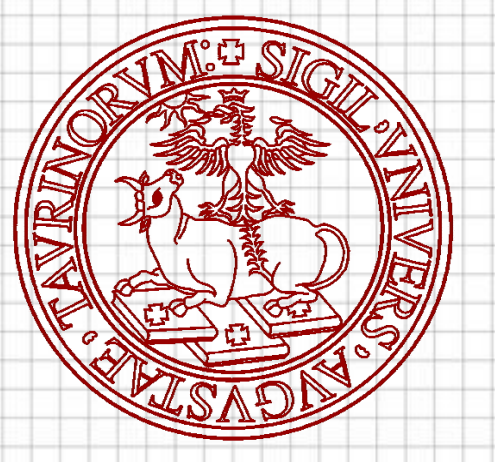


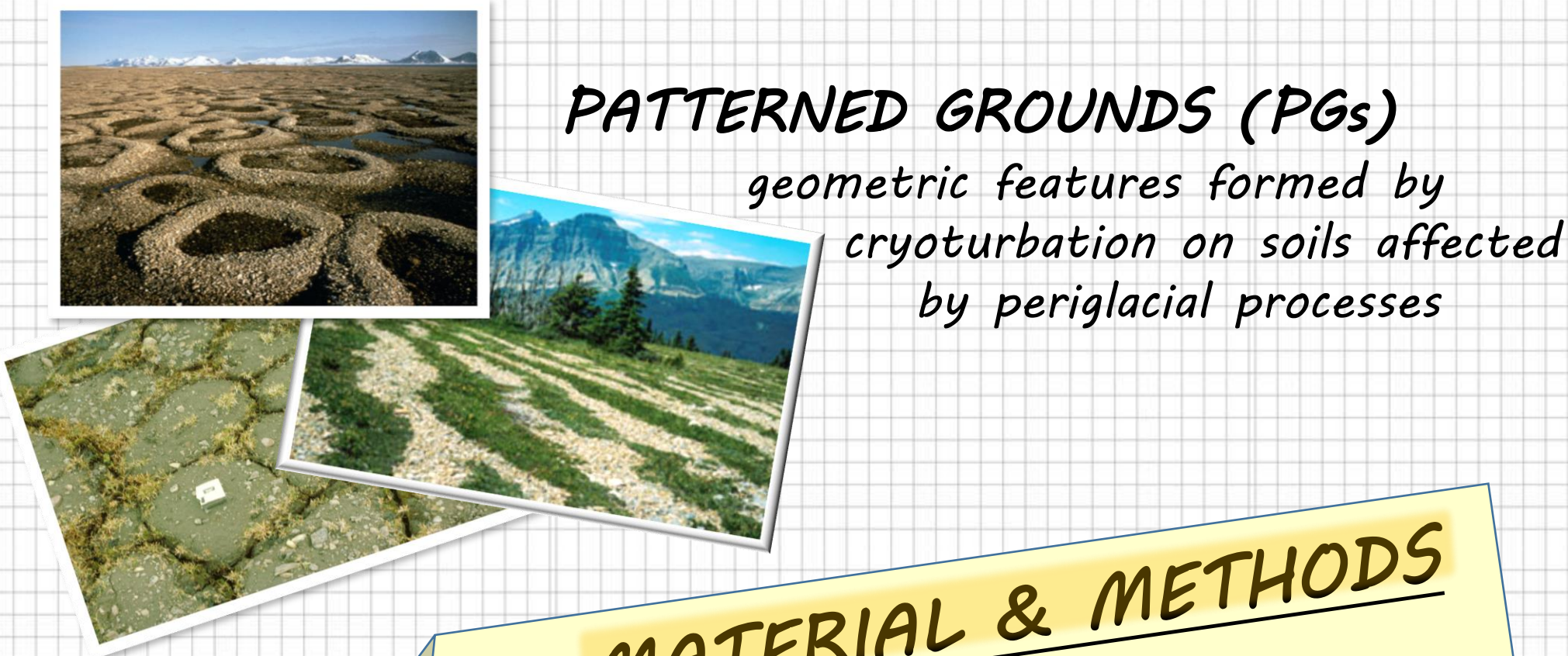
Diversity and small-scale distribution of microbial communities in Patterned Grounds

*Mania I., Freppaz M., D'Amico M., Gorra R.

