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Supplement of

Calcium carbonates: induced biomineralization with controlled macromorphology

Aileen Meier et al.

Correspondence to: Erika Kothe (erika.kothe@uni-jena.de)

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Supplemental Material

Tab. S1: Strains selected from each habitat used in this study. The four most representative strains from isolation plates for rock (r), groundwater (gw) and soil (s) samples from Middle Muschelkalk (MM) or Lower (LM) were selected. 16S rDNA sequence accession numbers are given in parentheses (Genbank).

rLM	rMM	gwLM	gwMM	sLM	sMM
<i>Bacillus</i> sp. rLMa (KX527723.1)	<i>Arthrobacter pascens</i> rMM19	<i>Flavobacterium limicola</i> S_5.3 (KR088468.1)	<i>Arthrobacter</i> sp. W_2.1 (KX570903.1)	<i>Agromyces cerinus</i> sLM10 (KX536506.1)	<i>Agrococcus jejuensis</i> sMM51 (KX527688.1)
<i>Bacillus muralis</i> rLMd (KX527725.1)	<i>Bacillus</i> sp. rMM8 (KX527696.1)	<i>Lelliottia amni-gena</i> S_H3 (KR088478.1)	<i>Planococcus</i> sp. W_1.2 (KR088481.1)	<i>Bacillus</i> sp. sLM42 (KX536514.1)	<i>Moraxella osloensis</i> sMM16 (KX527667.1)
<i>Bacillus simplex</i> 3.3F (KX527719.1)	<i>Psychrobacillus psychrodurans</i> rMM20 (KX527705.1)	<i>Pseudomonas</i> sp. S_H4 (KX573101.1)	<i>Rhodococcus erythropolis</i> W_Sd5 (KX570908.1)	<i>Streptomyces</i> sp. sLM17	<i>Sphingopyxis bauzanensis</i> sMM41 (KX527680.1)
<i>Micrococcus luteus</i> rLMc (KX527724.1)	<i>Ochrobactrum intermedium</i> rMM23 (KX527707.1)	<i>Rhizobium</i> sp. S_4.1a	<i>Advenella</i> sp. W_Sd3 (KR088492.1)	<i>Streptomyces</i> sp. sLM8 (KX536505.1)	<i>Streptomyces</i> sp. sMM10 (KX527665.1)

Tab. S2: Strains isolated from rock (r), groundwater (gw) and soil (s) samples from Middle Muschelkalk (MM) or Lower (LM) identified by 16S rDNA sequencing. The affiliations to kingdoms (classes for Proteobacteria) are given.

