

The Biofilm Lifestyle of AOA: Implications for Physiology and Nitrification Inhibition

ACTIONr Summer School-Greece

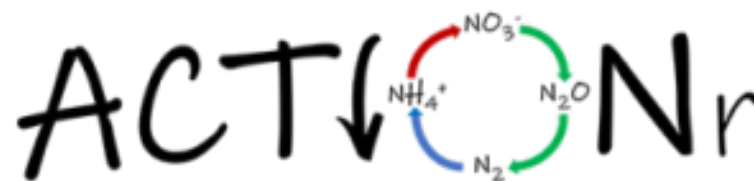
May 14, 2025

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University of Vienna-Schleper Lab



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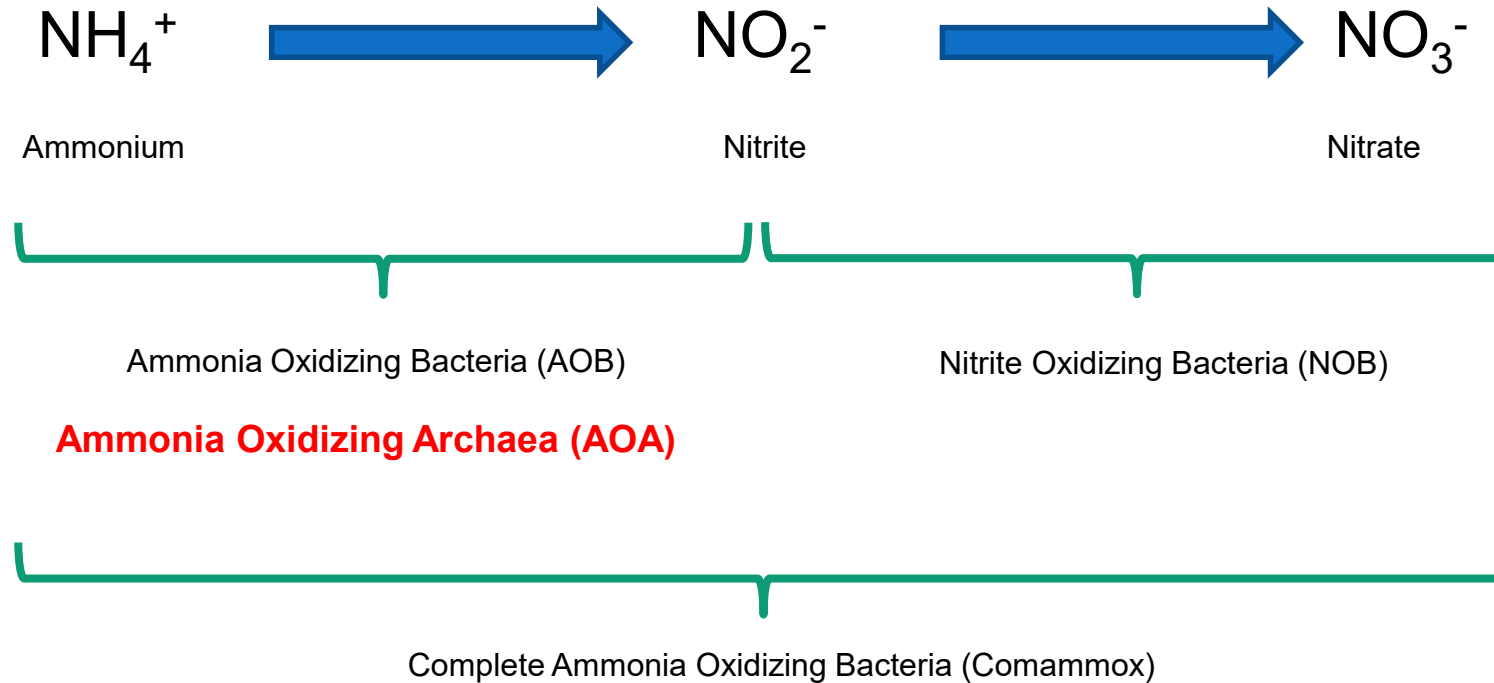


Outline

- Why we are interested in biofilms
- How we study and understand biofilms
 - Growth
 - Imaging
 - Transcriptomics
- Impacts of biofilms on nitrification inhibition

