Effects of elevated pCO_2 and temperature on prokaryotic community composition and respiration in mesopelagic waters of the NW Mediterranean Sea

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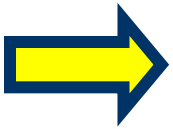
pCO_2, temperature and prokaryotic plankton

Effects of ocean acidification for the diversity and activity of prokaryotic plankton have been demonstrated in SOME studies with surface waters

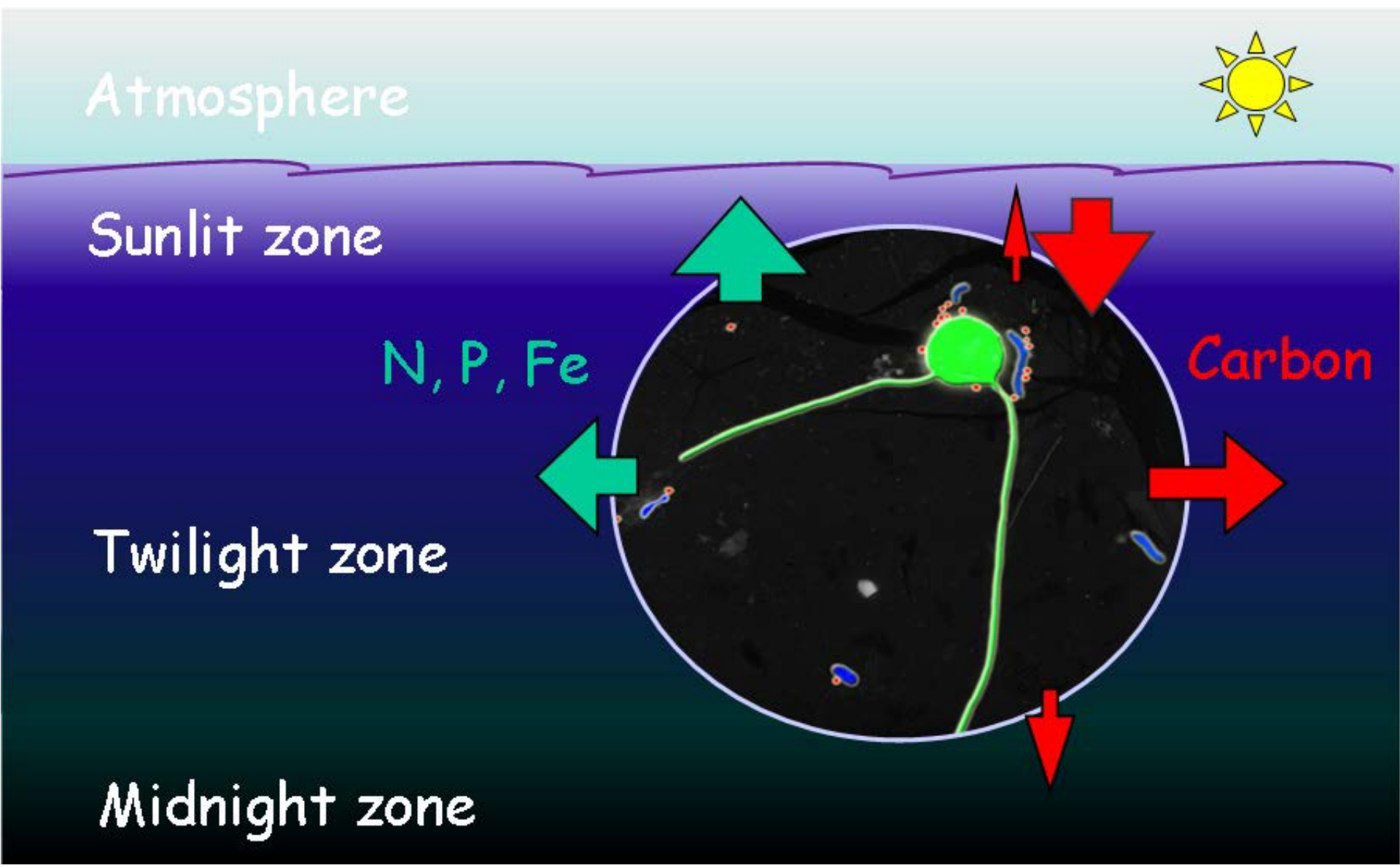
Elevated temperature should stimulate prokaryotic activity (respiration, enzymatic activity)



Nothing is known for mesopelagic prokaryotic plankton

Objective

To investigate the effects of elevated pCO_2 and temperature for the community composition and respiration of prokaryotic plankton in mesopelagic waters of the NW Mediterranean Sea



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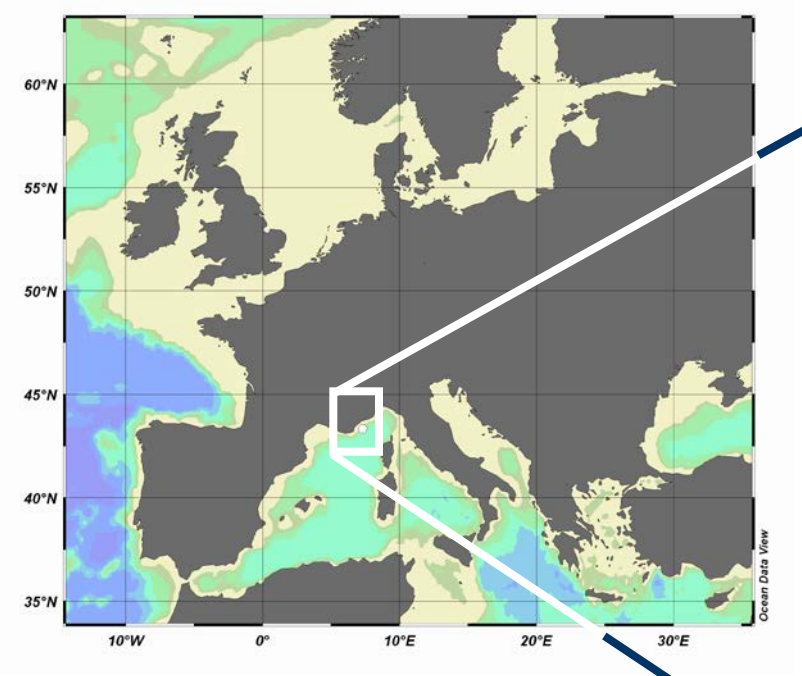
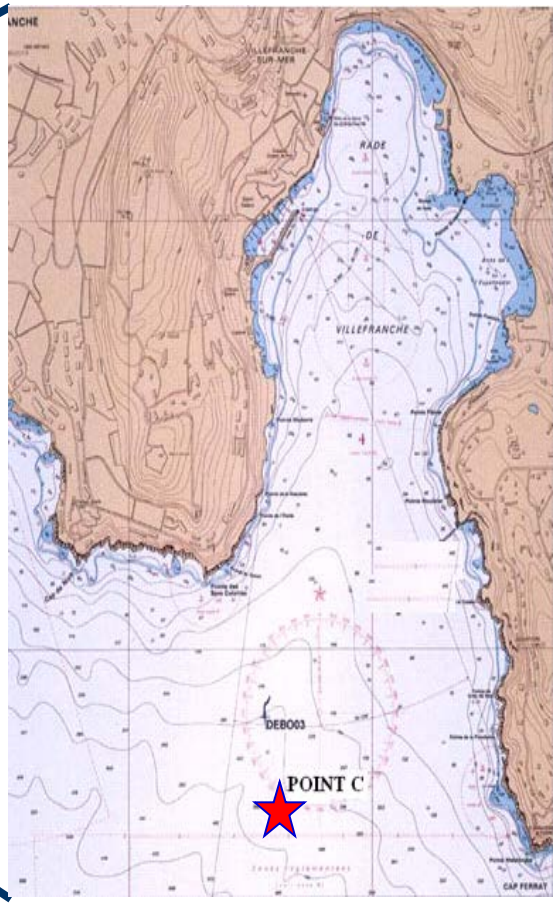
Study Site