DISAFA, University of Turin, Largo P. Braccini 2, 10095 Grugliasco (TO), Italy



A PRELIMINARY INVESTIGATION



PATTERNED GROUNDS (PGs)

geometric features formed by cryoturbation on soils affected by periglacial processes

Many studies describing PGs morphology and formative processes, BUT microbiological aspects yet greatly unexplored

Microbial communities may play important roles in nutrient availability, dynamics and stabilization in ecosystem evolution!

AIM: give insights on microbiological processes affecting PG features and find microbial markers potentially useful to explain and predict the evolution of cryoturbated ecosystems

MATERIAL & METHODS

•PCR-DGGE + band sequencing

Phylogenetic markers:

Archaeal and bacterial 16S
Fungal 26S

•qPCR

Phylogenetic markers:

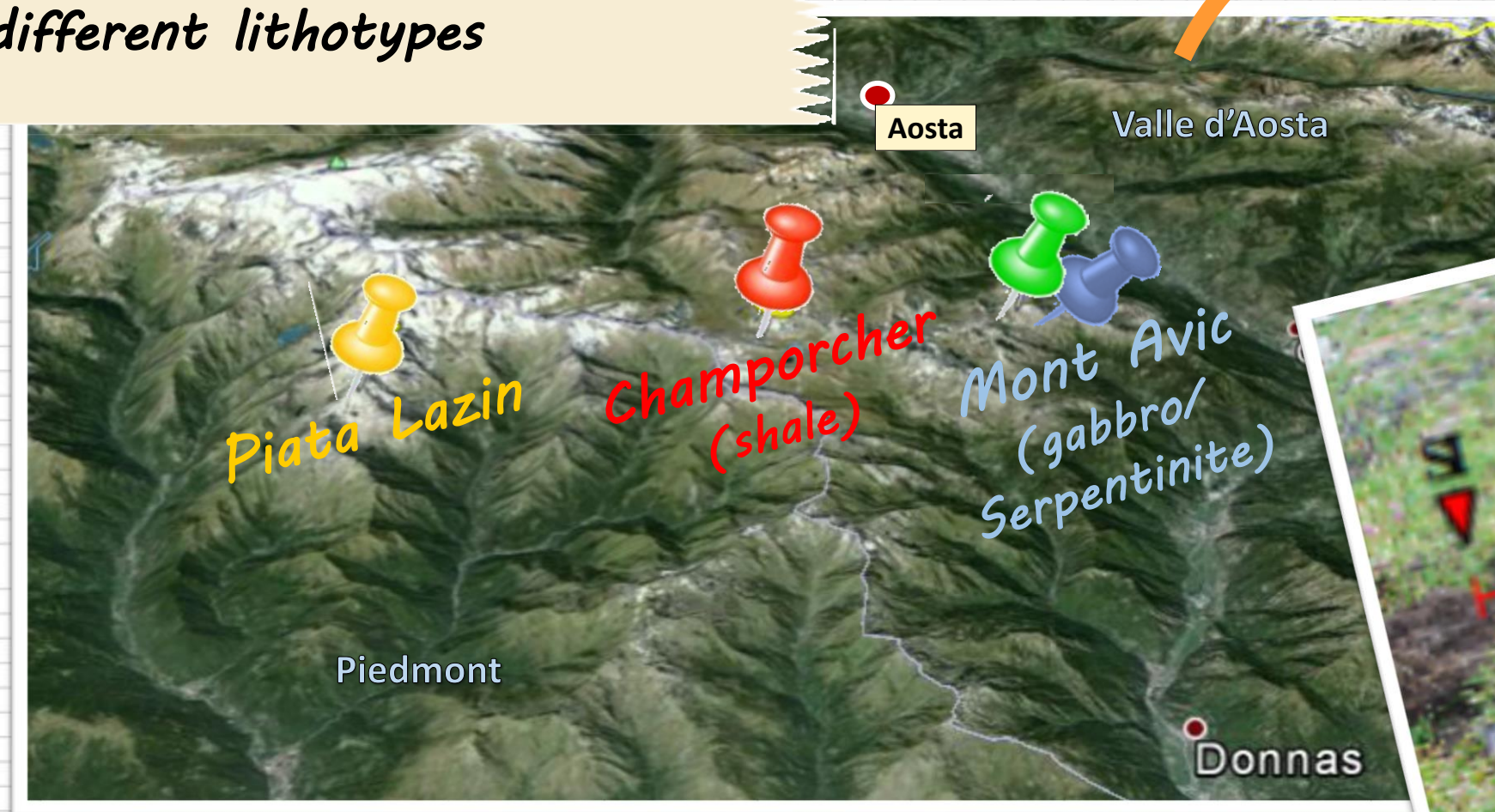
Archaeal and bacterial 16S
Fungal 26S

Diversity & structure

Abundance & distribution

EXPERIMENTAL PLAN

3 areas in NW alps (Italy),
4 different lithotypes

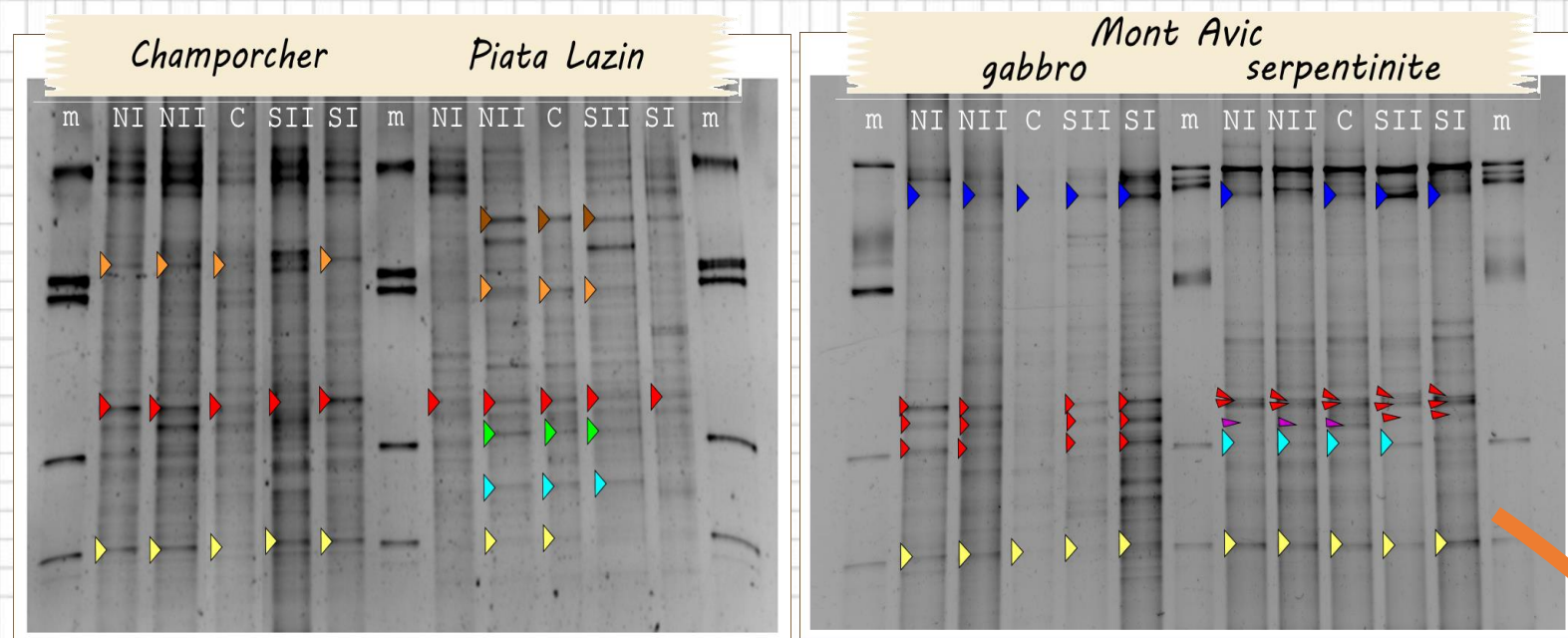


1 circular PG from each site

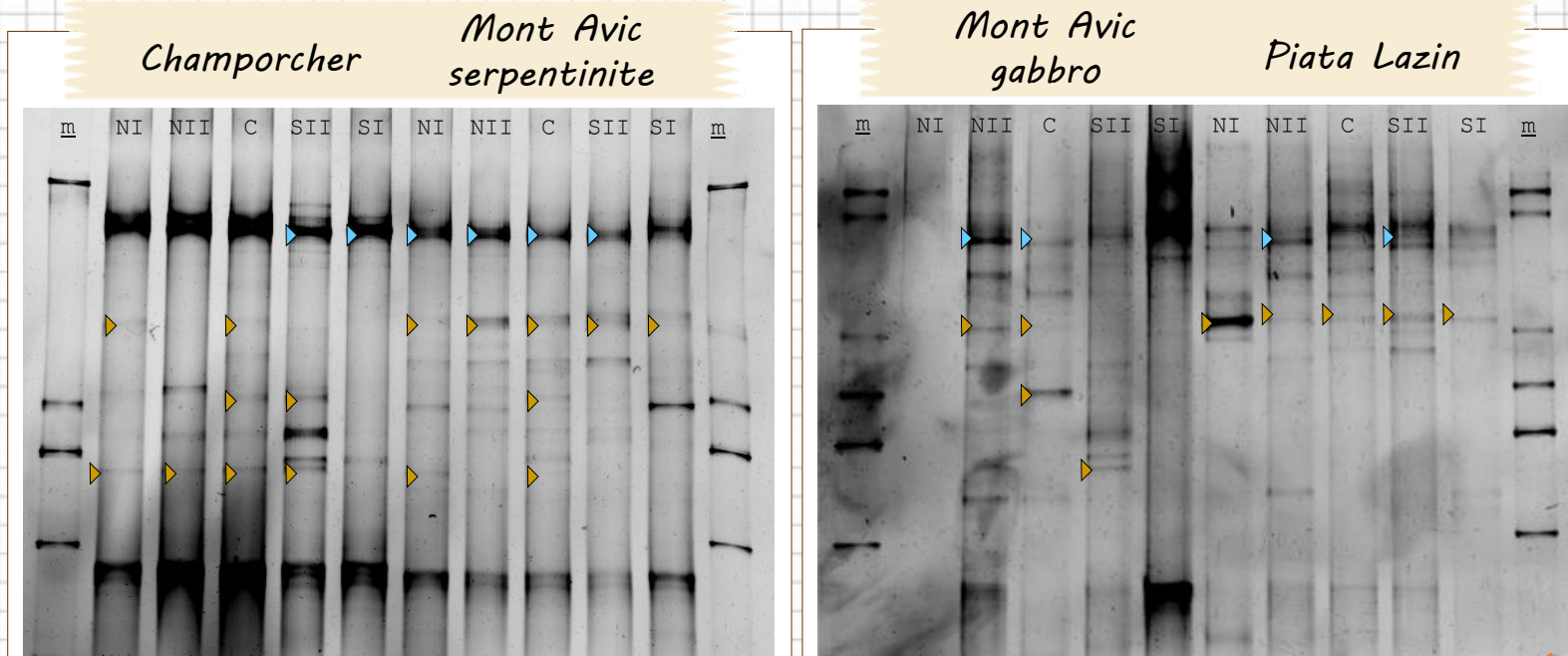
Each PG: 5 sampling points along a N-S transect