Nitrification and Archaea

Nitrification

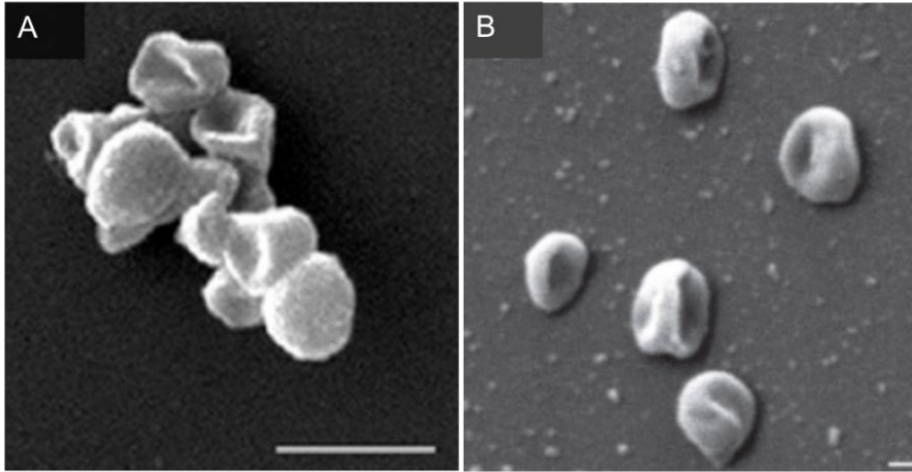


Winogradsky, 1890

Venter *et al.*, 2004
Treusch *et al.*, 2005
Könneke *et al.*, 2005

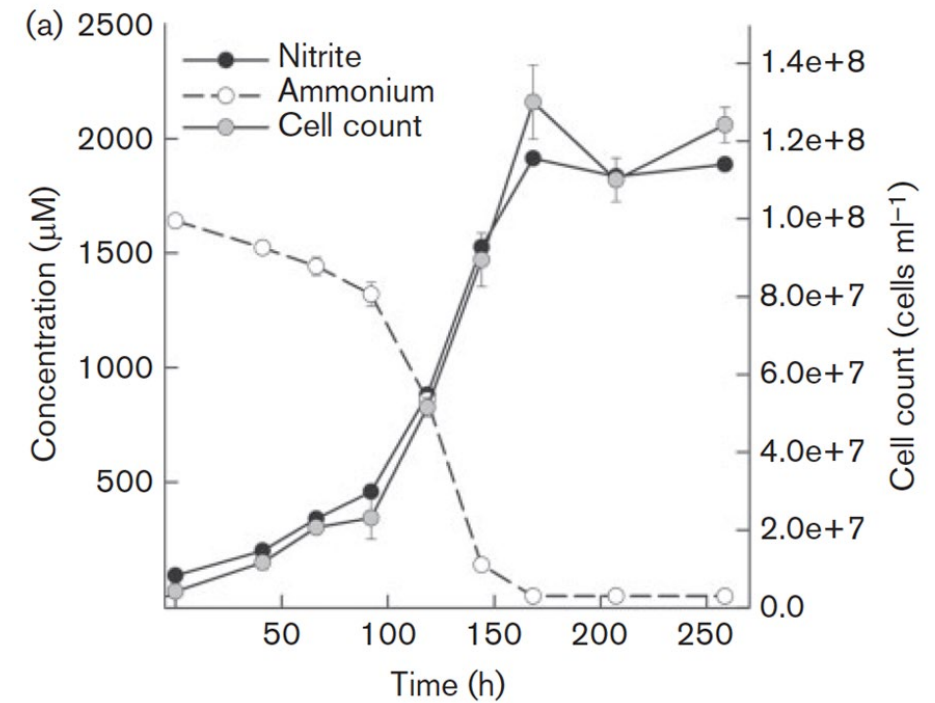
Daims *et al.*, 2015
van Kessel *et al.*, 2015

Nitrososphaera viennensis



Tourna *et al.* (2011) and Stieglmeier *et al.* (2014).

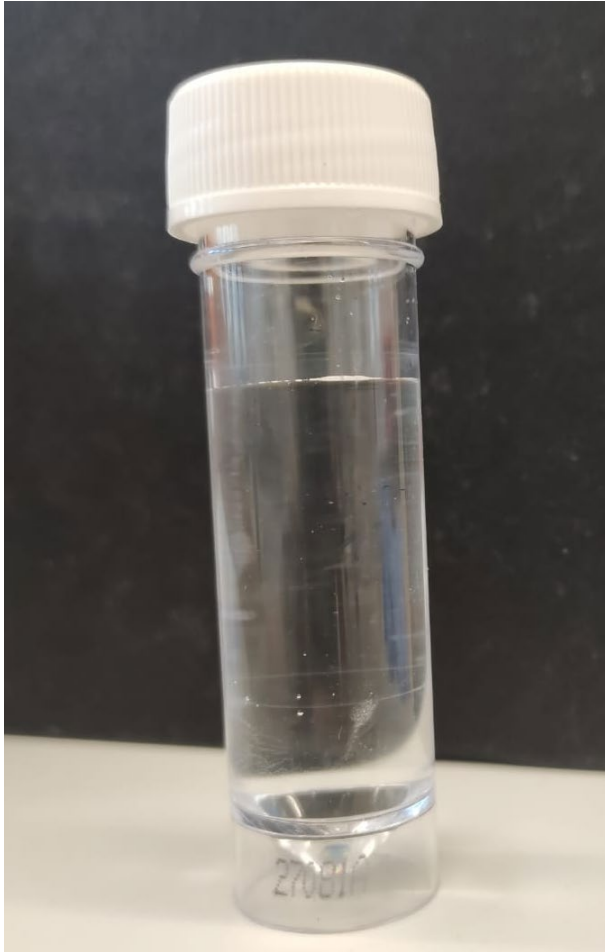
- First AOA isolated from soil.



Stieglmeier *et al.* (2014)



How do AOA grow in the environment?