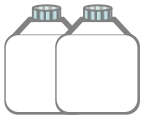
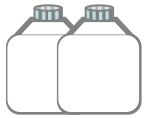


Sampling: Bay of Villefranche, France
Point C (Lat.43°40'N, Long.7°18'E)

Depth: 300 m

Short-term perturbation experiments

Five short-term experiments (5 days, between 2008 and 2009)

pCO2	**Temperature**	
	13° C	16° C
Pre-industrial		
Ambient (400 µatm)		
Two values higher than ambient		
End of century (1000 µatm)		
Higher than end of century		

Approach

Establishment of desired pCO2 levels by bubbling all treatments for 30 min with various mixtures of pCO2 reduced air and pure CO2.

Incubation of 5L bottles in a temperature controlled chamber in the dark with water tanks heated to 13˚ C and 16˚ C.

Prokaryotic respiration along the pCO2 gradient

Exp	**13° C**		**16° C**	
	T3d	T5d	T3d	T5d
STE-1			+	
STE-2			-	
STE-3	+		+	+
STE-4	Hump			
STE-5	+	+		-

+,-: pos or neg relationship based on linear, logarithmic, exponential or power functions

Hump: 2nd order polynomial function (in case +/- not significant; p>0.05)

Conclusions: short-term experiments

In nine out of 20 cases (five experiments times two time points times two temperatures), a significant relationship between PR and pCO2 levels was found, however, the trend was inconsistent.

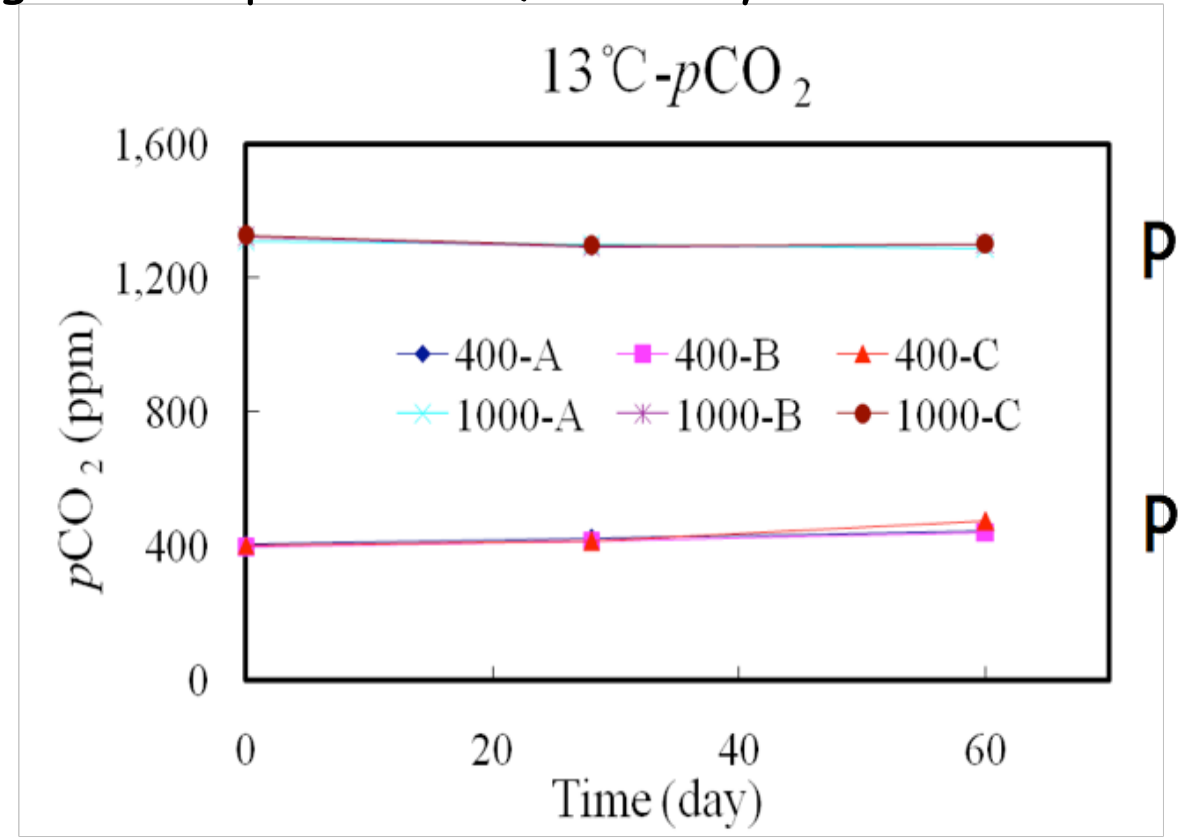
Average PR did not differ significantly between temperature treatments except for STE-8 (T3d); however, in five out of 20 cases, the PR vs pCO2 gradient patterns differed between temperature treatments.

Differences of metabolic and structural composition of communities could explain that and such differences have been detected for the communities collected for the experiments.

