

Highest diversity of cyanobacterial on granite substrates in the Sør Rondane Mountains

INTRODUCTION

Cyanobacteria form macroscopically visible crusts or thin biofilms on the surface of soils and rocks, or occupy endolithic niches in **ice-free regions of Antarctic mountains**.

Some taxa are able to fix atmospheric nitrogen, favouring the growth of microbial communities in oligotrophic terrestrial environments.

They are **key primary producers** in the terrestrial environments throughout the Poles.

GOAL OF OUR STUDY

Investigate the cyanobacterial diversity in the Sør Rondane Mountains and its link with the type of substrate (gneiss vs. granite).

METHODS

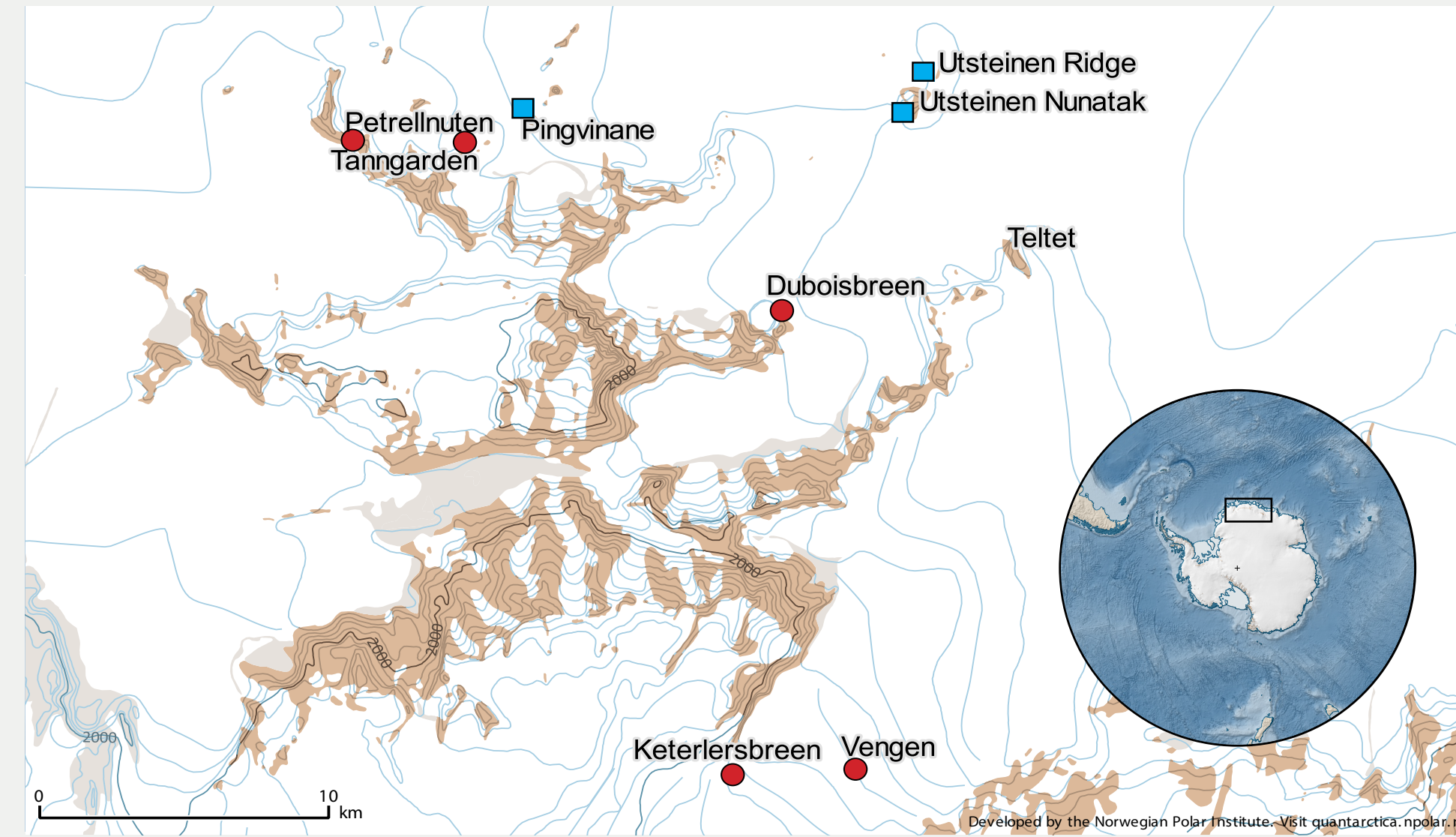


Fig. 1 Location of the sampling sites in the vicinity of the Princess Elisabeth Station (Utsteinen ridge). Red dots = gneiss; bluesquares=granite.