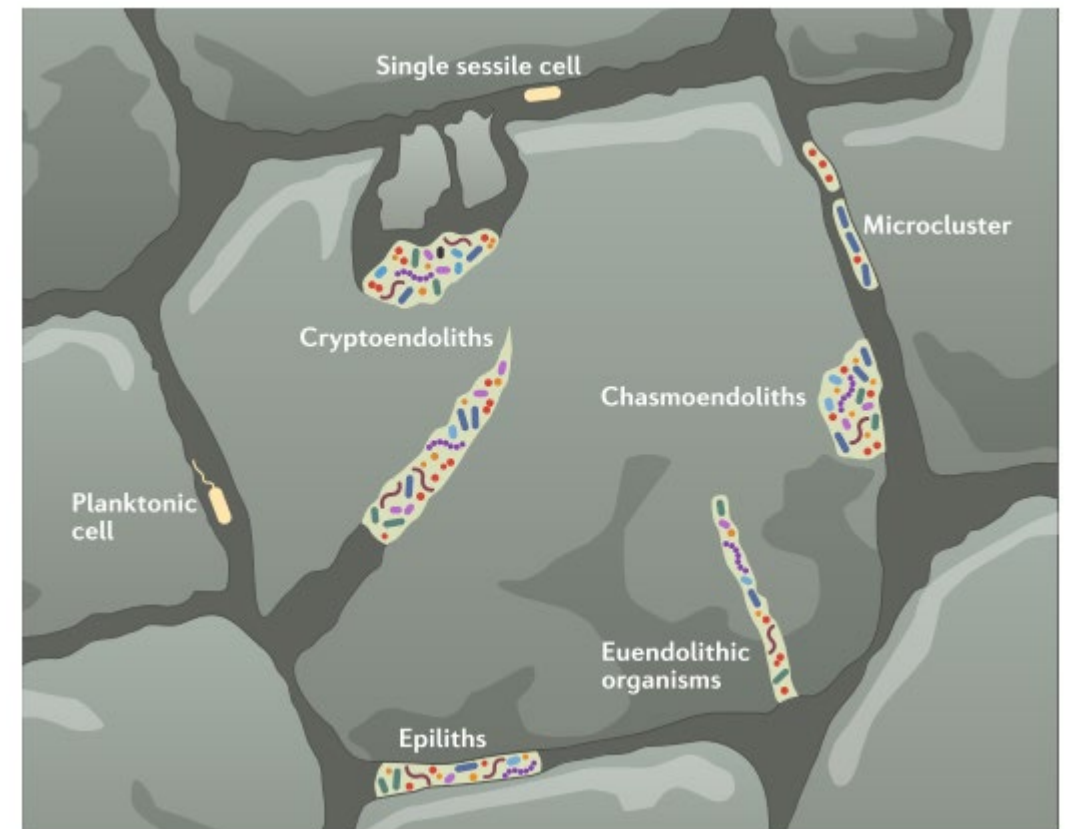


Majority of prokaryotes might exist as biofilms

Bacteria and archaea on Earth and their abundance in biofilms

Hans-Curt Flemming^{1,2*} and Stefan Wuerzt^{1,3*}

humans, animals and the phyllosphere, account for fewer cells by orders of magnitude. Biofilms dominate in all habitats on the surface of the Earth, except in the oceans, accounting for ~80% of bacterial and archaeal cells. In the deep subsurface, however, they cannot always be distinguished from single sessile cells; we estimate that 20–80% of cells in the subsurface exist as biofilms. Hence, overall, 40–80% of cells on Earth reside in biofilms. We conclude that biofilms drive all biogeochemical processes and represent the main way of active bacterial and archaeal life.



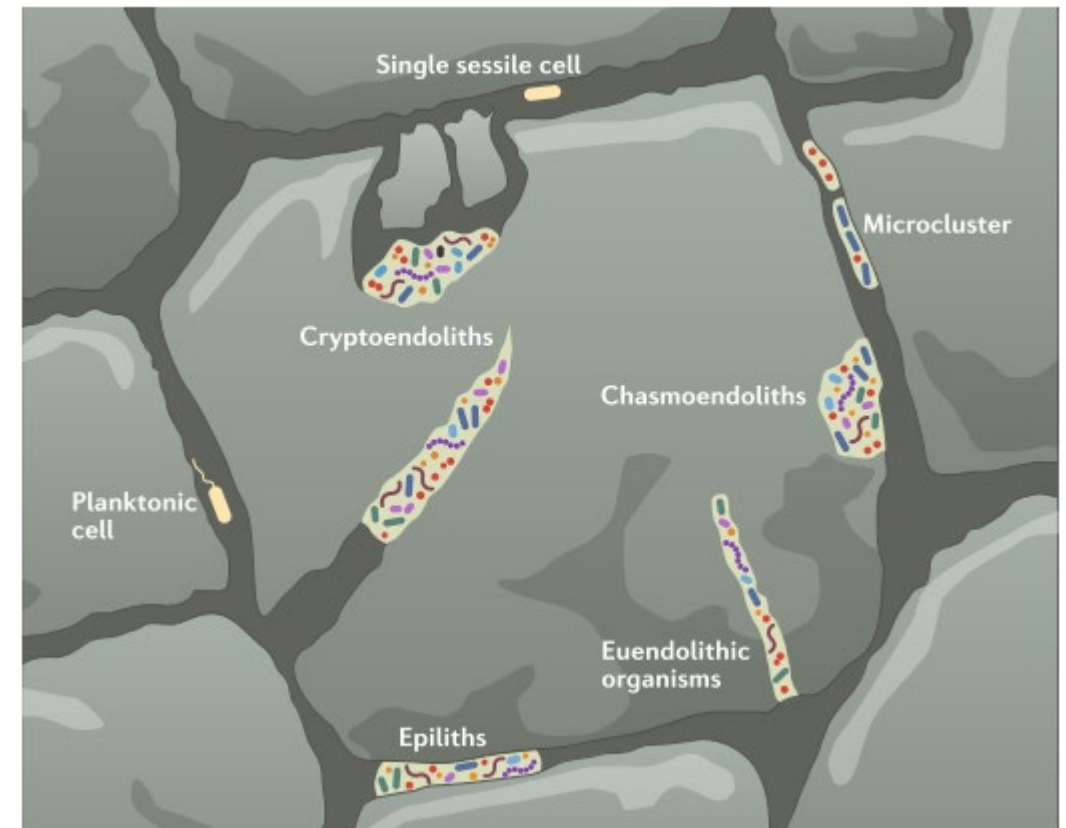
100% in soil?

Table 1 | Total and biofilm numbers of bacterial and archaeal cells in the most relevant habitats on Earth

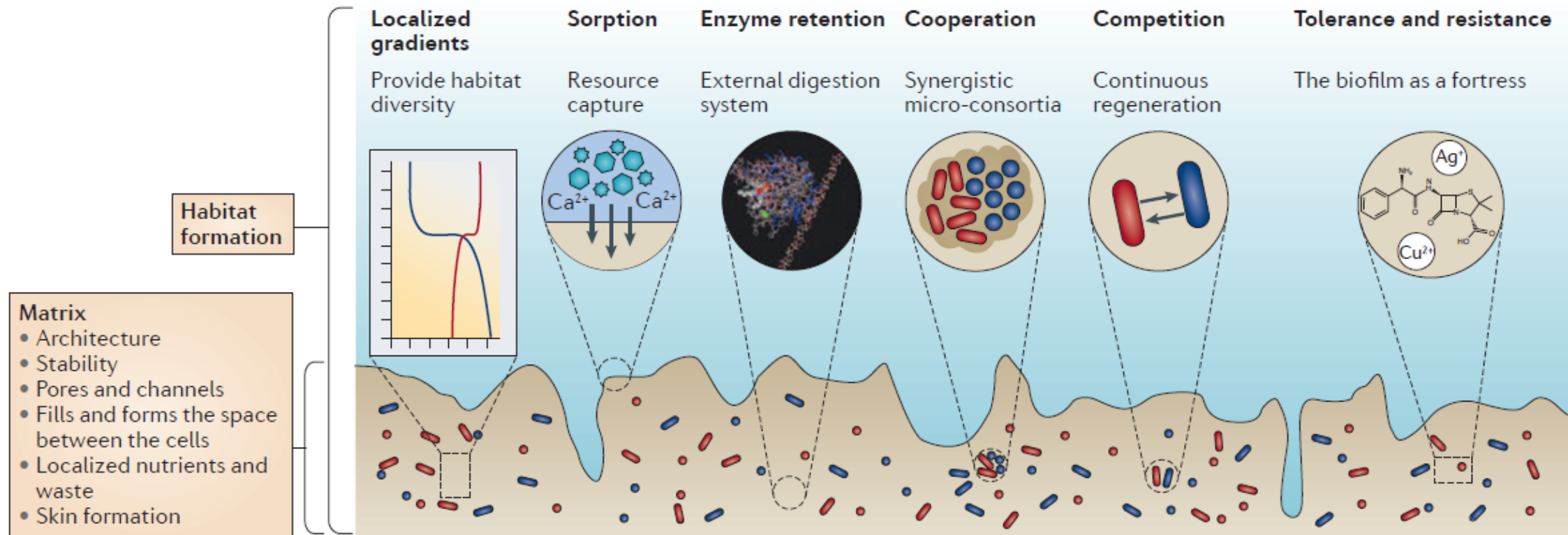
Habitat	Estimated total (bacterial and archaeal) cell number ^a	Estimated cell number in biofilms ^b	Refs
Total Earth	1.2×10^{30}	On surface of Earth: 3.5×10^{29} ; deep subsurface: large but as yet unknown, ranging from 4.9×10^{29} to 9.1×10^{29}	Total numbers estimated from values below (see Supplementary Box 1 for additional calculations)
Deep oceanic subsurface ^c	4×10^{29}	Most cells attached, either single or in clusters; 20–80% in biofilms based on microscopic and biogeochemical evidence	REF. ¹⁴ (additional references ^{29,38–40,46,67})
Deep continental subsurface ^d	3×10^{29}	Most cells attached, single and microclusters; 20–80% in biofilms based on microscopic and biogeochemical evidence	REF. ¹⁵ (additional references ^{14,21,27,38,40,86,203})
Top 10–50 cm of oceanic sediment ^e	5×10^{28}	5×10^{28}	Calculated from REF. ²⁸
→ Soil	3×10^{29}	3×10^{29}	REFS ^{14,37}
Open ocean	1×10^{29}	Large planktonic fraction, unknown numbers in marine snow, transparent exopolymer particles, gels, on mineral and debris particles, microplastics, plants and animals	REF. ¹⁴ (used geometric mean of REFS ^{27,127–129,131})