Alternatively, the observed patterns represent stochastic events and mesopelagic communities are insensitive or resistant to elevated levels of pCO2 or temperature.

pCO2 levels in LT-I

Two long term experiments (LTE; July 2009 and November 2009)



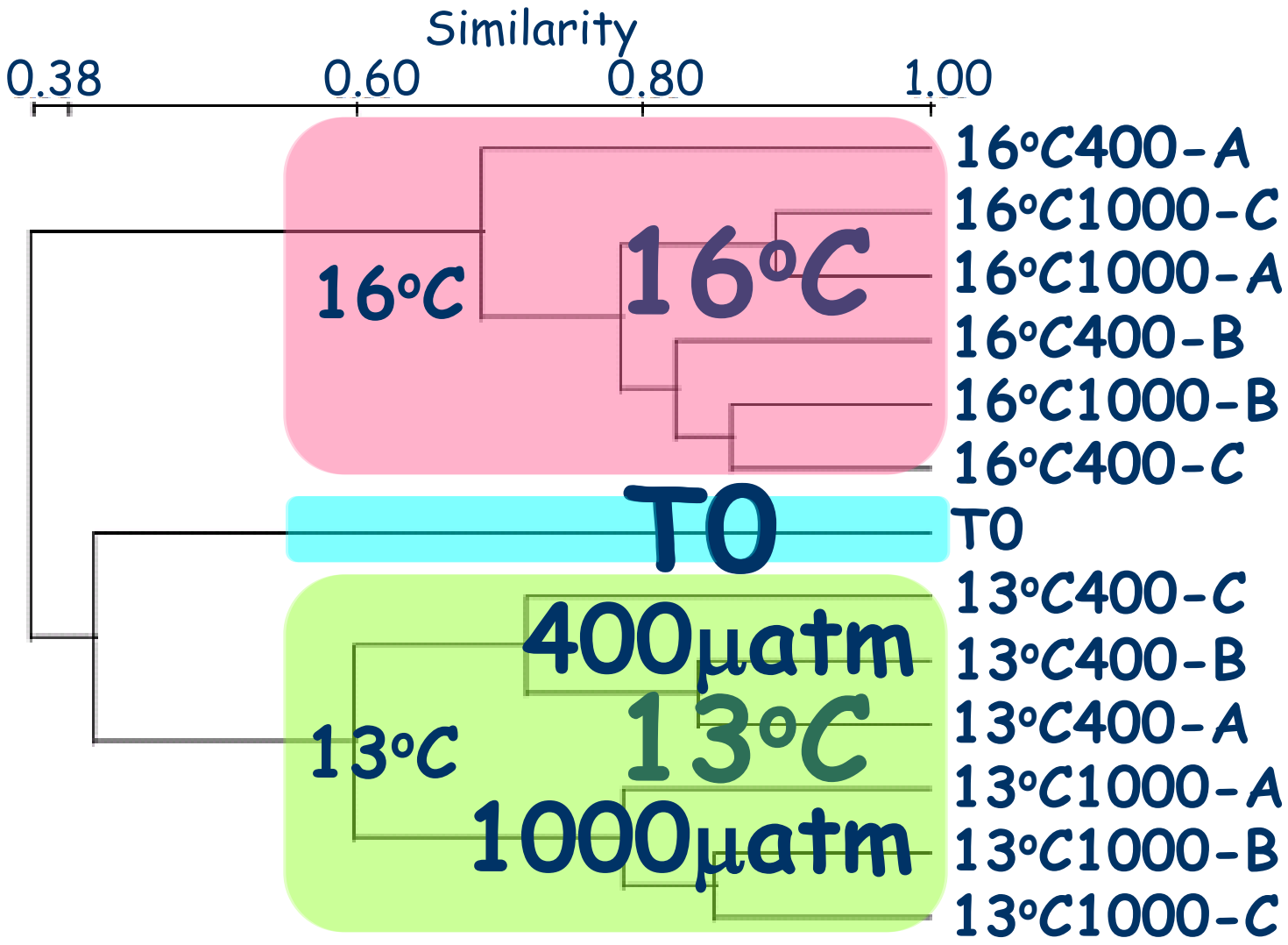
pH 7.63

pH 8.07

The experimental system was stable during the two months incubations with respect to the intended pCO2 manipulation (Same results for 16°C and for LT-2)

Cluster analysis of DGGE band patterns: LTE2

Genetic fingerprint (16S rRNA gene): Bacteria



Difference of DGGE pattern from control

		pCO_2	Temp	pCO_2 & Temp
Bacteria	LTE1	no	yes	yes
	LTE2	yes	yes	yes
Archaea	LTE1	no	yes	no
	LTE2	no	yes	no

Not only community composition, but specific bands were affected by pCO_2 and temperature, however, the trend across experiment were weak. Members of the Flavobacterium/Cytophaga/Bacteriodes group seemed the group affected most by the tested climate change factors.

Summary of effects on prokaryotic respiration

		pCO_2	Temp	pCO_2 & Temp
LTE-1	T28d	-	+	-
	T59d	no	+	+
LTE-2	T29d	no	+	no
	T60d	-	no	no

Elevated pCO2 had a neutral or neg effect of PR, whereas elevated temperature had a neutral or pos effects on PR (the latter also at T0d), whereas the for the combined ‘stressors’ no consistent effect a found.

Summary: long-term experiments

* Elevated pCO2 levels had neutral or negative effect on PR

* Elevated temperature had a neutral or positive effect on PR

* Temperature effects were more consistent than pCO2 effects

* No additive affects were detected; rather the effects of pCO2 and temperature seemed to neutralize each other

Potential consequences for the twilight zone

* Reduced PR at elevated pCO2 levels suggest reduced remineralization and thus likely enhanced carbon export (priming the biological carbon pump)
* Enhanced PR at elevated temperatures suggest enhanced remineralization and thus likely reduced carbon export (short-circuiting the biological carbon pump)
* The data suggest antagonistic effects of OA and global warming for prokaryotic respiration
* Our study suggests that an assessment of pCO2 scenarios for microorganisms needs to include the effect of global warming
* Finally, the climate change related experiments suggest an influence on bacterial and archaeal community composition; consequences are difficult to predict