Strain	Organism	Affiliation	Strain	Organism	Affiliation	Strain	Organism	Affiliation
Rock Lower Muschelkalk, outcrop Jena Formation (51125583, 11707340/57)			Groundwater Lower Muschelkalk, Stöben (5660183, 4478864)			Soil Lower Muschelkalk, quarry Bad Kösen on Jena formation (51125376/427, 11709132/319)		
rLM1.4	<i>Bacillus niacini</i>	Firmicutes	S_1.1	<i>Pseudomonas</i> sp.	Gamma-proteobacteria	sLM2	<i>Streptomyces</i> sp.	Actinobacteria
rLM1.5	<i>Bacillus flexus</i>	Firmicutes	S_1.13	<i>Microbacterium</i> sp.	Actinobacteria	sLM5	<i>Streptomyces</i> sp.	Actinobacteria
rLM1.6	<i>Bacillus pumilus</i>	Firmicutes	S_1.16	<i>Pantoea ananatis</i>	Gamma-proteobacteria	sLM6	<i>Rhodococcus</i> sp.	Actinobacteria
rLM1.9	<i>Bacillus altitudinis</i>	Firmicutes	S_1.18	<i>Paenibacillus glycanilyticus</i>	Firmicutes	sLM8	<i>Streptomyces</i> sp.	Actinobacteria
rLM2.3	<i>Bacillus anthracis</i>	Firmicutes	S_2.5	<i>Pseudomonas migulae</i>	Gamma-proteobacteria	sLM10	<i>Agromyces cerinus</i>	Actinobacteria
rLM2.4	<i>Bacillus subtilis</i>	Firmicutes	S_2.6	<i>Pseudomonas fluorescens</i>	Gamma-proteobacteria	sLM11	<i>Bacillus badius</i>	Firmicutes
rLM2.6	<i>Bacillus massiliensis</i>	Firmicutes	S_2.9	<i>Pseudomonas</i> sp.	Gamma-proteobacteria	sLM13	<i>Bacillus simplex</i>	Firmicutes
rLM2.7	<i>Bacillus strato-sphericus</i>	Firmicutes	S_2.10	<i>Microbacterium</i> sp.	Actinobacteria	sLM15	<i>Bacillus pumilus</i>	Firmicutes
rLM4.3	<i>Kocuria</i> sp.		S_3.1	<i>Aeromonas sharmana</i>	Gamma-proteobacteria	sLM17	<i>Streptomyces</i> sp.	Actinobacteria
rLM3.1F	<i>Bacillus pumilus</i>	Firmicutes	S_3.6	<i>Aeromonas salmonicida</i>	Gamma-proteobacteria	sLM18	<i>Phyllobacterium</i> sp.	Alphaproteobacteria
rLM3.2F	<i>Paenibacillus</i> sp.	Firmicutes	S_3.7	<i>Pseudomonas protegens</i>	Gamma-proteobacteria	sLM29	<i>Paenibacillus</i> sp.	Firmicutes
rLM3.3F	<i>Bacillus simplex</i>	Firmicutes	S_3.8	<i>Acinetobacter calcoaceticus</i>	Gamma-proteobacteria	sLM39	<i>Streptomyces</i> sp.	Actinobacteria
rLM3.5F	<i>Bacillus</i> sp.	Firmicutes	S_4.1a	<i>Rhizobium</i> sp.	Alphaproteobacteria	sLM41	<i>Streptomyces phaeochromogenes</i>	Actinobacteria
rLM3.6F	<i>Paenibacillus amylolyticus</i>	Firmicutes	S_5.2	<i>Janthinobacterium lividum</i>	Actinobacteria	sLM42	<i>Bacillus</i> sp.	Firmicutes
rLM4.1F	<i>Bacillus cereus</i>	Firmicutes	S_5.3	<i>Flavobacterium limicola</i>	Bacteroidetes	sLM43	<i>Bacillus</i> sp.	Firmicutes
rLMa	<i>Bacillus</i> sp.	Firmicutes	S_Sd4	<i>Massilia aurea</i>	Betaproteobacteria	sLM47	<i>Bacillus pumilus</i>	Firmicutes
rLMc	<i>Micrococcus luteus</i>	Actinobacteria	S_Sd8	<i>Acidovorax facilis</i>	Betaproteobacteria	sLM48	<i>Streptomyces anulatus</i>	Actinobacteria
rLMd	<i>Bacillus muralis</i>	Firmicutes	S_Sd9	<i>Pseudomonas peli</i>	Gamma-proteobacteria	sLM50	<i>Bacillus pumilus</i>	Firmicutes
			S_Sd13	<i>Aeromonas</i> sp.	Gamma-proteobacteria	sLM1E4	<i>Caballeronia glathei</i>	Firmicutes
			S_Sd16	<i>Pseudomonas</i> sp.	Gamma-proteobacteria	sLM2A3	<i>Pseudomonas brenneri</i>	Gammaproteobacteria
			Sd20	<i>Microbacterium</i> sp.	Actinobacteria			
			S_A2	<i>Pseudomonas</i>	Gamma-			