Bacteria and archaea on Earth and their abundance in biofilms

Hans-Curt Flemming^{1,2*} and Stefan Wuerzt^{1,3*}



Role of Biofilms in the environment



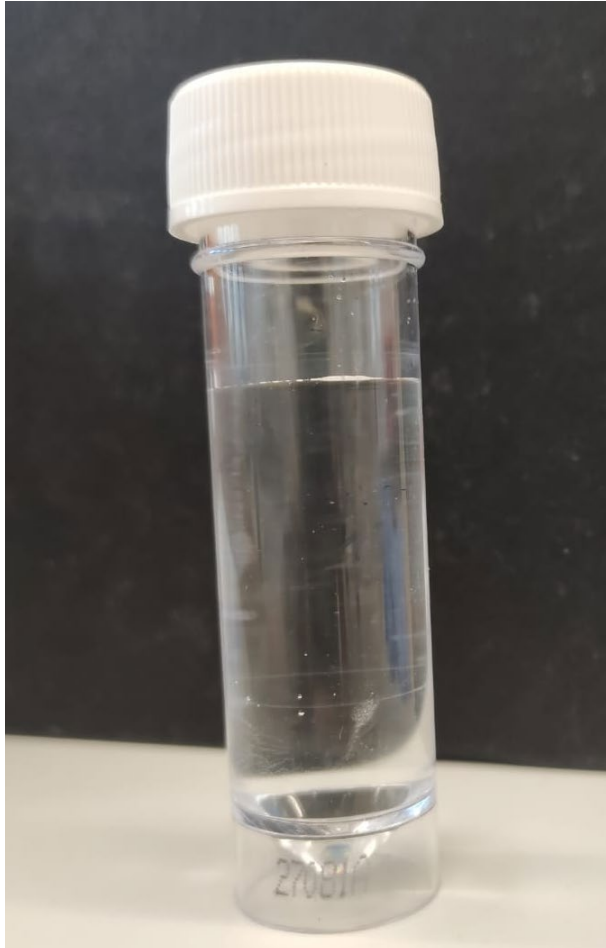
Review Article | Published: 11 August 2016

Biofilms: an emergent form of bacterial life

Hans-Curt Flemming , Jost Wingender, Ulrich Szewzyk, Peter Steinberg, Scott A. Rice & Staffan Kjelleberg

Nature Reviews Microbiology **14**, 563–575 (2016) | [Cite this article](#)

How do AOA grow in the environment?