Samples were collected in **10 sites** characterized by both granite and gneiss substrates around the Belgian Station Princess Elisabeth (Fig. 1) between 2007 (before the building of the Station), 2009 and 2010. **126 samples** were analyzed through **light microscopy** and a **selection of 27** was further studied by **DGGE** (Denaturing Gradient Gel Electrophoresis) based on the **16S rRNA gene**. A **new DNA extraction protocol** was especially designed for taxa presenting large polysaccharidic sheaths.

RESULTS

Morphological observations

- **15 morphotypes** (Fig. 3, Table 1);
- The **most representative taxa** in all samples were *Aphanocapsa* sp., *Coleodesmium* sp. or *Nostoc* sp. characterized by yellow, red, brown or dark-blue pigments and thick sheaths;
- **Heterocystous cyanobacteria** were present in all the 28 crust samples, but more sporadically in the other sample types;
- **Crusts** followed by gravel were the **richest sample types**;
- **Granitic rocks** hosted the **most diverse communities**.

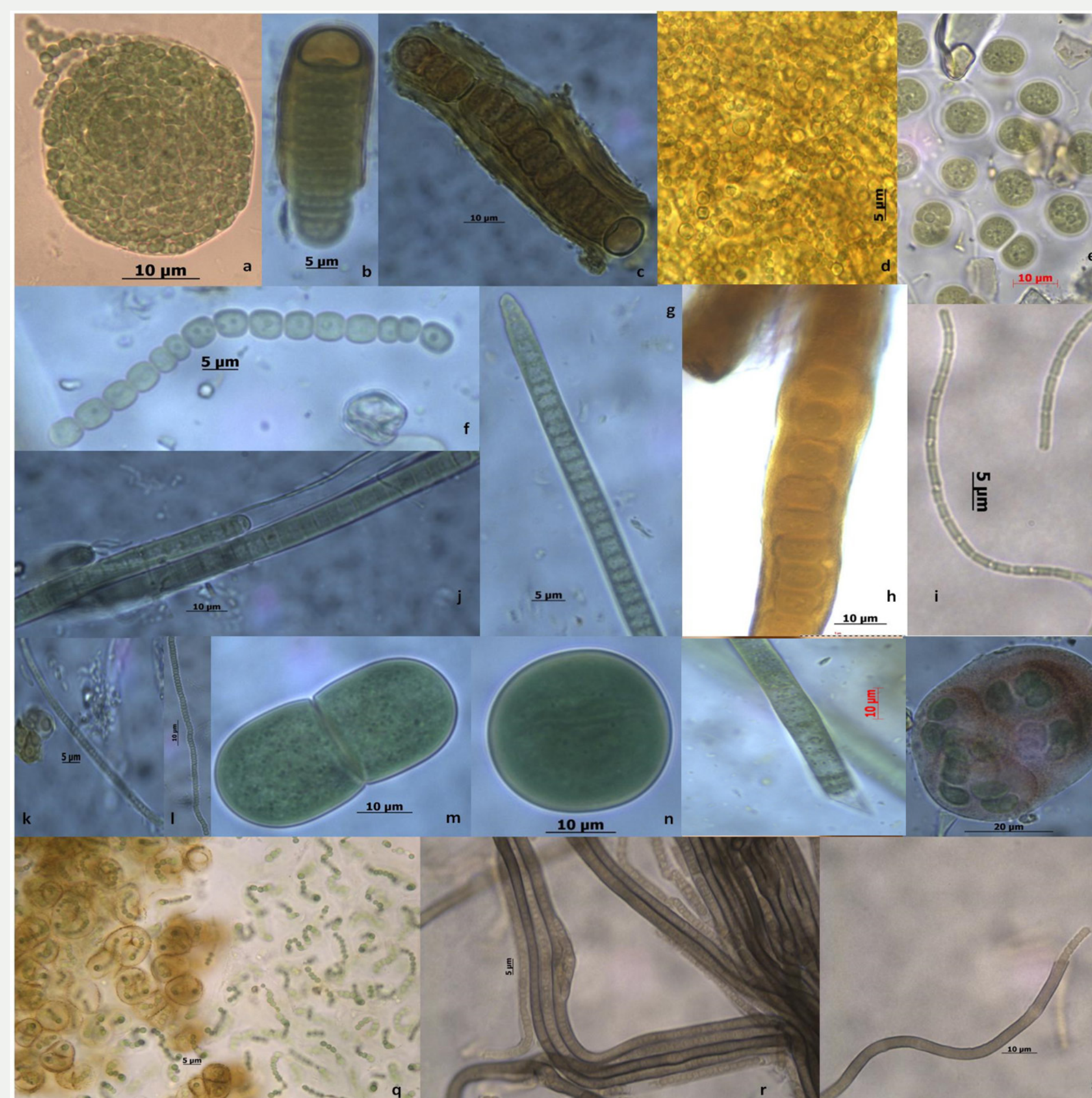


Fig. 3 Morphological identification of cyanobacteria (a) *Nostoc commune* (b,c,e,f) *Coleodesmium* sp. (e) *Chroococcus* sp. (j,g) *Phormidium* sp. (h,o) *Phormidium autumnale* (i) *Leptolyngbya antarctica* (k,l) *Phormidium priestleyi* (m,n) *Cyanotheca aeruginosa* (p) *Asterocapsa* sp. (q) *Nostoc commune* culture (r,s) *Phormidium* sp. culture.

Table 1. Distribution of the 15 morphotypes

	KE	NUN	PE	PI	RUN	TA	VN	
<i>Phormidium autumnale</i>	+	+	+	+	+	+	+	Filamentous cyanobacteria with thin sheath
<i>Ph. priestleyi</i>	-	+	-	+	+	+	-	
<i>Leptolyngbya</i> sp.	+	+	-	+	+	+	-	
Oscillatoria	-	+	+	+	-	-	-	Heterocystous cyanobacteria with thick sheath
<i>Calothrix</i> sp.	-	+	-	+	+	-	-	