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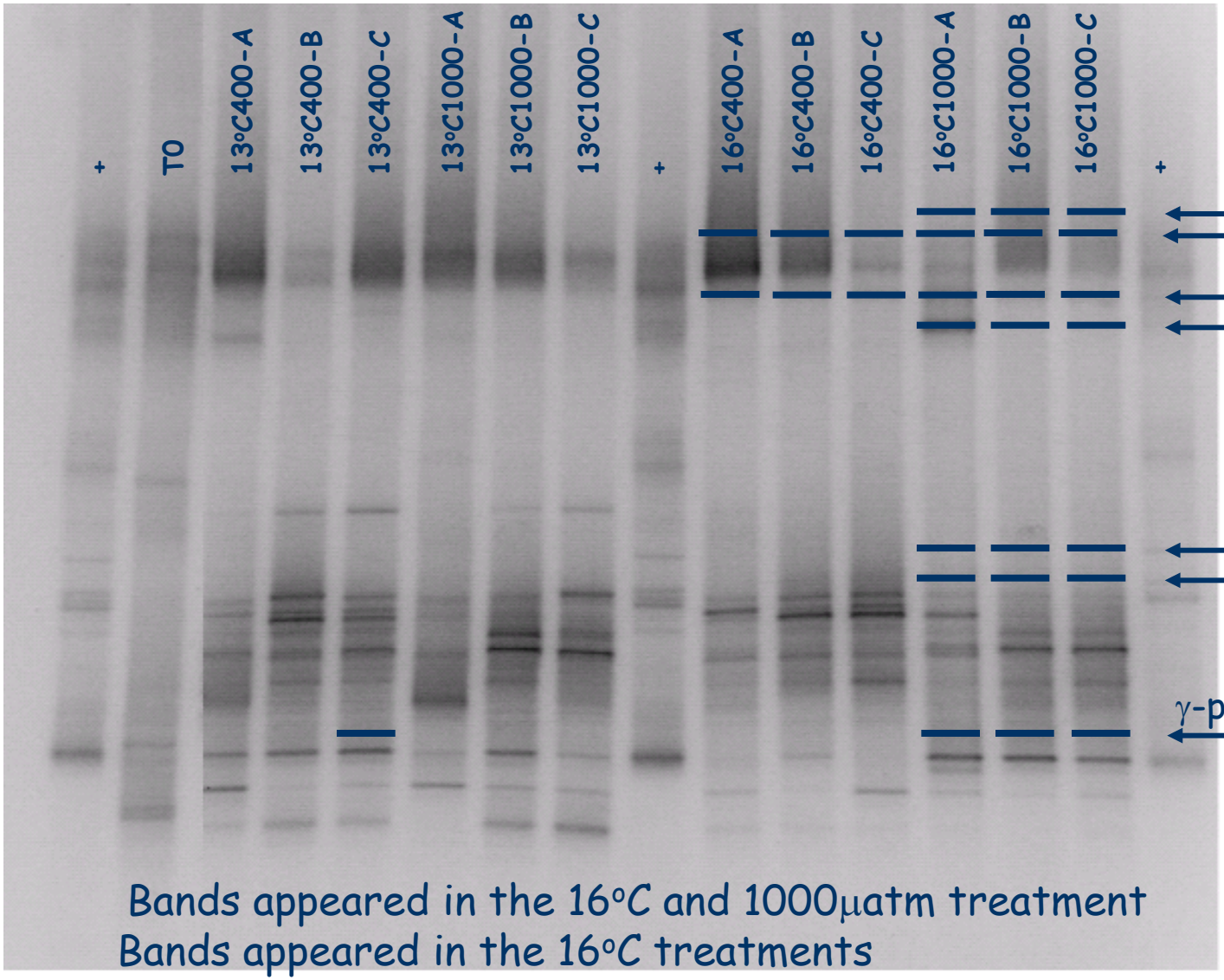
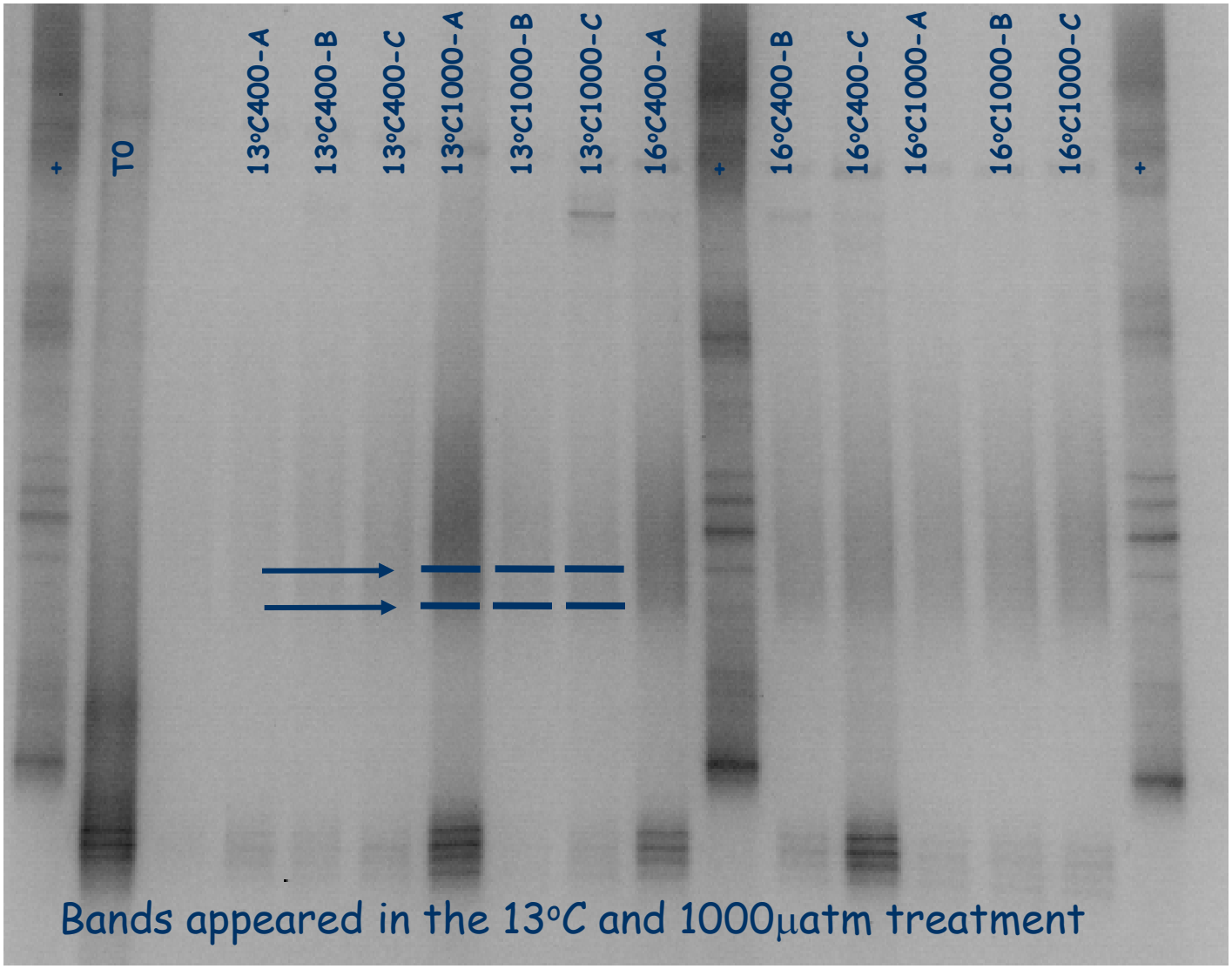
Sailors of the Observatoire d’Océanographie de Villefranche