Max Dreer

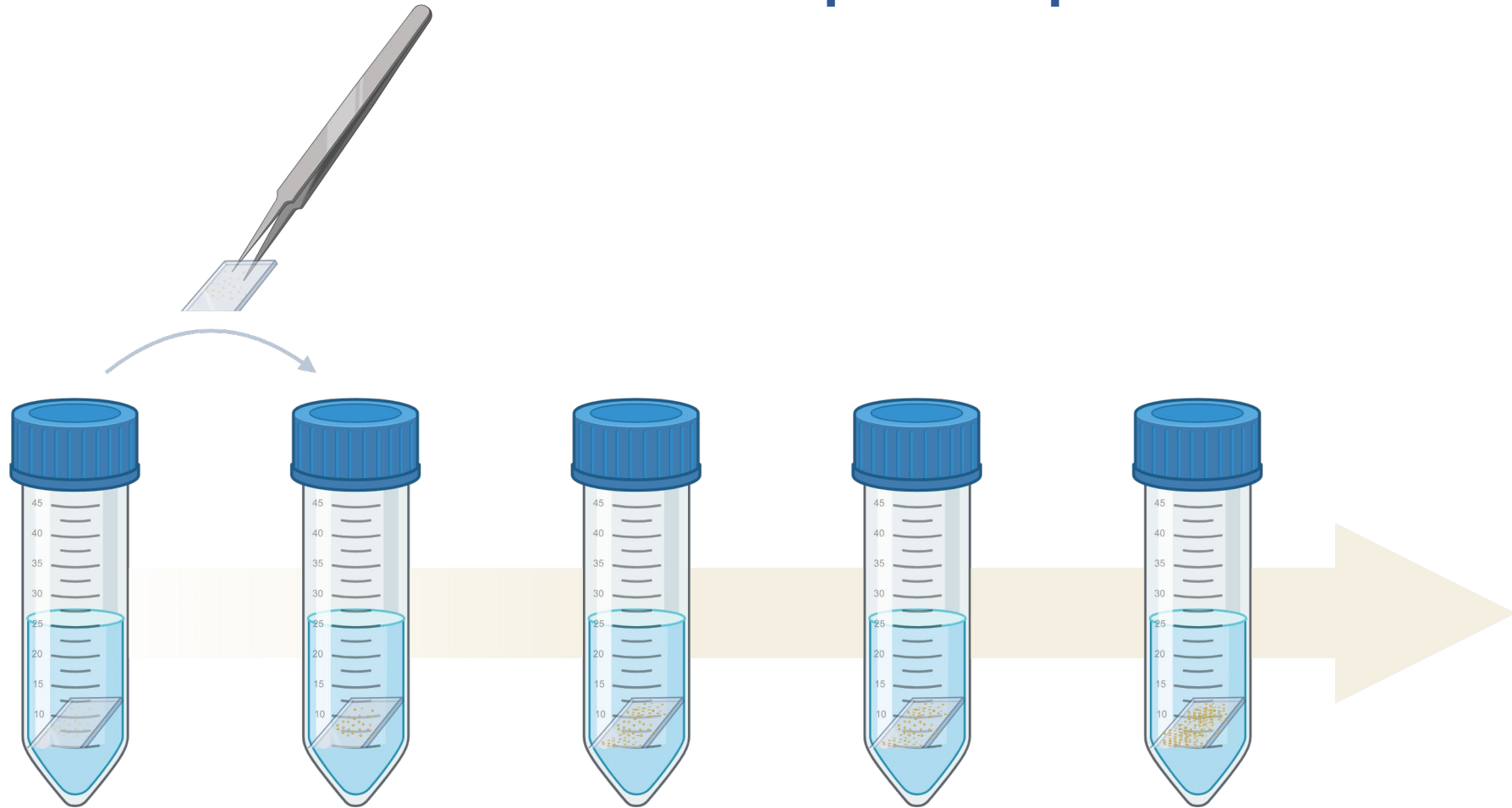


Thomas Pribasnig

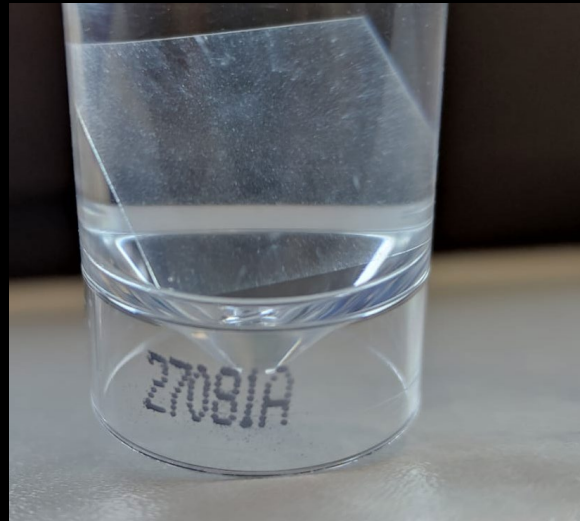
Questions

- Do AOA form biofilms?
- Are there physiological responses associated with biofilms?
- Does biofilm growth affect nitrification?