<i>Tolypothrix</i> sp.	+	+	+	+	+	+	+	
<i>Coleodesmium</i> sp.	-	+	+	+	+	+	-	
<i>Nostoc commune</i>	+	+	+	+	+	+	+	
Nostocales	-	+	+	+	+	+	-	Unicellular cyanobacteria with thick sheath
<i>Stigonema</i> sp.	-	+	-	+	+	-	-	
<i>Aphanocapsa</i> sp.	+	-	-	+	+	-	-	Unicellular cyanobacteria without sheath
<i>Gloeocapsa</i> sp. (<i>Asterocapsa</i> sp.)	-	+	-	+	+	-	-	
<i>Chroococcus</i> sp.	-	+	-	+	+	-	-	
<i>Synechococcus</i> sp.	-	-	-	+	-	-	-	Unicellular cyanobacteria without sheath
<i>Cyanotheca aeruginosa</i>	+	+	+	+	+	+	-	

DU: Duboisbreen, KE: Katerlersbreen dry valley, NUN: Utsteinen nunatak north, PE: Petrelnutten nunatak, PI: Pingvinane nunataks, RUN: Utsteinen ridge north, TA: Tanngarden, VN: Vengen, UN: Utsteinen nunatak, UR: Utsteinen ridge.

DGGE observations

- **34 OTUs** (Operational Taxonomic Unit) sharing $\geq 97.5\%$ of 16S rRNA similarity (from the 130 obtained sequences; Fig. 4);
- The **OTUs' richness** varied between 1 and 5 per sample.
- Morphotypes were higher in number compared to the OTUs in most samples;
- ***Phormidium* / *Microcoleus* sp.** was the most frequently observed OTU;
- **No OTU was common** to all the studied sites;
- **Utsteinen ridge, Utst. nunatak and Pingvinane nunataks** were the **richest in OTUs**. The latter two sites shared 6 OTUs.

CONCLUSION

Granites are highly stable rocks that probably favor the cyanobacterial community development. The common local cyanobacterial diversity may be explained by similar environmental conditions and local dissemination by winds. New field campaigns in the frame of the **MICROBIAN** project (www.microbian.ugent.com) will give new insights into the cyanobacterial diversity, functioning and distribution in the Sør Rondane Mountains, which will be also of interest for the designation of ASPA sites.