Metagenomic DNA extraction

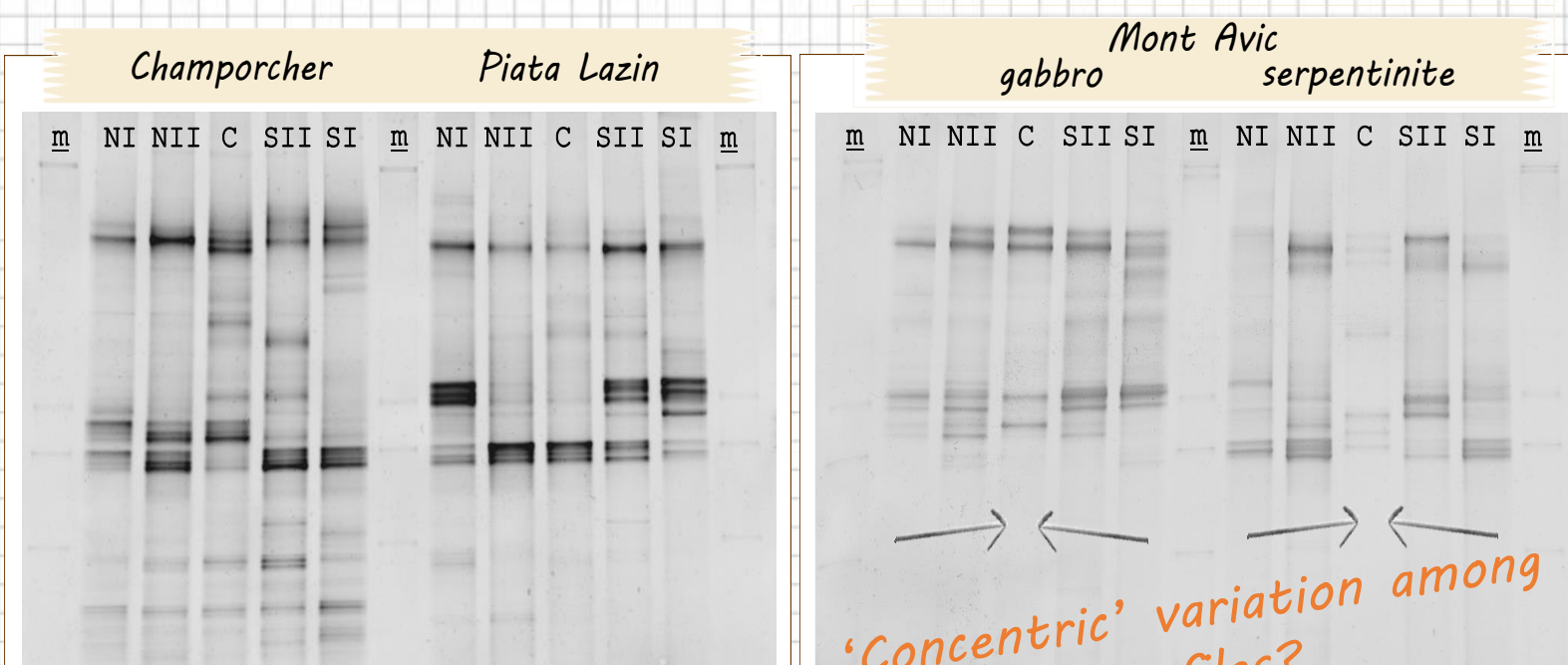
Bacteria



Fungi



Archaea



'Concentric' variation among profiles?

