

Supplementary Information

Living lithic and sublithic microbial communities in Namibian drylands

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Figure S2: Abundances of bacterial 16S rRNA gene revealed by quantitative PCR from Tsauchab Valley, Namibia. Limestone, quartz-rich shale and quartz-rich sandstone were quantified by three intersections across their weathering profile from unaltered core over the subsurface to the surface and compared to adjacent soil. Standard deviations are indicated by an error bar

Table S1: Sampling list including sample alias and location.

Table S2: Identification of microorganisms from limestone and quartz-rich sandstone based on Sanger sequencing. Medium R2S for facultative heterotrophic aerobes and SSM for mineral solubilizing bacteria (sucrose salt medium). N: Number of isolates

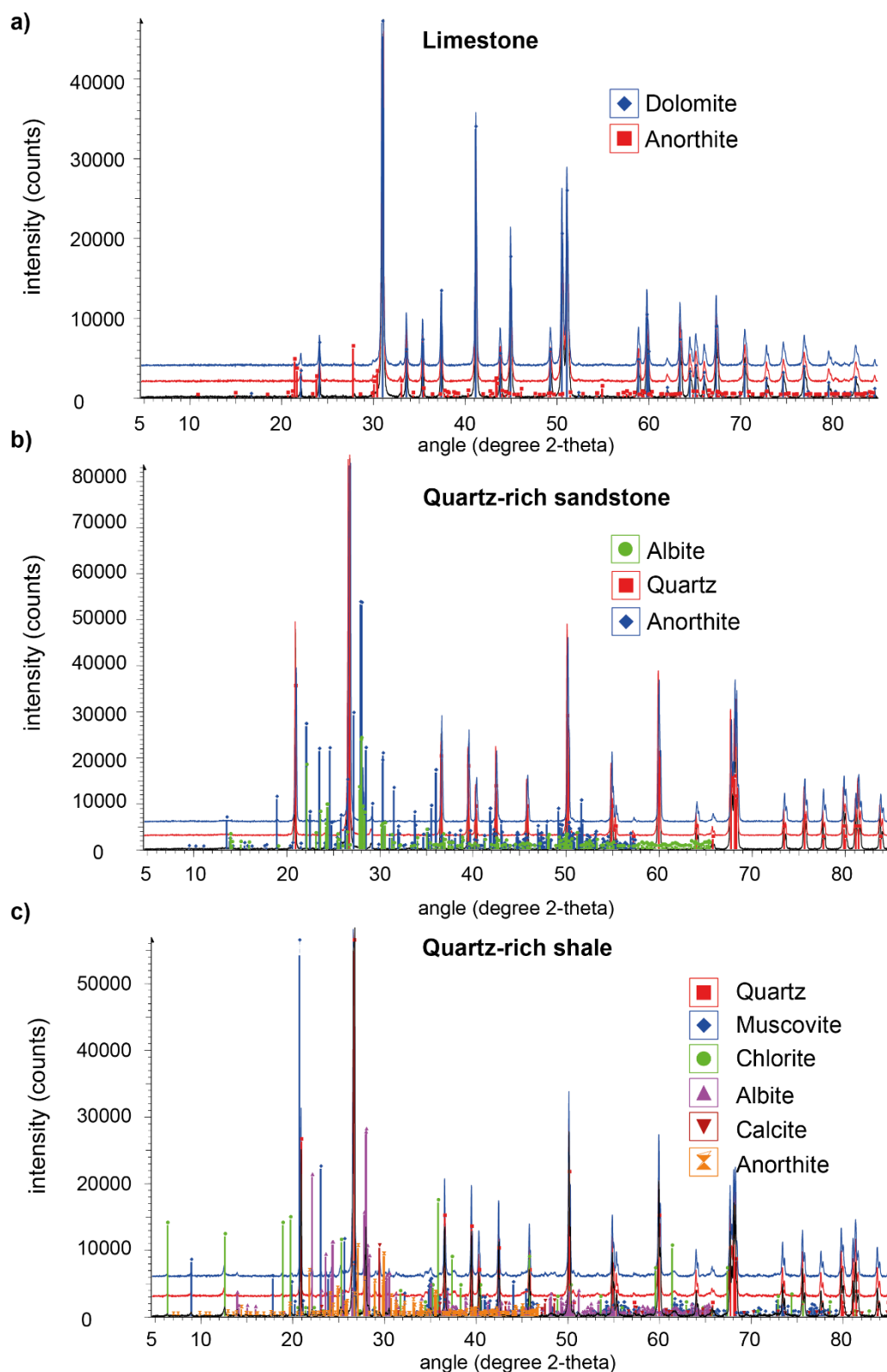


Figure S1: Mineral composition of rock samples using XRD.