			S_B2	<i>baetica</i> <i>Agrobacterium</i> sp.	proteobacteria Alphaproteo- bacteria			
			S_G4	<i>Pseudomonas</i> <i>umsongensis</i>	Gamma- proteobacteria			
			S_H1	<i>Rahnella</i> sp.	Gamma- proteobacteria			
			S_H3	<i>Lelliottia</i> <i>amnigena</i>	Gamma- proteobacteria			
			S_H4	<i>Pseudomonas</i> sp.	Gamma- proteobacteria			
Rock Middle Muschelkalk, outcrop Kartstadt formation (51126206, 11704266-11704280)			Groundwater Middle Muschelkalk, Wichmar (5655906, 4478030)			Soil Middel Muschelkalk, quarry Bad Kösen, Kartstadt formation (5665596-5665733_4479366-4479449)		
rMM4	<i>Arthrobacter phenantrenivorans</i>	Actinobacteria	W_1.1	<i>Staphylococcus succinus</i>	Firmicutes	sMM5	<i>Bacillus</i> sp.	Firmicutes
rMM7	<i>Ramlibacter tataouinensis</i>	Betaproteobacteria	W_1.3	<i>Staphylococcus xylosus</i>	Firmicutes	sMM6	<i>Kocuria rhizophila</i>	Actinobacteria
rMM8	<i>Bacillus</i> sp.	Firmicutes	W_2.1	<i>Arthrobacter</i> sp.	Actinobacteria	sMM7	<i>Rathayibacter caricis</i>	Actinobacteria
rMM9	<i>Bacillus</i> sp.	Firmicutes	W_3.1b	<i>Sporosarcina aquimarina</i>	Firmicutes	sMM10	<i>Streptomyces</i> sp.	Actinobacteria
rMM10	<i>Bacillus</i> sp.	Firmicutes	W_3.2	<i>Glucamicibacter arilaitensis</i>	Actinobacteria	sMM13	<i>Paracoccus yeei</i>	Alphaproteobacteria
rMM11	<i>Streptomyces</i> sp.	Actinobacteria	W_3.7	<i>Pantoea</i> sp.	Gamma- proteobacteria	sMM16	<i>Moraxella osloensis</i>	Gammaproteobacteria
rMM12	<i>Arthrobacter</i> sp.	Actinobacteria	W_4.1a	<i>Pseudomonas</i> sp.	Gamma- proteobacteria	sMM17	<i>Promicromonospora umidemergens</i>	Actinobacteria
rMM13	<i>Arthrobacter phenantrenivorans</i>	Actinobacteria	W_4.1b	<i>Lelliottia amnigena</i>	Gamma- proteobacteria	sMM19	<i>Streptomyces beijiagensis</i>	Actinobacteria
rMM14	<i>Bacillus</i> sp.	Firmicutes	W_5.1a	<i>Stenotrophomonas rhizophila</i>	Gamma- proteobacteria	sMM21	<i>Dermacoccus</i> sp.	Actinobacteria
rMM16	<i>Bacillus niabensis</i>	Firmicutes	W_5.3a	<i>Shingobacterium kitahiroshimense</i>	Bacteroidetes	sMM23	<i>Arthrobacter pascens</i>	Actinobacteria