RESULTS

Autotrophy + heterotrophy

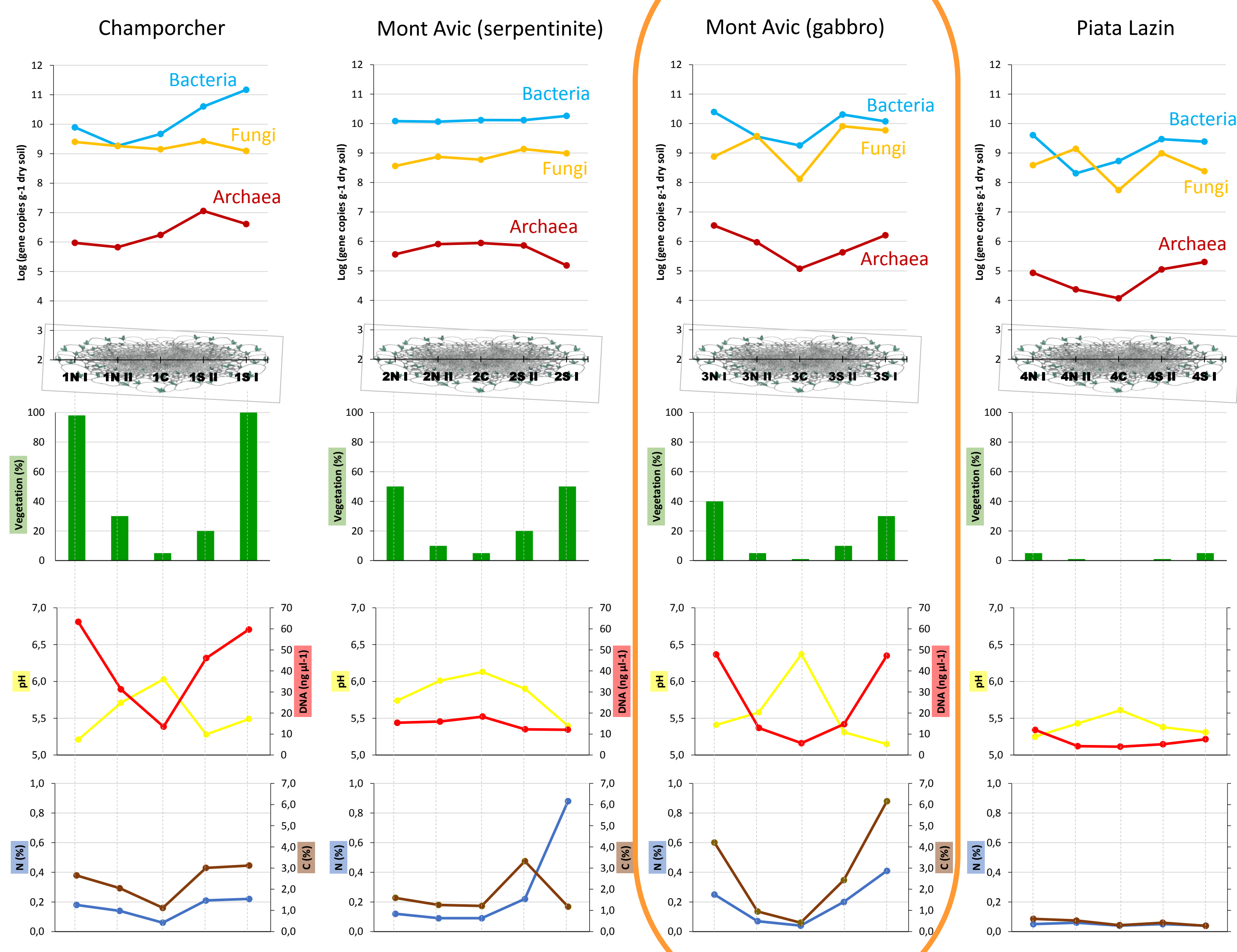
Closest relative	Isolation source/habitat	Similarity	Phylum	Closest described relative	Similarity	Presence in different sites			
						1	2	3	4
						Cham	MA (serp)	MA (gab)	Piata L
<i>Nitrobacter winogradskyi</i> (NR_074324)	soil	100	Alphaproteobacteria	<i>Nitrobacter winogradskyi</i> (NR_074324)	100	X	X	X	X
Uncultured bacterium clone BB-80 (KF494605)	permafrost	99	Alphaproteobacteria	<i>Snorhizobium fredii</i> (NR_102919)	97	X	X		X
Uncultured bacterium isolate DGGE gel band 02_F2 clone O1 (JX986102)	soil	99	Alphaproteobacteria	<i>Phaeosporium fulvum</i> (NR_025836)	94	X	X	X	X
Uncultured bacterium clone KA13 (JQ973360)	forest soil	96	Alphaproteobacteria	<i>Microvirga guangxiensis</i> (NR_044563)	95	X	X	X	X
Bacterium PE03-55G21 (AB127830)	eutrophic lake	97	Alphaproteobacteria	<i>Filomicrobium insigne</i> (NR_044095)	95	X		X	
Uncultured bacterium clone GD25:G9RADRH03H1H4 (JX808480)	soil (Lava Beds National Monument)	84	Alphaproteobacteria	<i>Bradyrhizobium</i> sp. (X70403)	85		X		
<i>Edaphobacter aggregans</i> (NR_043898)	forest soil	95	Acidobacteria	<i>Edaphobacter aggregans</i> (NR_043898)	95	X	X	X	X
Uncultured SOIL BACTERIUM clone GC0AAAZA03P1 (JQ919779)	soil	96	Bacteroidetes	<i>Pedobacter borealis</i> (NR_044381)	88		X	X	
<i>Pseudomonas antarctica</i> (NR_025586)	McMurdo Valley, Antarctica	100	Gammaproteobacteria	<i>Pseudomonas antarctica</i> (NR_025586)	100	X			X