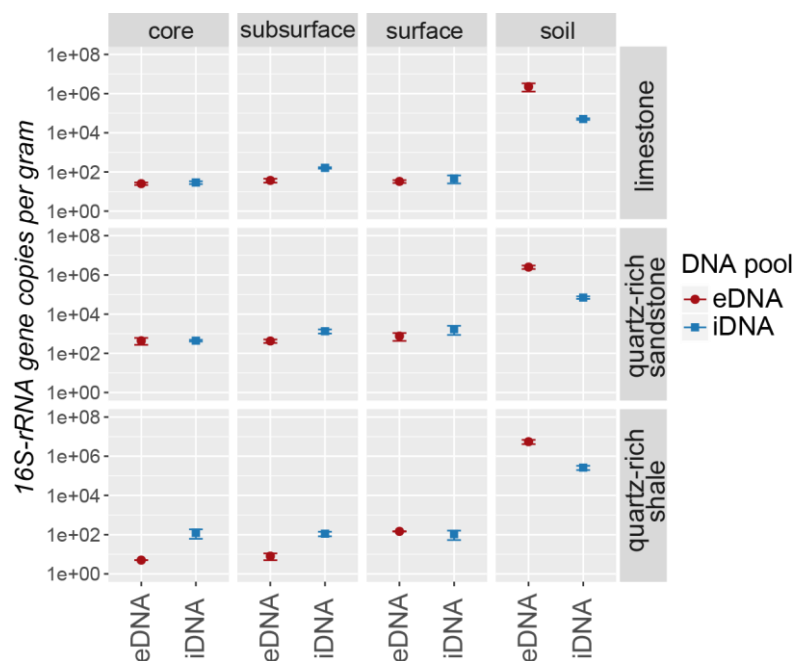


Figure S2: Abundances of bacterial 16S rRNA gene revealed by quantitative PCR from Tsauchab Valley, Namibia. Limestone, quartz-rich shale and quartz-rich sandstone were quantified by three intersections across their weathering profile from unaltered core over the subsurface to the surface and compared to adjacent soil. Standard deviations are indicated by an error bar.

Table S1: Sampling list including sample alias and location.

Project	03G0861B		
short title	Lithic microbial communities of dryland samples		
Collection date	18.03.2017		
location	Namibia		
geographic location	24°26,37'S,		
geographic location	016°10,31'E		
geographic elevation	1160 m		
geographic region	Tsauchab River Valley, Namibia		
sample alias	DNA pool	material	section
A1103	eDNA	limestone	surface
A1201	eDNA	limestone	core
A1202	eDNA	limestone	subsurface
A1203	eDNA	limestone	surface
A1401	eDNA	quartz-rich sandstone	core
A1402	eDNA	quartz-rich sandstone	subsurface
A1403	eDNA	quartz-rich sandstone	surface
A1501	eDNA	quartz-rich sandstone	core
A1502	eDNA	quartz-rich sandstone	subsurface
A1503	eDNA	quartz-rich sandstone	surface
A1601	eDNA	quartz-rich shale	core
A1602	eDNA	quartz-rich shale	subsurface
A1603	eDNA	quartz-rich shale	surface
B1101	iDNA	limestone	core
B1202	iDNA	limestone	subsurface
B1203	iDNA	limestone	subsurface
B1402	iDNA	quartz-rich sandstone	subsurface
B1403	iDNA	quartz-rich sandstone	core
B1601	iDNA	quartz-rich shale	core
B1602	iDNA	quartz-rich shale	subsurface
B1602	iDNA	quartz-rich shale	subsurface
A1106	eDNA	soil	limestone
A1206	eDNA	soil	limestone
A1406	eDNA	soil	quartz-rich sandstone
A1506	eDNA	soil	quartz-rich sandstone
A1606	eDNA	soil	quartz-rich shale
B1106	iDNA	soil	limestone
B1206	iDNA	soil	limestone
B1406	iDNA	soil	quartz-rich sandstone
B1506	iDNA	soil	quartz-rich sandstone
B1606	iDNA	soil	quartz-rich shale
	negative		
X00000	control		
Z11111	positive control	E. coli	

Table S2: Identification of microorganisms from limestone and quartz-rich sandstone based on Sanger sequencing. Medium R2S for facultative heterotrophic aerobes and SSM for mineral solubilizing bacteria (sucrose salt medium). N: Number of isolates

Phylum Identification		Medium	N	% GenBank accession Identity number
Limestone	 <i>Protaetiibacter</i> sp.	R2A	1	97 CP059987
	 <i>Arthrobacter</i> sp.	R2A, SSM	2	98 – 99 CP019304
	 <i>Kocuria rosea</i>	R2A	1	98 LR134391
	 <i>Streptomyces</i> sp.	R2A, SSM	2	99 – 100 KC336160, CP050504
	 <i>Streptomyces</i>	SSM	1	100 AB184448
	 <i>ansochromogenes</i>			
	 <i>Bacillus axarquiensis</i>	R2A	1	98 KY608836
	 <i>Bacillus paralicheniformis</i>	R2A	2	99 CP033198
	 <i>Bacillus niacini</i>	R2A	1	98 BCVA01000102
	 <i>Microvirga</i> sp.	R2A	1	99 CP029481
Quartz-rich sandstone	 <i>Massilia</i> sp.	R2A	2	97 – 98 CP012640
	 <i>Microbacterium</i> sp.	R2A, SSM	3	99 – 100 CP043430
	 <i>Arthrobacter</i> sp.	R2A	1	98 AY618581
	 <i>Lechevalieria</i> sp.	R2A	1	99 FJ911538
	 <i>Streptomyces</i> sp.	SSM	3	99 – 100 LC429299, KC336160, CP050504
	 <i>Streptomyces reticuli</i>	SSM	1	100 LN997842
	 <i>Bacillus subtilis</i>	R2A, SSM	4	99 – 100 MN704542, MT643824, MT641205, CP018184
	 <i>Bacillus tequilensis</i>	R2A	1	99 MT326211
	 <i>Actinobacteria</i>			
	 <i>Firmicutes</i>			
	 <i>Proteobacteria</i>			