rMM17	<i>Arthrobacter phenantrenivorans</i>	Actinobacteria	W_5.3b	<i>Comamonas koreensis</i>	Betaproteobacteria	sMM27	<i>Promicromonospora sukumoe</i>	Actinobacteria
rMM19	<i>Arthrobacter pascens</i>	Actinobacteria	W_5.4	<i>Flavobacterium</i> sp.	Bacteroidetes	sMM28	<i>Ramlibacter tataouinensis</i>	Betaproteobacteria
rMM20	<i>Psychrobacillus psychrodurans</i>	Firmicutes	W_6.5b	<i>Pseudomonas</i> sp.	Gamma- proteobacteria	sMM31	<i>Stenotrophomonas maltophilia</i>	Gammaproteobacteria
rMM21	<i>Cryocolla</i> sp.	Actinobacteria	W_Sd1	<i>Glacihabitans tibetensis</i>	Actinobacteria	sMM32	<i>Micrococcus</i> sp.	Actinobacteria
rMM23	<i>Ochrobactrum intermedium</i>	Alphaproteobacteria	W_Sd2	<i>Rathayibacter</i> sp.	Actinobacteria	sMM33	<i>Stenotrophomonas</i> sp.	Gammaproteobacteria
			W_Sd3	<i>Advenella</i> sp.	Betaproteobacteria	sMM35	<i>Micrococcus luteus</i>	Actinobacteria
			W_Sd4	<i>Pseudomonas</i> sp.	Gamma- proteobacteria	sMM36	<i>Arthrobacter</i> sp.	Actinobacteria
			W_Sd5	<i>Rhodococcus erythropolis</i>	Actinobacteria	sMM40	<i>Streptomyces astroliivaceus</i>	Actinobacteria
			W_Sd8	<i>Mycoplana</i> sp.	Alphaproteobacteria	sMM41	<i>Sphingopyxis bauzanensis</i>	Alphaproteobacteria
			W_Sd9	<i>Enterobacter</i> sp.	Gamma- proteobacteria	sMM43	<i>Micrococcus yunnanensis</i>	Actinobacteria
			W_Sd11	<i>Stenotrophomonas rhizophila</i>	Gamma- proteobacteria	sMM44	<i>Streptomyces ederensis</i>	Actinobacteria
			W_Sd13	<i>Rhodococcus</i> sp.	Actinobacteria	sMM45	<i>Streptomyces spororaveus</i>	Actinobacteria
			W_B4	<i>Pedobacter daejeonensis</i>	Bacteroidetes	sMM46	<i>Bacillus</i> sp.	Firmicutes
			W_B5	<i>Chryseobacterium</i> sp.	Bacteroidetes	sMM47	<i>Kocuria palustris</i>	Actinobacteria
			W_B6	<i>Stenotrophomonas humi</i>	Gamma- proteobacteria	sMM48	<i>Streptomyces atratus</i>	Actinobacteria
			W_B10	<i>Serratia proteamaculans</i>	Gamma- proteobacteria	sMM49	<i>Micrococcus yunnanensis</i>	Actinobacteria
						sMM51	<i>Agrococcus jejunensis</i>	Actinobacteria
						sMMB1	<i>Pseudomonas</i> sp.	Gammaproteobacteria
						sMMB2	<i>Serratia proteamaculans</i>	Gammaproteobacteria