Changes in bacterial community composition -LTE1-



Changes in Archaeal community composition -LTE1-



Bands appeared in the 13°C and 1000μatm treatment

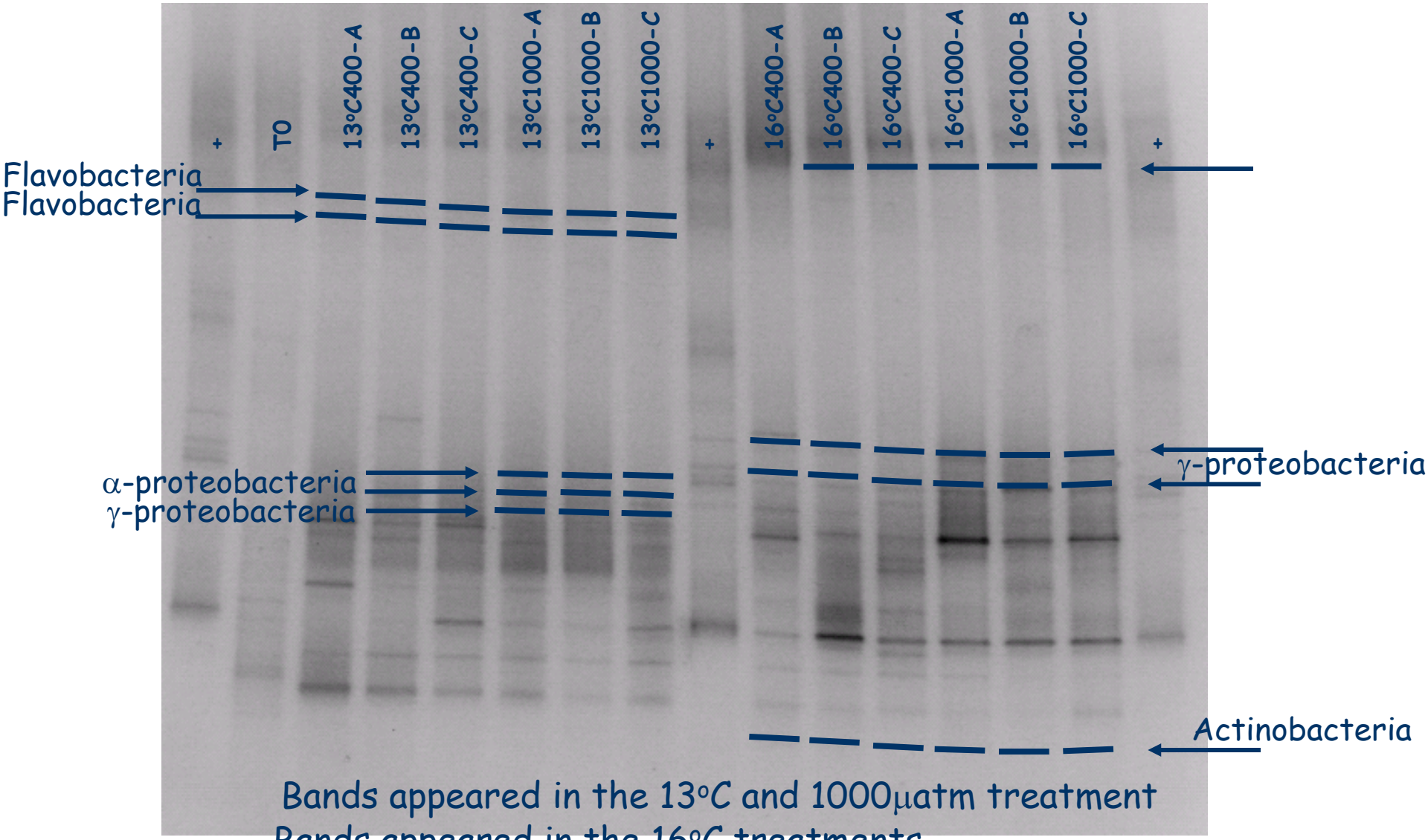
Summary

- In LTE1, bacterial community composition clearly differed between ambientand elevated temperature treatments. At elevated temperature, the bacterial community differed between the two pCO_2 levels.

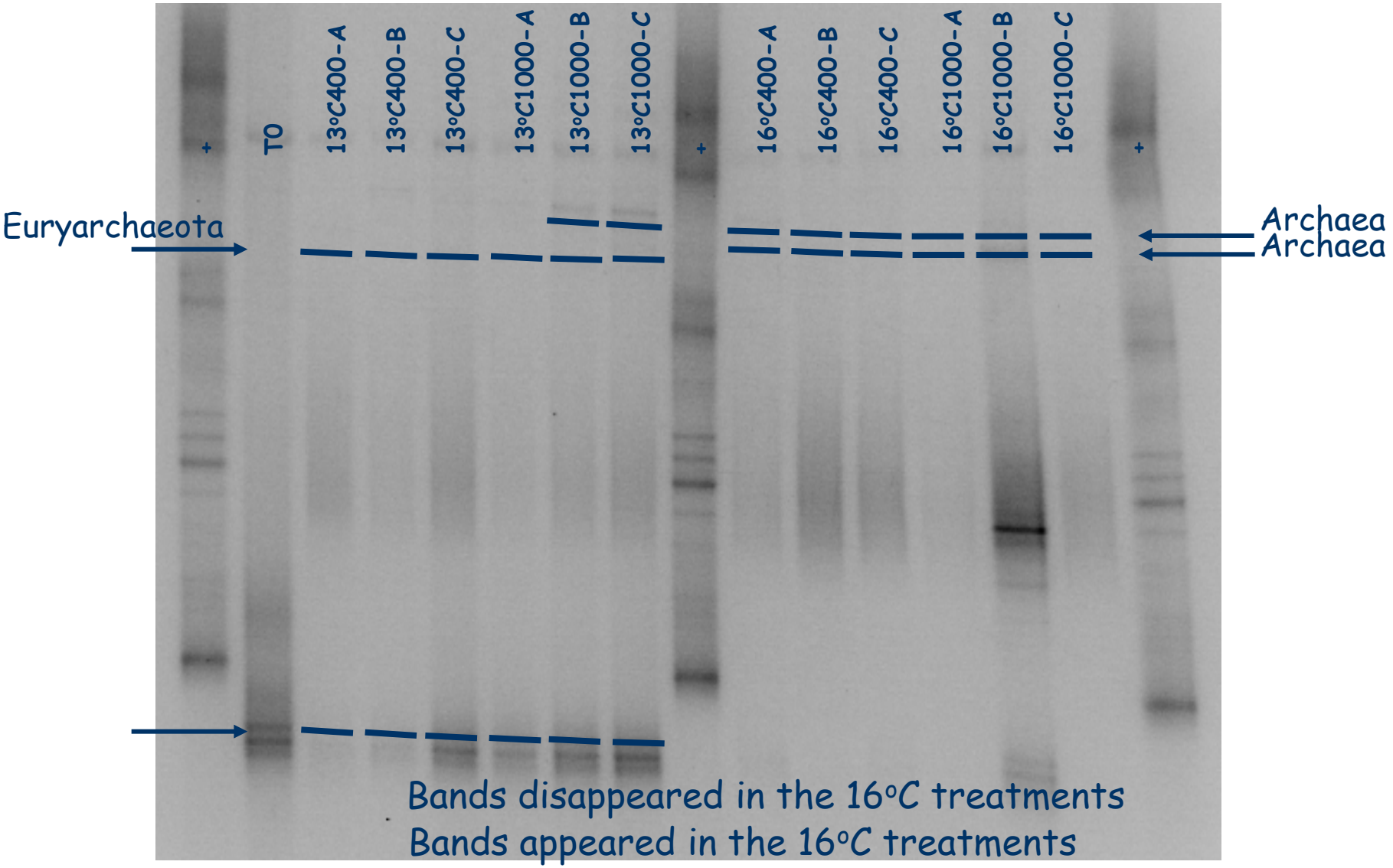
- In LTE2, both bacterial and archaeal communities responded to changes in temperature, but inconsistent with the LTE1, bacterial community clearly differed between the two pCO_2 levels at control temperature