<i>Arthrobacter ramosus</i> (AF387692)	Himalaya	90	Actinobacteria	<i>Arthrobacter ramosus</i> (AF387692)	90		X		
<i>Chloroflexi bacterium</i> Ellin7237 (AY673403)	soil	86	Actinobacteria	<i>Tetrasphaera australiensis</i> (NR_024975)	82				X
Uncultured bacterium clone HF127 (KJ037272)	soil	97	Betaproteobacteria	<i>Nitrosospora multiformis</i> (NR_074736)	93		X		
Uncultured bacterium clone P15-43 (GQ287601)	periglacial soil, Himalaya	100	Verrucomicrobia	<i>Prostheco bacterium fluvialis</i> (NR_041608)	86	X			
Uncultured bacterium isolate 111286939975 (HQ11871)	forest soil	95	Verrucomicrobia	Bacterium Ellin507 (AY960770)	90				X
<i>Chroococcales cyanobacterium</i> PE566 (HE805950)	lake water	86	Cyanobacteria	<i>Cyanobium gracile</i> (NR_102447)	85				X
Uncultured fungus clone 126_NA10_P32_C19 (KC966197)	Patterned Grounds (North America)	98	Ascomycota	<i>Coniochaeta</i> sp. (AB752287)	97	X	X	X	
<i>Pleiosporales</i> sp. (JX244063)	<i>Populus deltoides</i> roots	95	Ascomycota	<i>Pleiosporales</i> sp. (JX244063)	95	X	X	X	
Uncultured fungus clone 112_NA3_P31_P17 (KC966078)	Patterned Grounds (North America)	97	Ascomycota	<i>Geomyces</i> sp. (AB752279)	97	X	X	X	X
<i>Cortinarius cf. saniosus</i> (FN687648)	Alpine soil (Salix herbacea roots)	97	Basidiomycota	<i>Cortinarius cf. saniosus</i> (FN687648)	97	X	X		
<i>Clavulina cf. cristata</i> (AF238225)	Guiana Massif	89	Basidiomycota	<i>Clavulina cf. cristata</i> (AF238225)	89			X	X