sMMB6	<i>Enterobacter</i> sp.	Gamma proteobacteria
sMMB10	<i>Enterobacter ludwigii</i>	Gamma proteobacteria
sMMB14	<i>Bacillus tequilensis</i>	Firmicutes

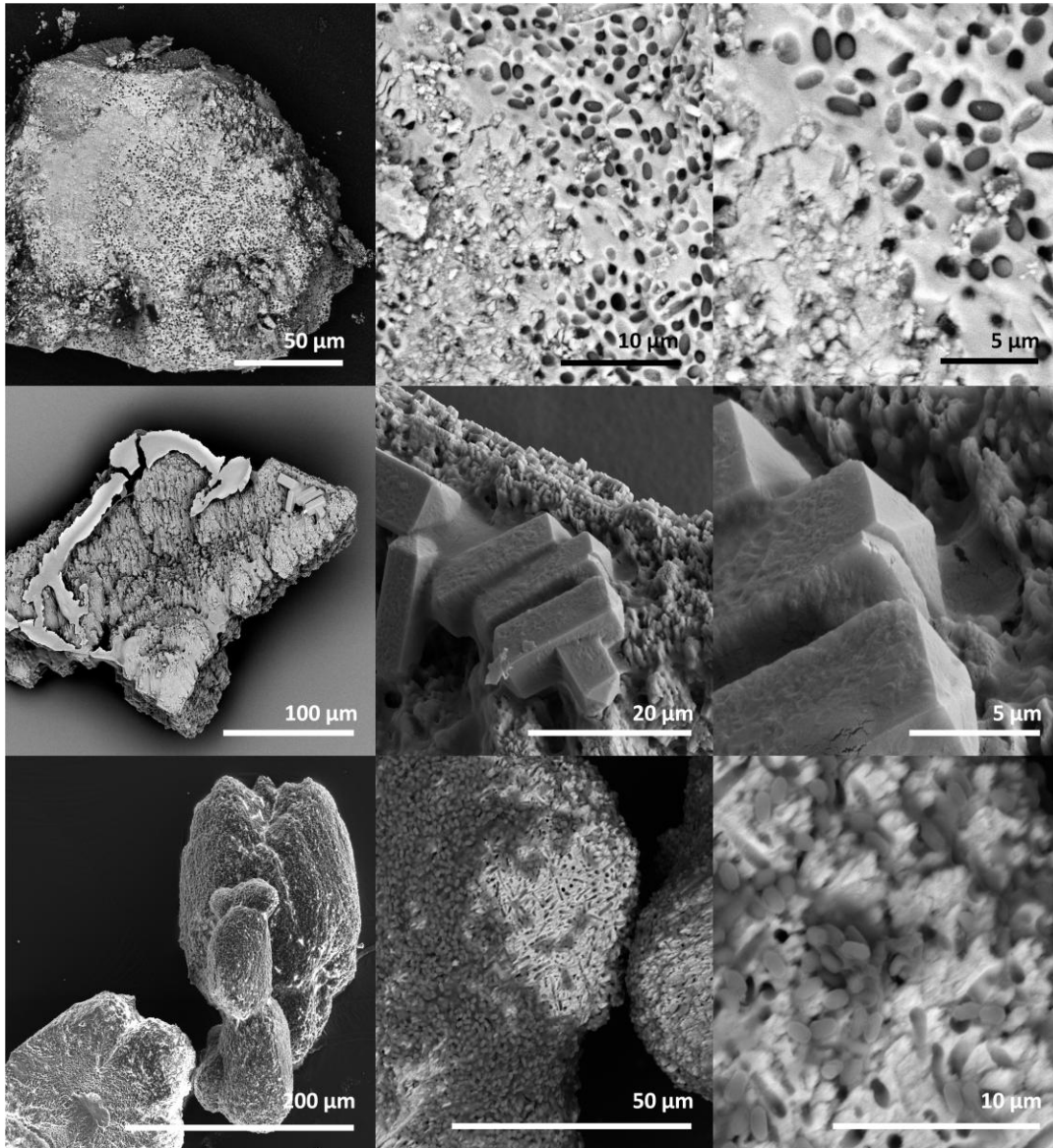


Fig. S1: Biominerals visualized by scanning electron microscopy. *Bacillus flexus* rLM1.5 (A), *Comamonas koreensis* W_5.3b (B), *Bacillus* sp. rMM10 (C) are shown, each for an overview of crystal shapes, partly covered with organic matrix, and high magnification to give insight into surface and microcrystalline structures. Some minerals are settled by bacterial cells leaving holes after lysis.

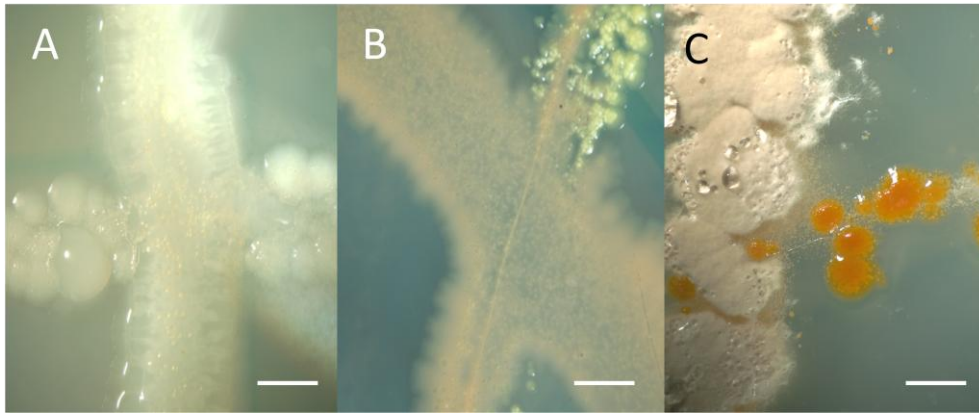


Fig. S2: Interactions with effects on formation of biominerals. More crystals were produced in the interaction zone between *L. amnigena* S_H3 and *Pseudomonas* sp. (A), crystal formation was reduced at the contact zone between *Micrococcus luteus* rLMc and *Bacillus muralis* rLMd (B). *Moraxella osloensis* sMM16 vs. *Agrococcus jejunensis* sMM51 showed overgrowth (C).