Temperature and pCO_2 changes can potentially affect prokaryotes community composition; temperature changes had a stronger effect on the mesopelagic prokaryotic community.

Changes in bacterial community composition -LTE2-



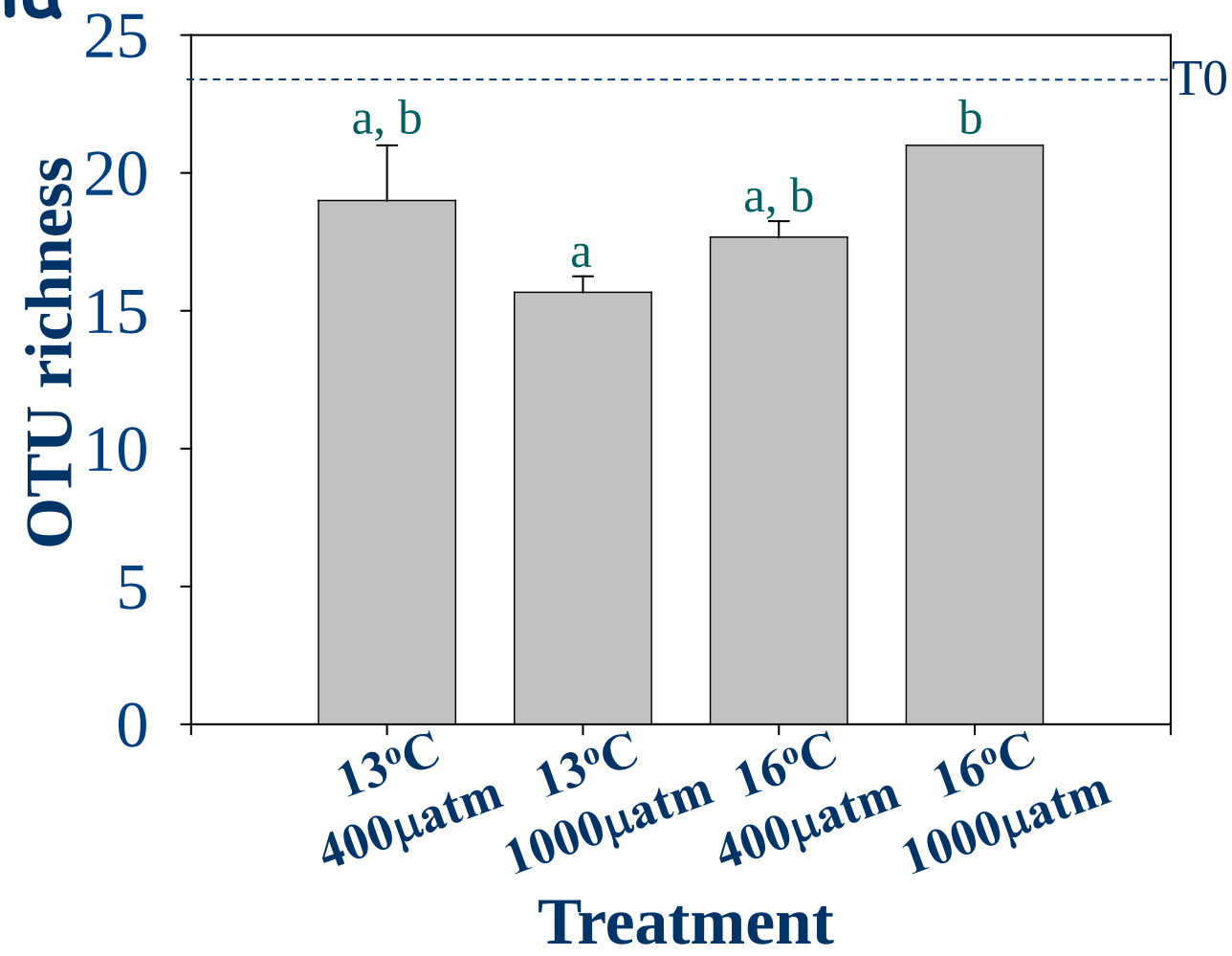
Changes in Archaeal community composition -LTE2-