Setup – Borosilicate coverslip in liquid medium



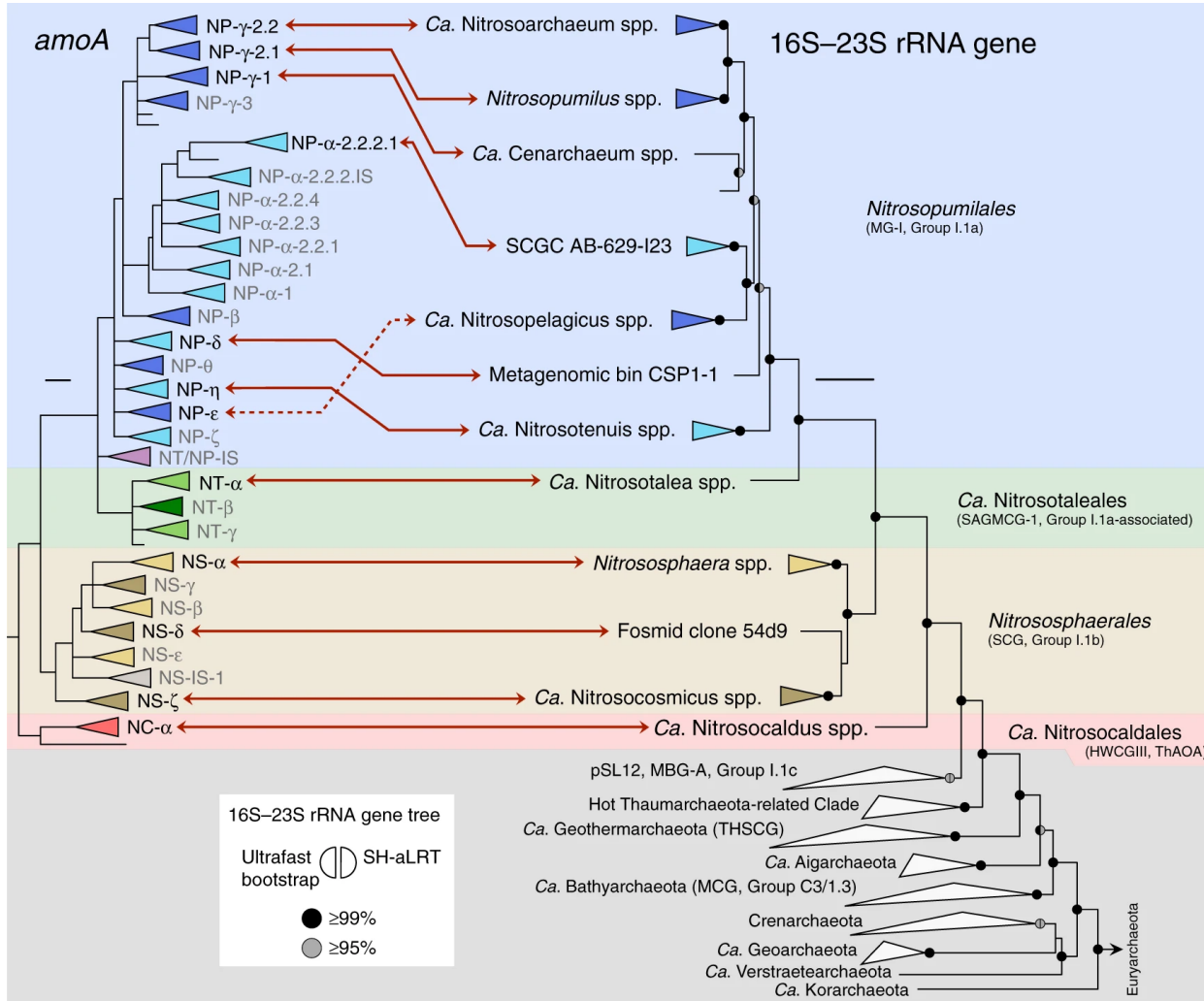
Macroscopically visible BF - ~2 months



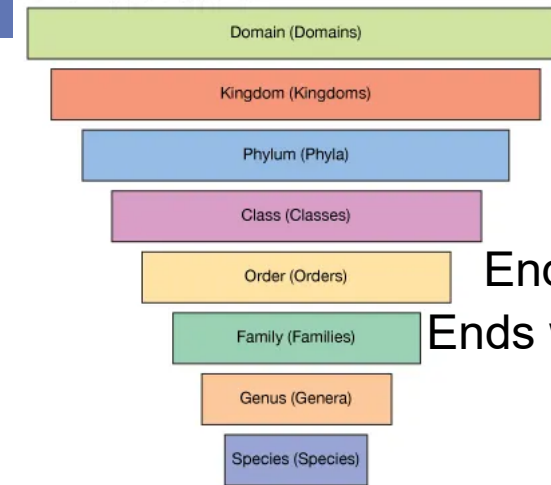
Which Species?-A Classification Detour

Thaumarchaeota

NCBI: Nitrososphaerota (phylum) Grouped by Orders



How animals are classified

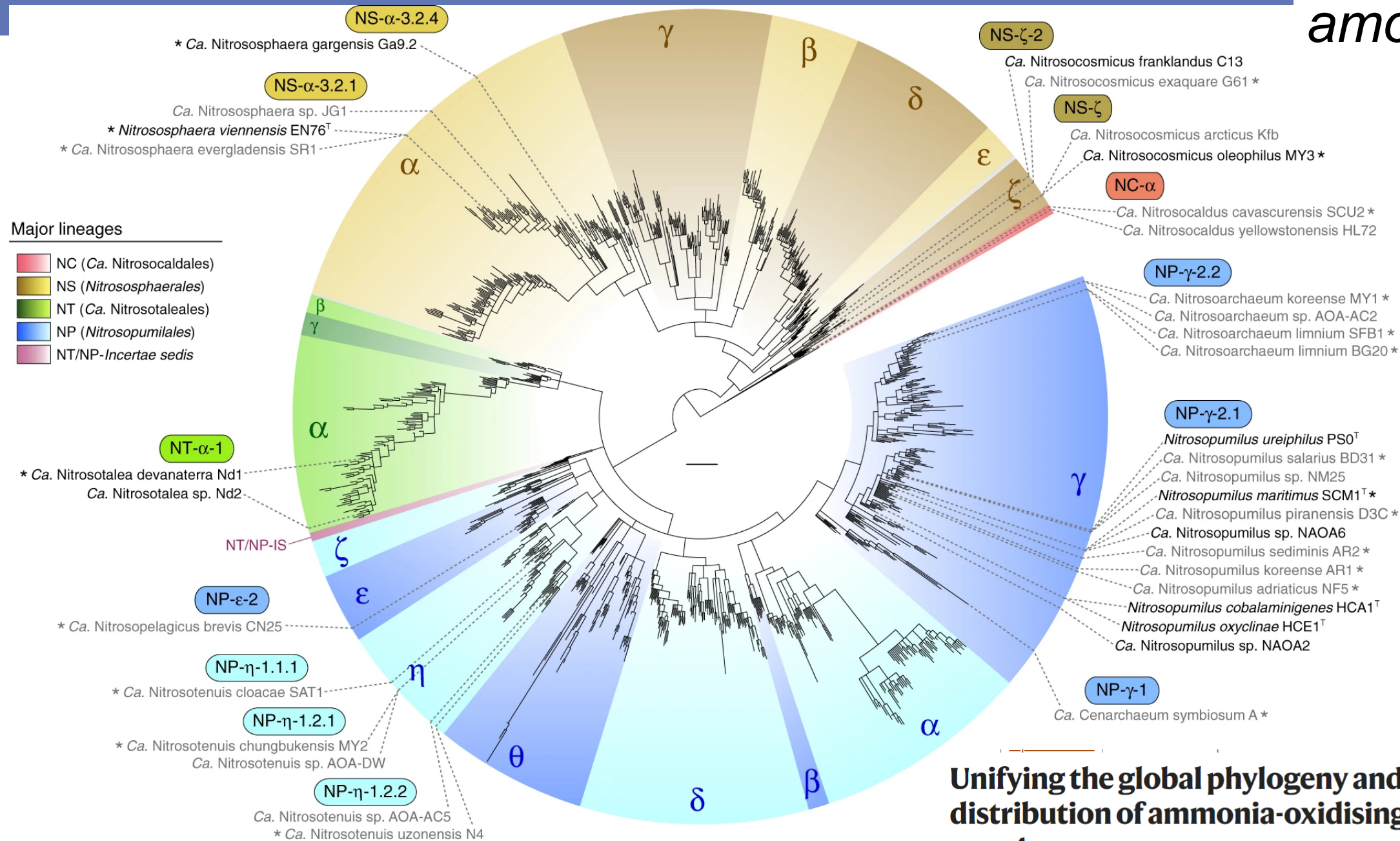


Ends with -ales

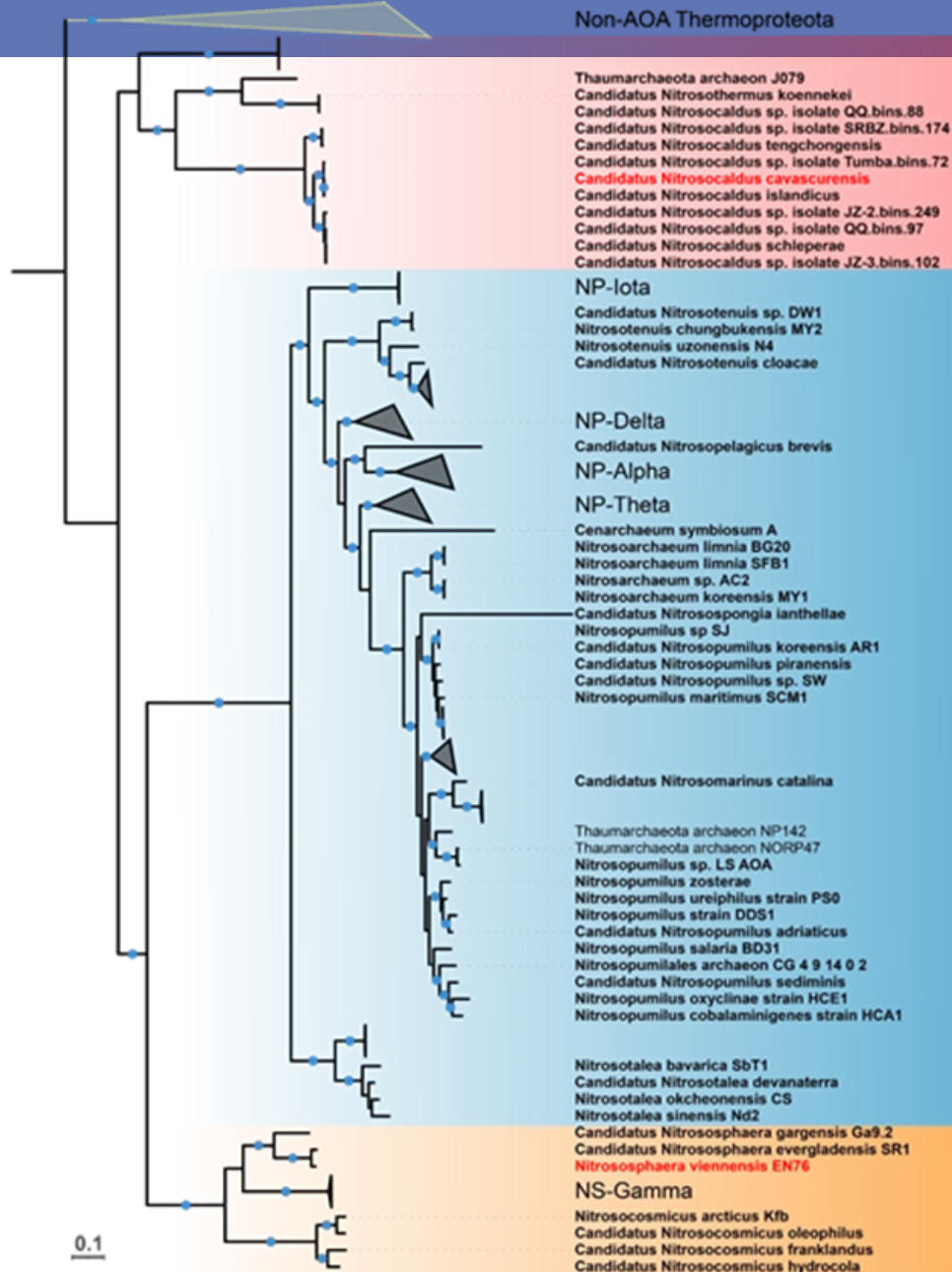
Ends with -aceae

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amoA Clades



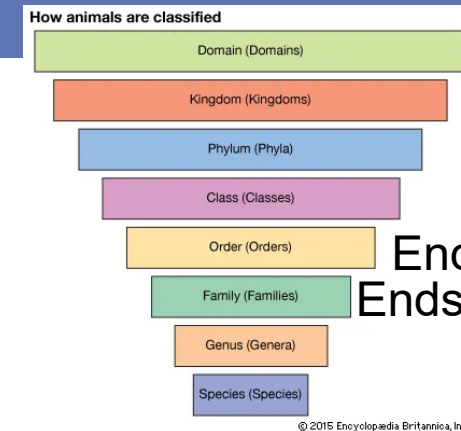
Unifying the global phylogeny and environmental distribution of ammonia-oxidising archaea based on *amoA* genes



Nitrosocaldaceae
(Thermophilic)

Nitrosopumilaceae
(Marine Group)

Nitrososphaeraceae (Soil Group)



Ends with -ales
Ends with -aceae

*Genome Taxonomy Database (GTDB)
nomenclature (Rinke et al. 2021)

*Different than NCBI

A standardized archaeal taxonomy for the Genome Taxonomy Database

[Christian Rinke](#), [Maria Chuvpochina](#), [Aaron J. Mussig](#), [Pierre-Alain Chaumeil](#), [Adrián A. Davín](#), [David W. Waite](#), [William B. Whitman](#), [Donovan H. Parks](#) & [Philip Hugenholtz](#)

