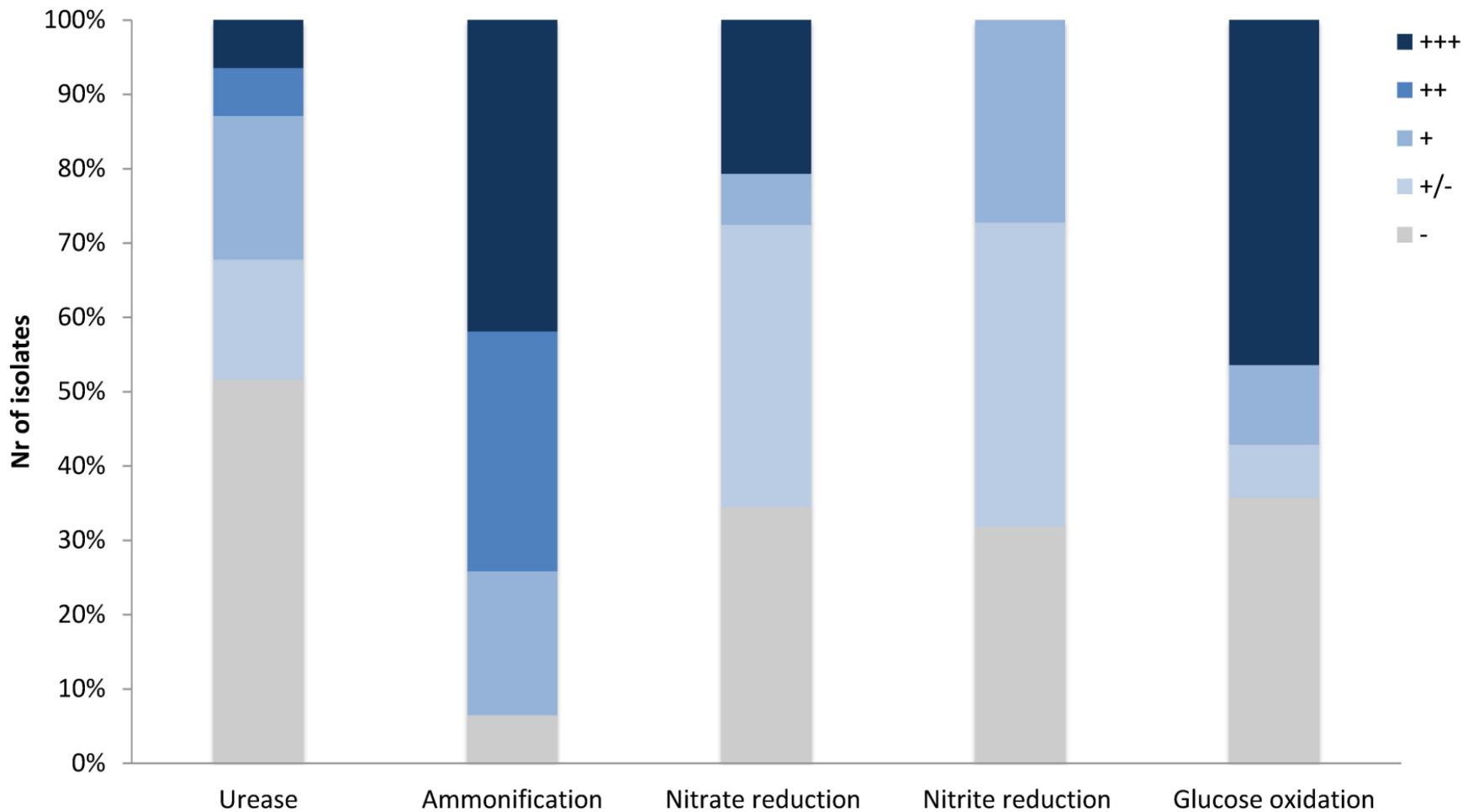
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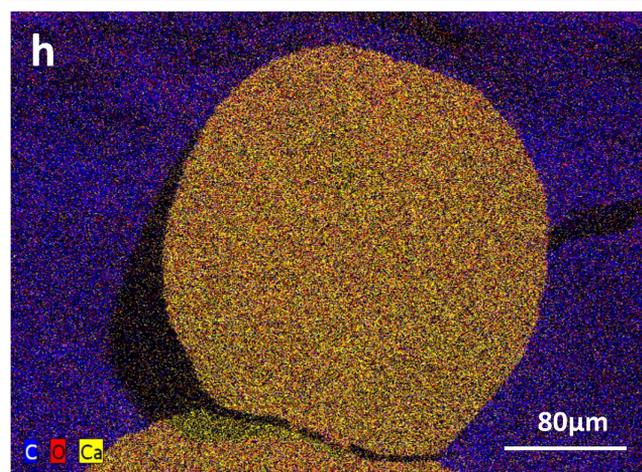
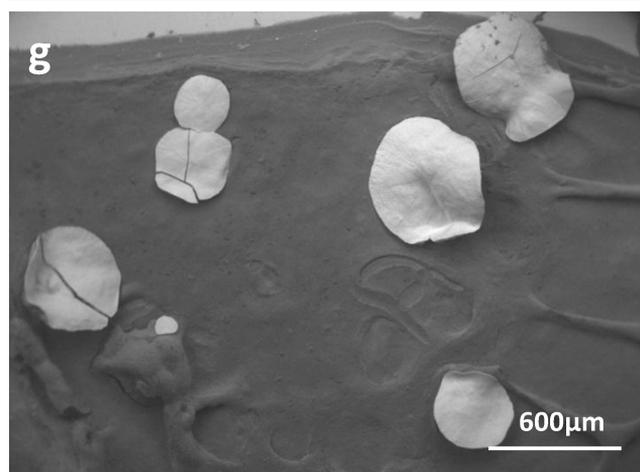
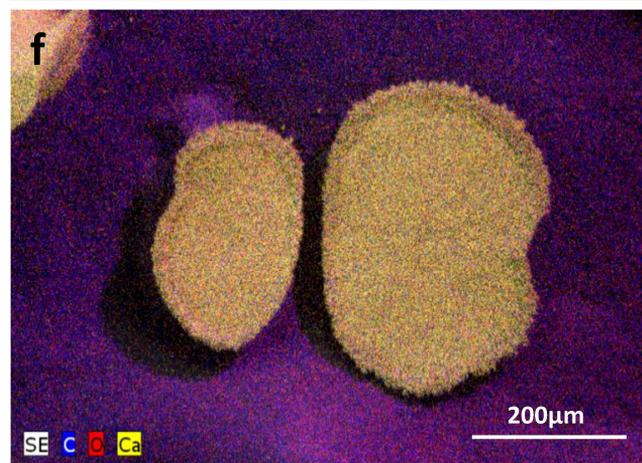
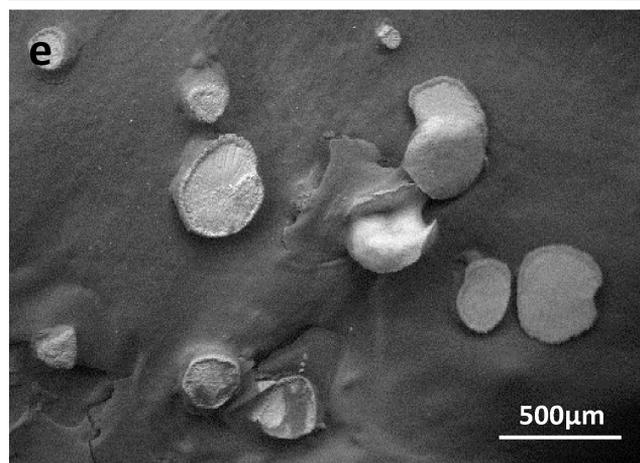
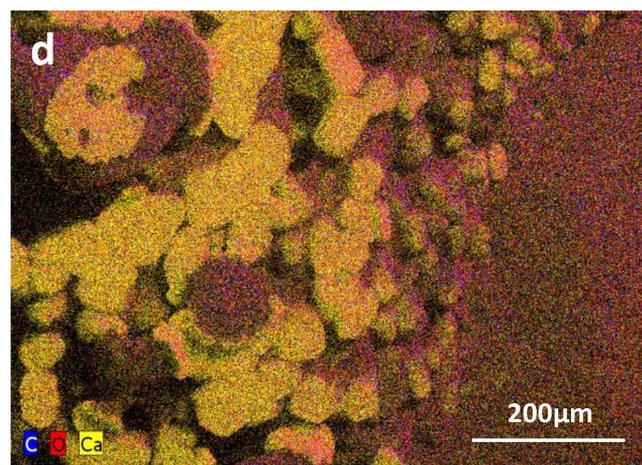