Ubiquitous phylotypes: Alphaproteobacteria and Acidobacteria

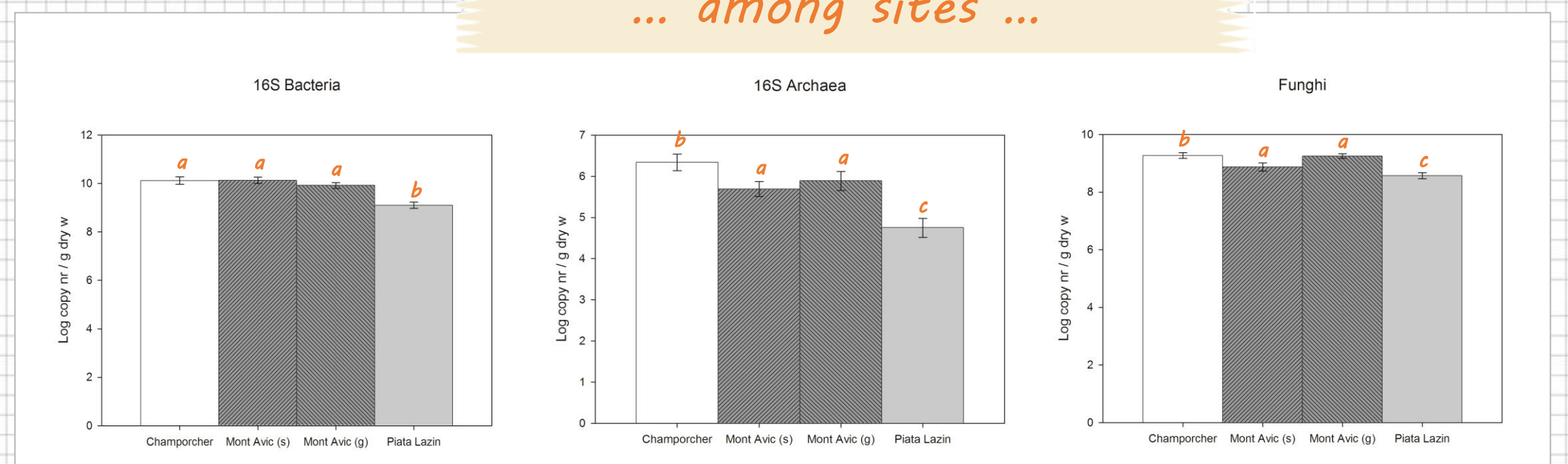
Microbial structure analysis revealed:

- relatively homogeneous community within circles, but also among different PGs
- presence of several phylotypes previously observed in other PGs and cold environments (*)
- only for Archaea stronger differences in community composition on small-scale

... small scale ...

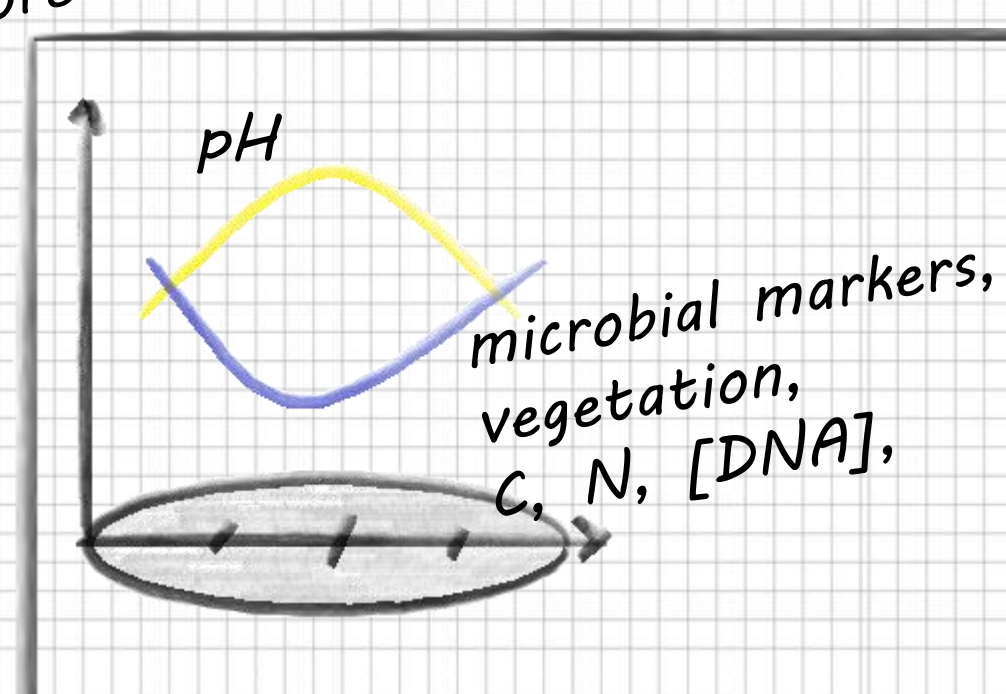


... among sites ...



Significant differences in abundance among sites BUT low variability between Mont Avic PGs (same area, different lithology)

Concentric distribution of microbial markers, coherent with trend of physicochemical parameters (more evident in Mont Avic - gabbro)



Strong correlation (P < 0.05) Microbial markers vs C/N

Conclusions

These first results highlight the importance of cryoturbation in shaping microbial communities in permafrost soils, particularly affecting their quantitative distribution. If, on one hand, this could be linked to a mere mechanical sorting activity exercised on microbial biomass by soil and water mixing, on the other the presence of a concentrically differentiated archaeal population suggest a more complex situation, with microorganisms actively involved in ecosystem modelling and evolution.

More information from functional genes?

Diversity & Structure

Abundance & Distribution