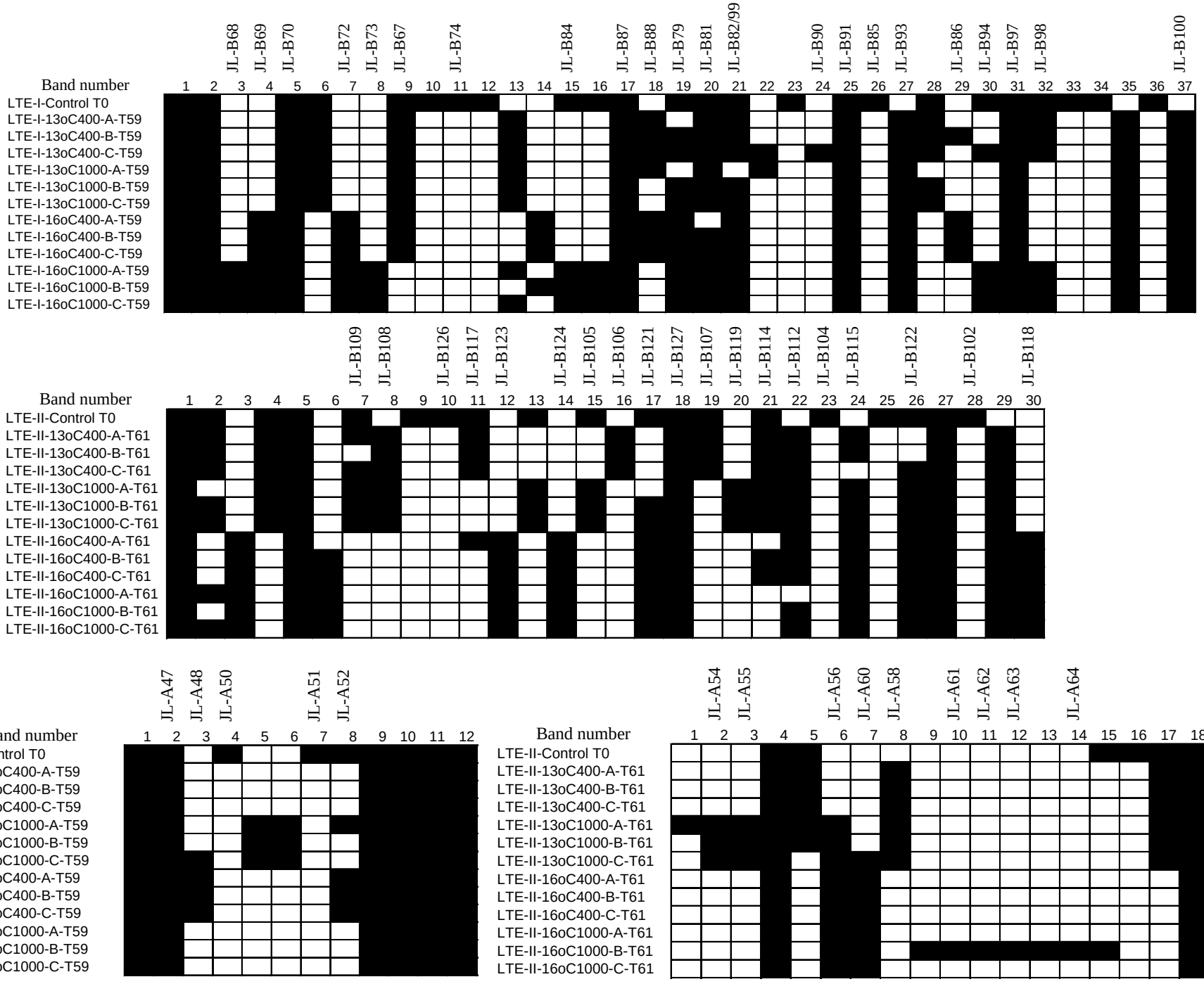
OTU richness
-LTE1-

Bacteria

ANOVA p<0.05



Significant differences in OTU richness between 16°C·1000µatm and 13°C·1000µatm


JL-B68
JL-B69
JL-B70
JL-B72
JL-B73
JL-B67
JL-B74
JL-B84
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JL-B88
JL-B79
JL-B81
JL-B82/99
JL-B90
JL-B91
JL-B85
JL-B93
JL-B86
JL-B94
JL-B97
JL-B98
JL-B100
Band number
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37
LTE-I-Control T0
LTE-I-13oC400-A-T59
LTE-I-13oC400-B-T59
LTE-I-13oC400-C-T59
LTE-I-13oC1000-A-T59
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LTE-I-13oC1000-C-T59
LTE-I-16oC400-A-T59
LTE-I-16oC400-B-T59
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JL-B109
JL-B108
JL-B126
JL-B117
JL-B123
JL-B124
JL-B105
JL-B106
JL-B121
JL-B127
JL-B107
JL-B119
JL-B114
JL-B112
JL-B104
JL-B115
JL-B122
JL-B102
JL-B118
Band number
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30
LTE-II-Control T0
LTE-II-13oC400-A-T61
LTE-II-13oC400-B-T61
LTE-II-13oC400-C-T61
LTE-II-13oC1000-A-T61
LTE-II-13oC1000-B-T61
LTE-II-13oC1000-C-T61
LTE-II-16oC400-A-T61
LTE-II-16oC400-B-T61
LTE-II-16oC400-C-T61
LTE-II-16oC1000-A-T61
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JL-A47
JL-A48
JL-A50
JL-A51
JL-A52
Band number
1 2 3 4 5 6 7 8 9 10 11 12
LTE-I-Control T0
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LTE-I-13oC400-B-T59
LTE-I-13oC400-C-T59
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LTE-I-16oC1000-B-T59
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JL-A54
JL-A55
JL-A56
JL-A60
JL-A58
JL-A61
JL-A62
JL-A63
JL-A64
Band number
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
LTE-II-Control T0
LTE-II-13oC400-A-T61
LTE-II-13oC400-B-T61
LTE-II-13oC400-C-T61
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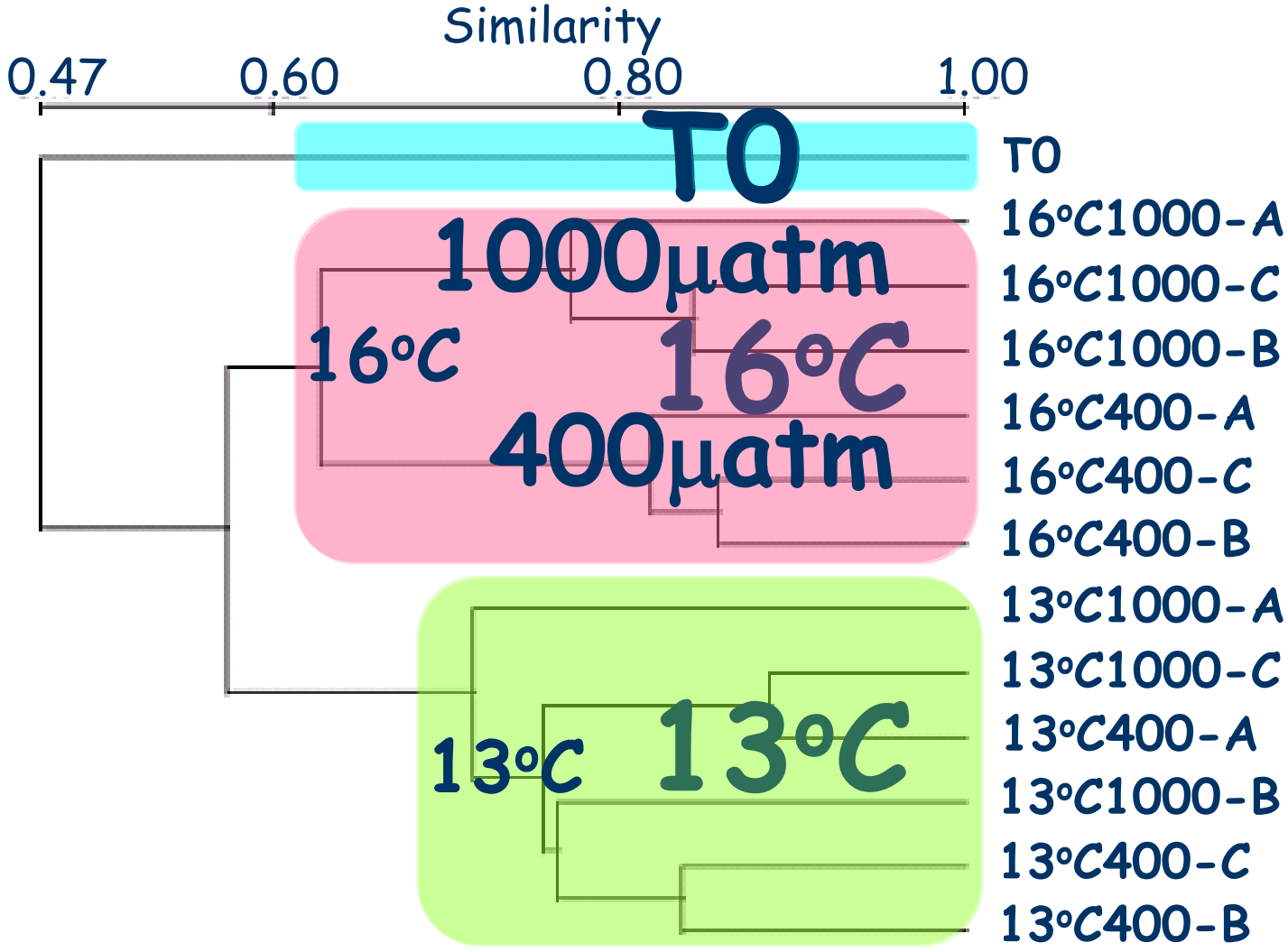
LTE-II-16oC400-A-T61
LTE-II-16oC400-B-T61
LTE-II-16oC400-C-T61
LTE-II-16oC1000-A-T61
LTE-II-16oC1000-B-T61
LTE-II-16oC1000-C-T61