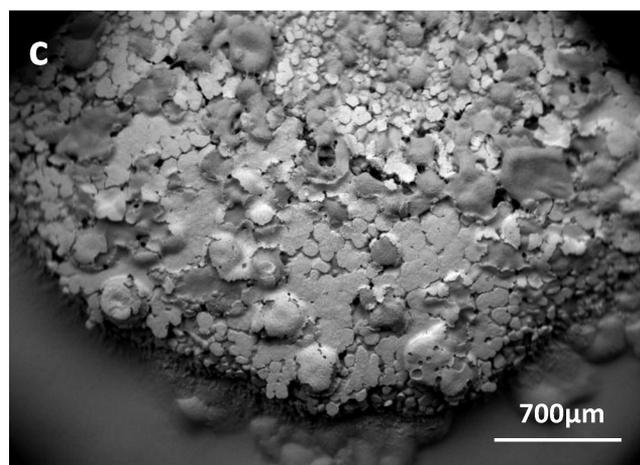
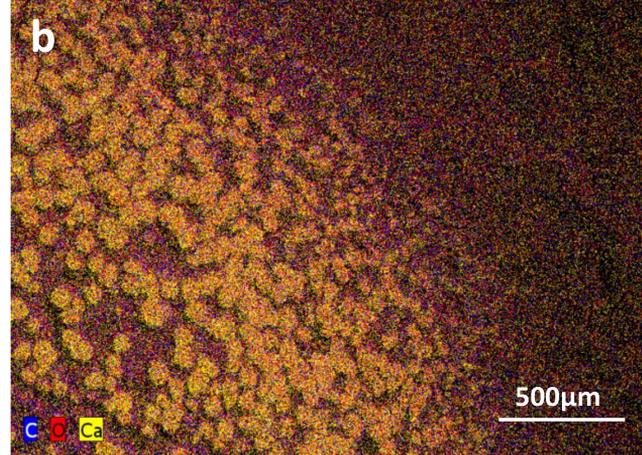
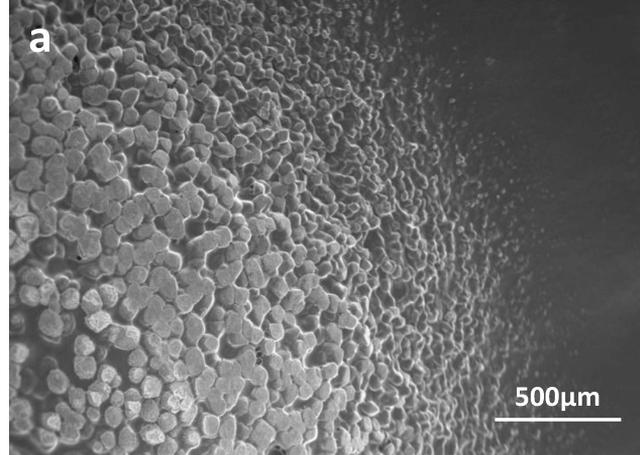
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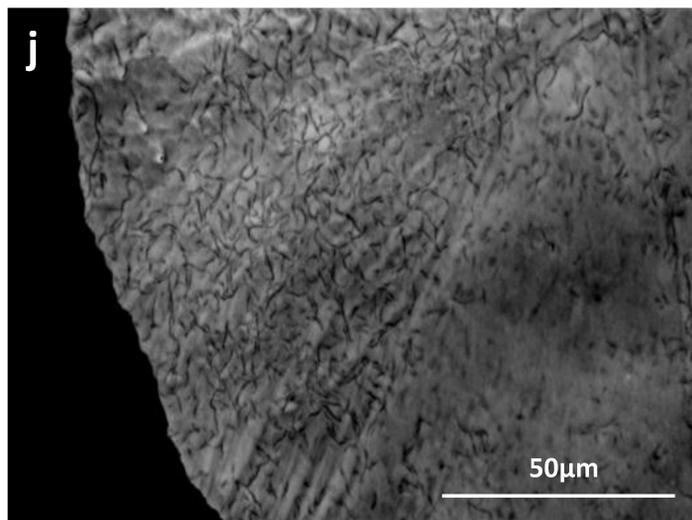
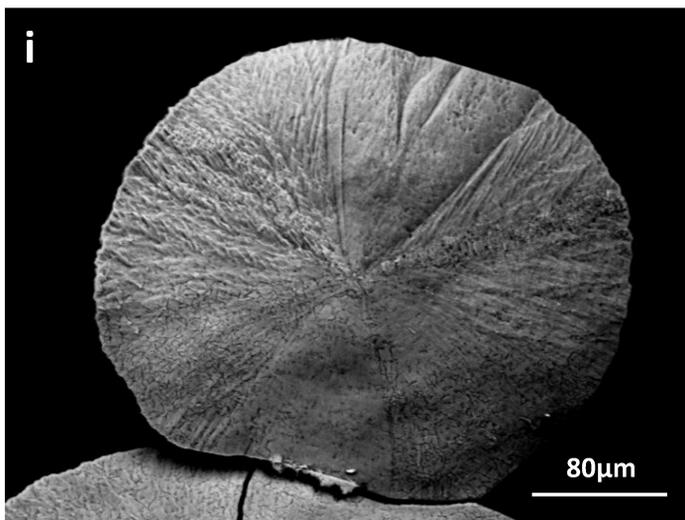
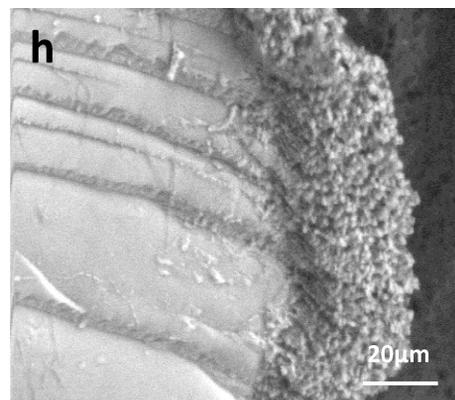
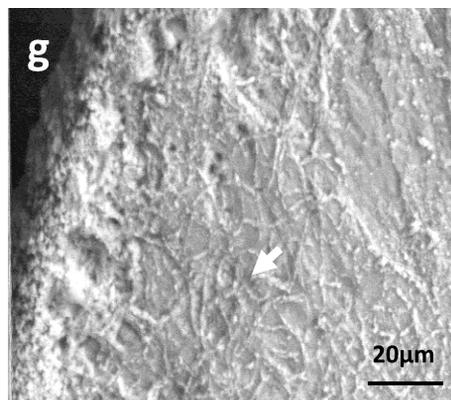