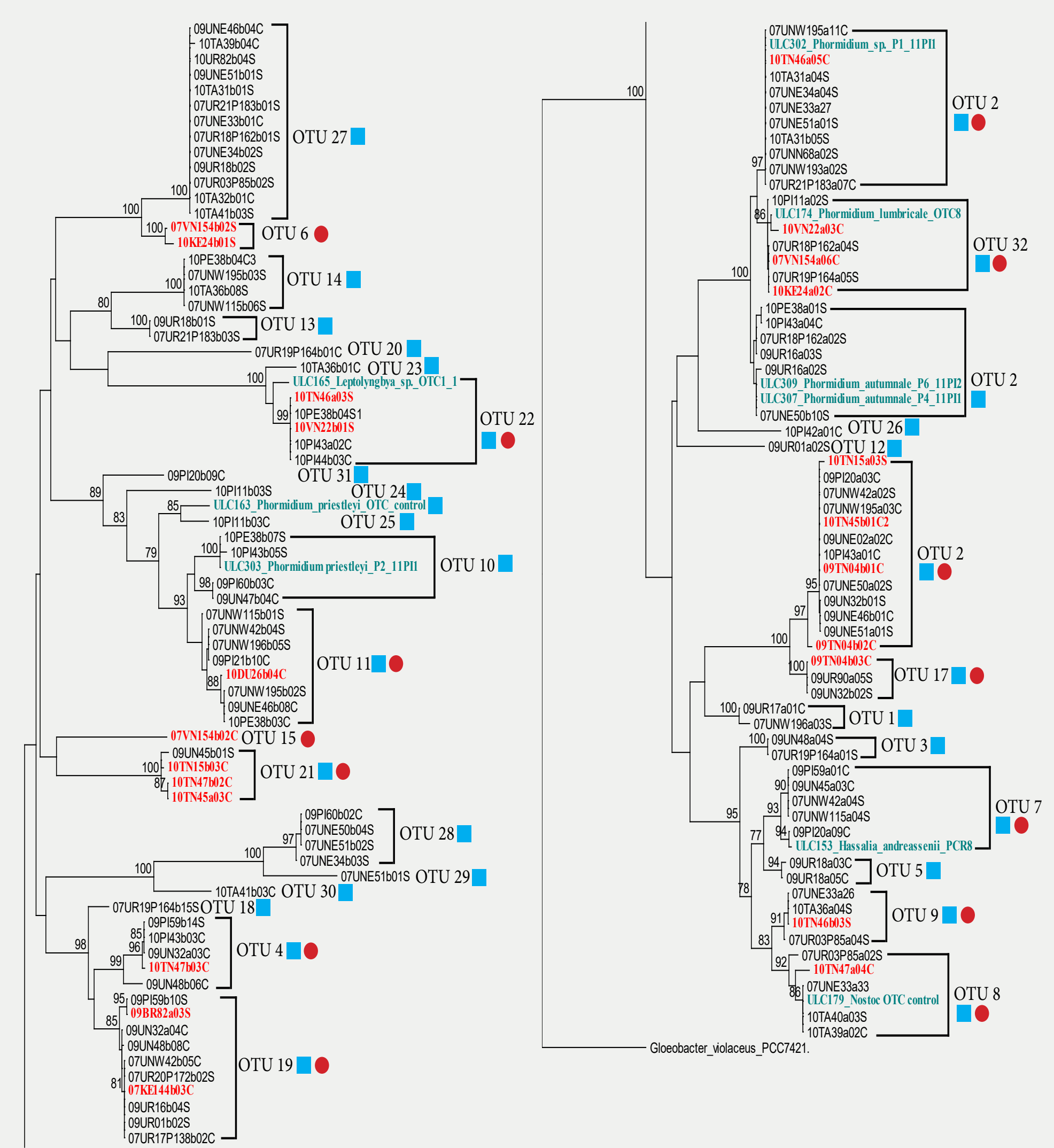


Fig. 4 Neighbor-joining tree based on the 16S rRNA sequences from DGGE bands. A bootstrap analysis was performed with 500 resampled trees. Red dots = gneiss; blue squares= granite.