Cluster analysis of DGGE band patterns -LTE1-

Bacteria

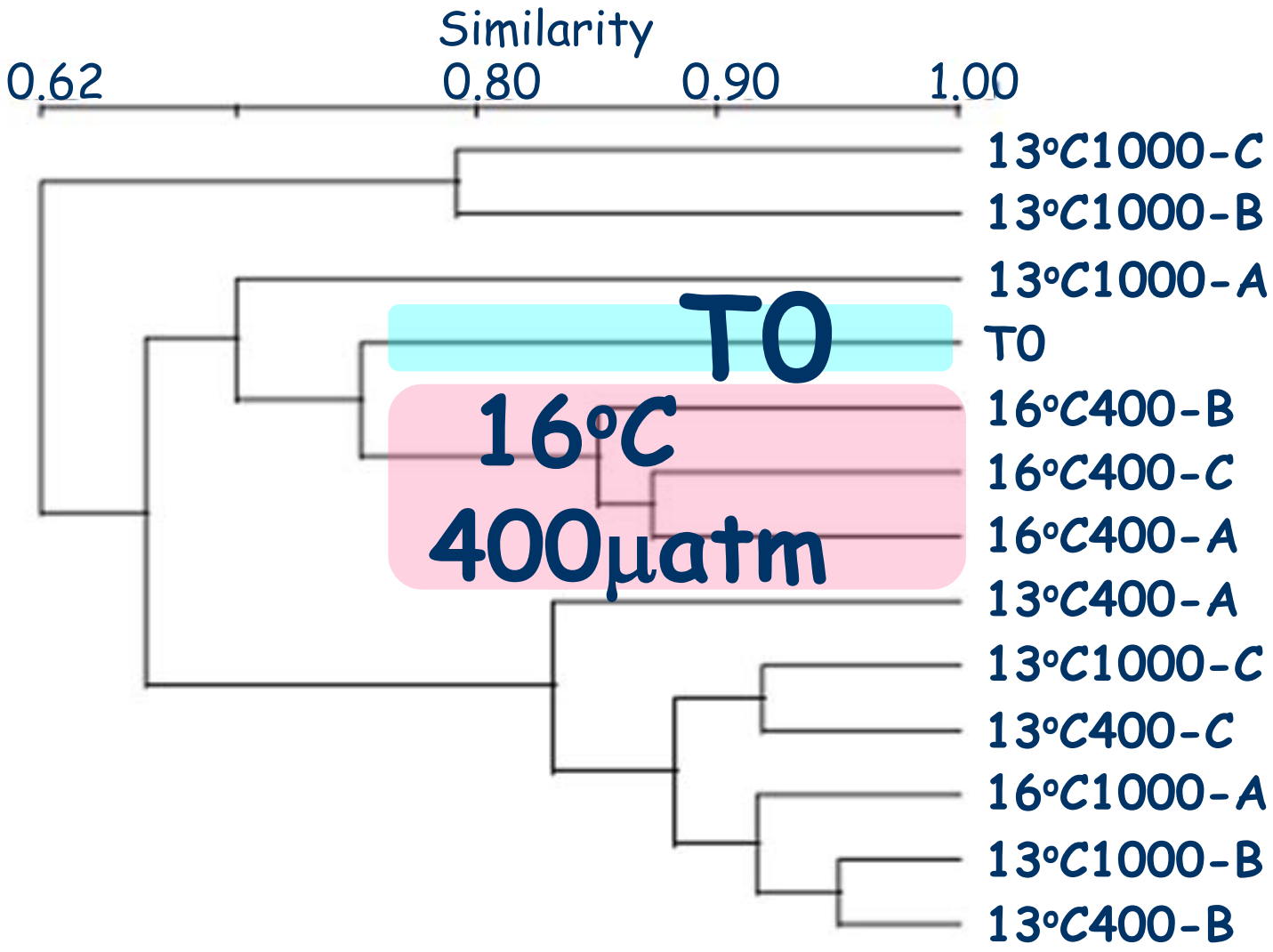
UPGAMA, Dice coefficient



Cluster analysis of DGGE band patterns -LTE1-

Archaea

UPGAMA, Dice coefficient



Cluster analysis of DGGE band patterns -LTE2-

Archaea

UPGAMA, Dice coefficient