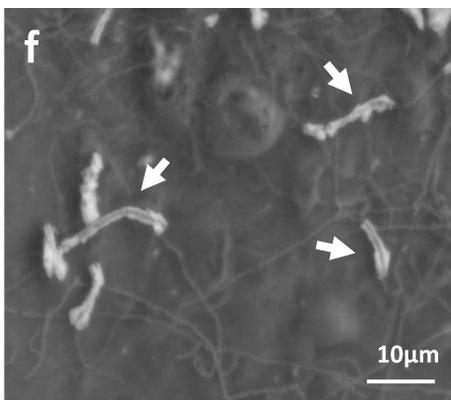
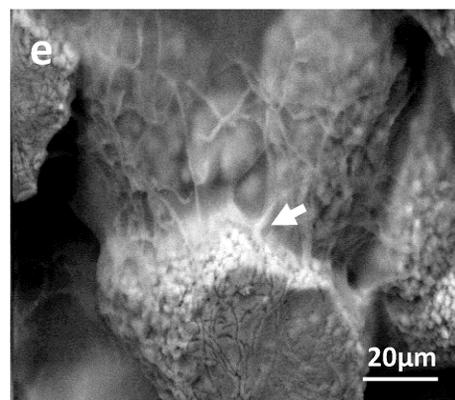
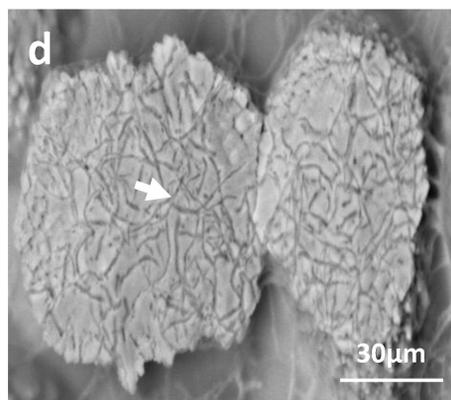
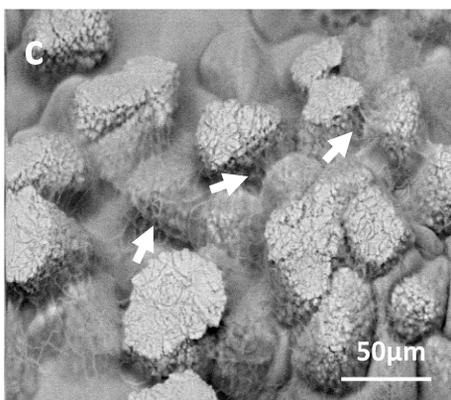
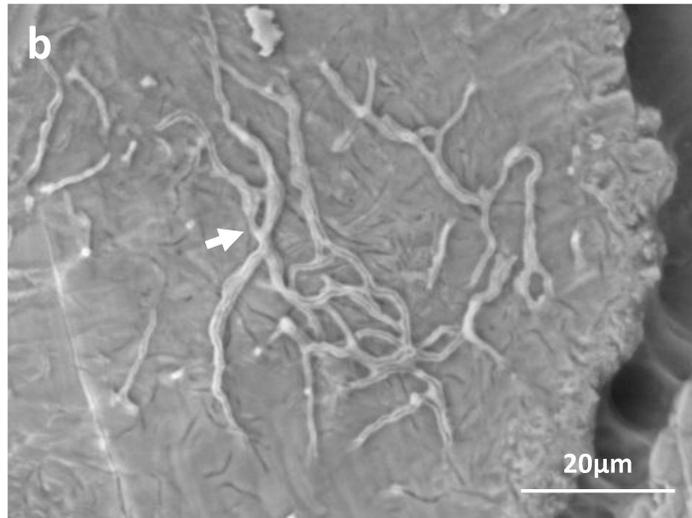
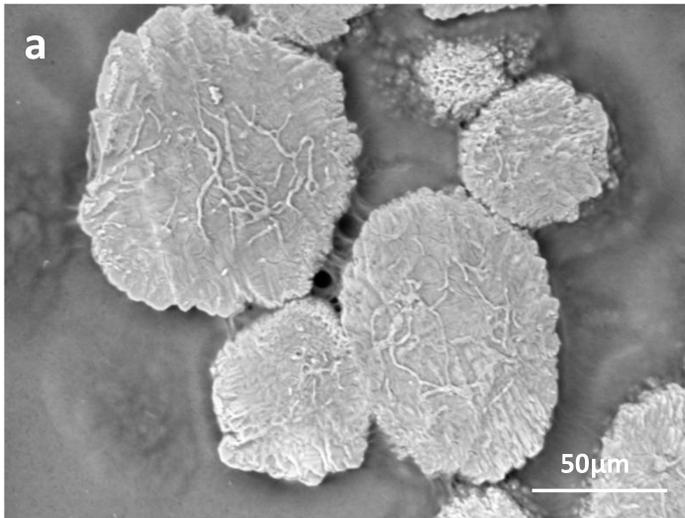


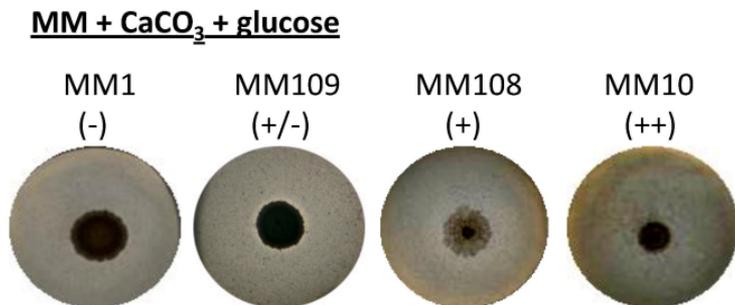
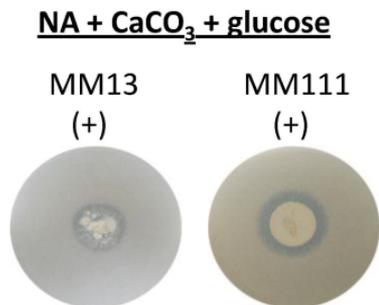
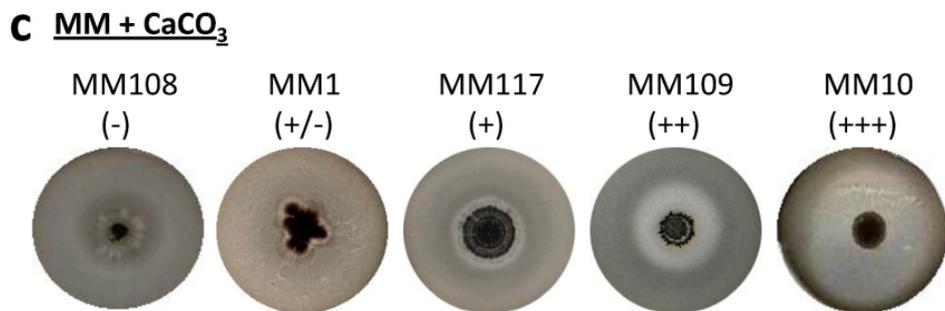
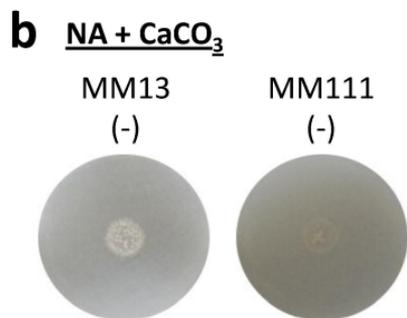
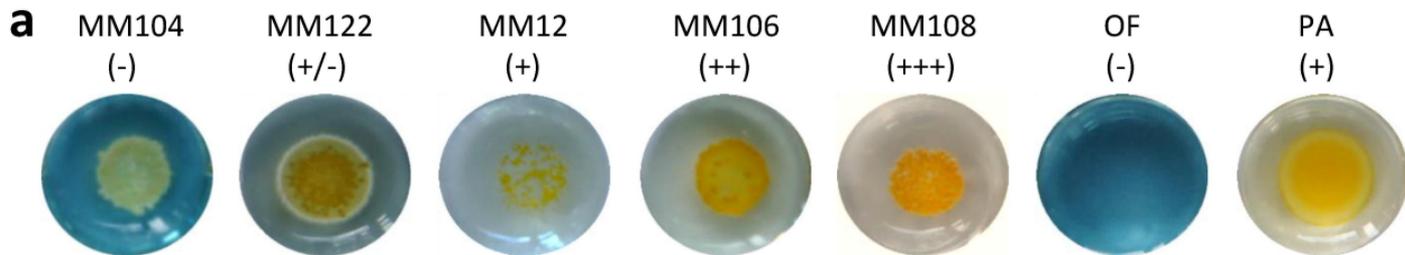
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MM48	0	3	3	4	0
MM17	0	3	3	0	1
MM6	0	0	0	0	3
MM104	0	4	4	0	1
MM1	0	0	0	0	3
MM24	5	3	8	0	2
MM12	0	2	2	1	0
MM100	4	4	8	3	1
MM117	0	2	2	2	1
MM122	6	4	10	4	3
MM99	6	3	9	4	1
MM14	4	4	8	1	0
MM105	4	3	7	1	3
MM111	4	3	7	0	0
MM108	5	4	9	1	0
MM106	0	4	4	4	2
MM128	0	2	2	0	0
MM10	1	3	4	4	1
MM13	0	2	2	1	2
MM68	1	3	4	1	3
MM59	3	4	7	1	3
MM5	4	4	8	1	1
MM107	0	2	2	0	2
MM109T	0	3	3	4	0
MM19	0	3	3	1	2
MM7	0	3	3	3	3
MM44	2	4	6	0	3
MM21	2	4	6	0	1
MM23	0	4	4	1	2
MM3	2	4	6	1	3
MM90	0	2	2	2	1

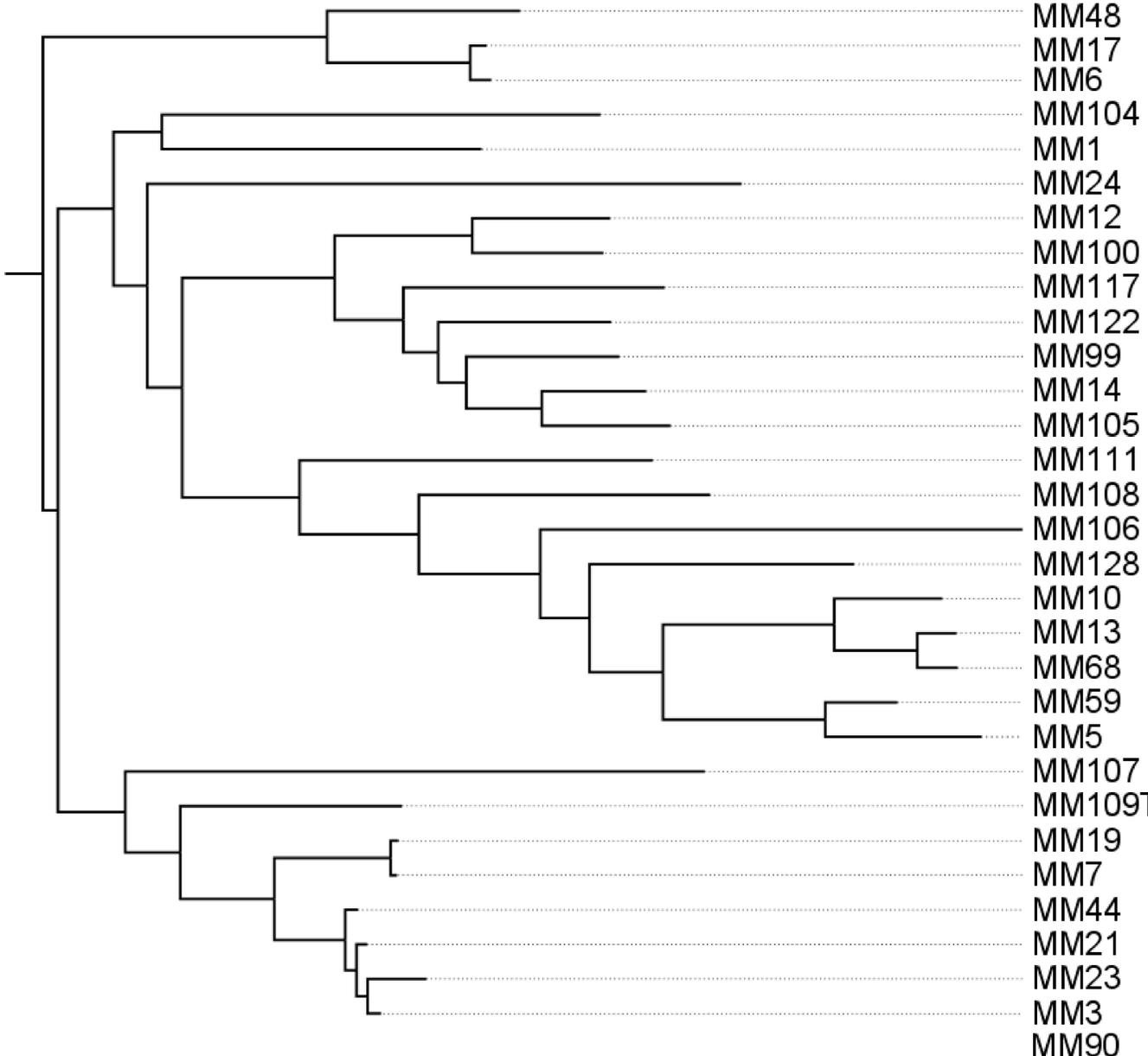
0.04











	O	MM	MMg	NA	NAg
MM48	4	4	1	0	0
MM17	0	4	0	0	0
MM6	0	4	0	0	0
MM104	0	2	0	0	0
MM1	0	1	0	0	0
MM24	4	1	0	0	0
MM12	2	0	0	0	0
MM100	0	2	0	0	0
MM117	4	2	0	0	0
MM122	1	2	0	0	0
MM99	0	3	0	0	0
MM14	4	3	1	0	0
MM105	4	2	0	0	1
MM111	4	1	2	0	2
MM108	4	0	2	0	0
MM106	3	0	0	0	0
MM128	2	4	3	0	1
MM10	2	4	3	0	0
MM13	4	0	0	0	1
MM68	4	4	3	0	1
MM59	0	3	0	0	0
MM5	0	3	0	0	0
MM107	0	1	0	0	0
MM109T	4	3	1	0	0
MM19	0	0	0	0	0
MM7	3	4	0	0	0
MM44	4	1	0	0	1
MM21	4	3	0	0	0
MM23	1	0	1	0	1
MM3	4	3	0	0	0
MM90	3	2	0	0	1

0.04