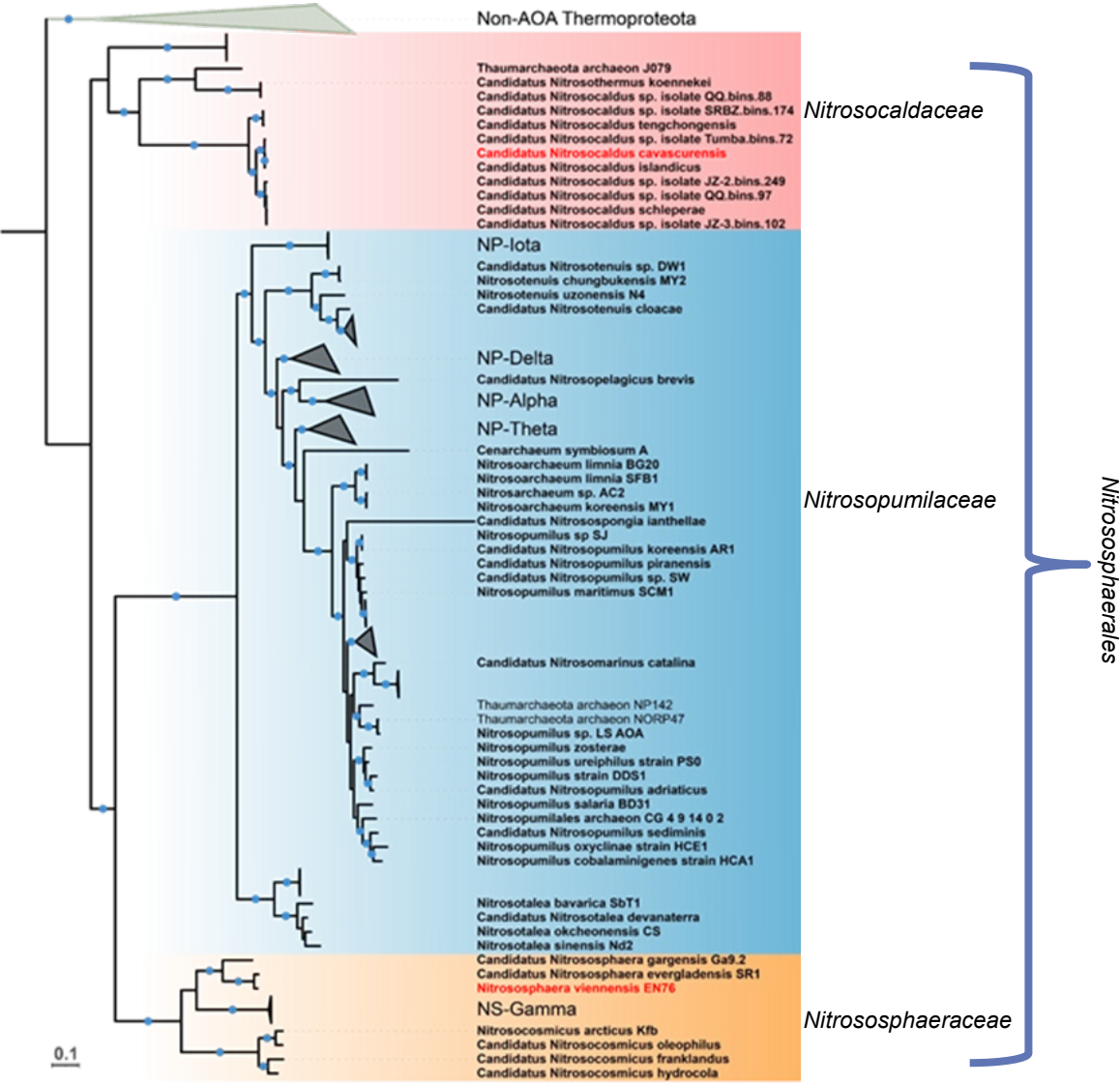
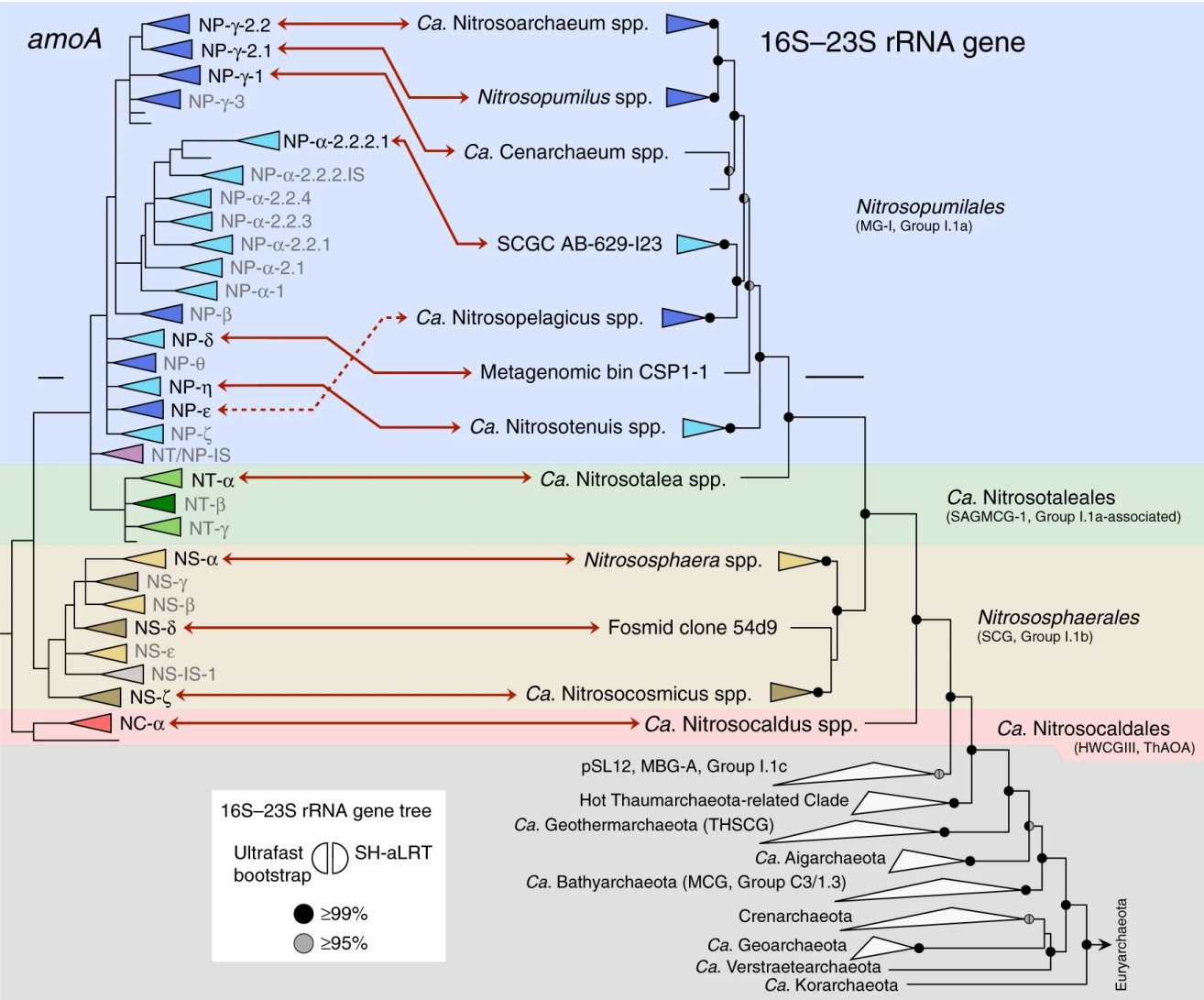
Thermoproteota (phylum)

Grouped by family. Acidic soil strains are now in the marine group (family).

All AOA are in the order Nitrososphaerales

NCBI

GTDB



GTDB

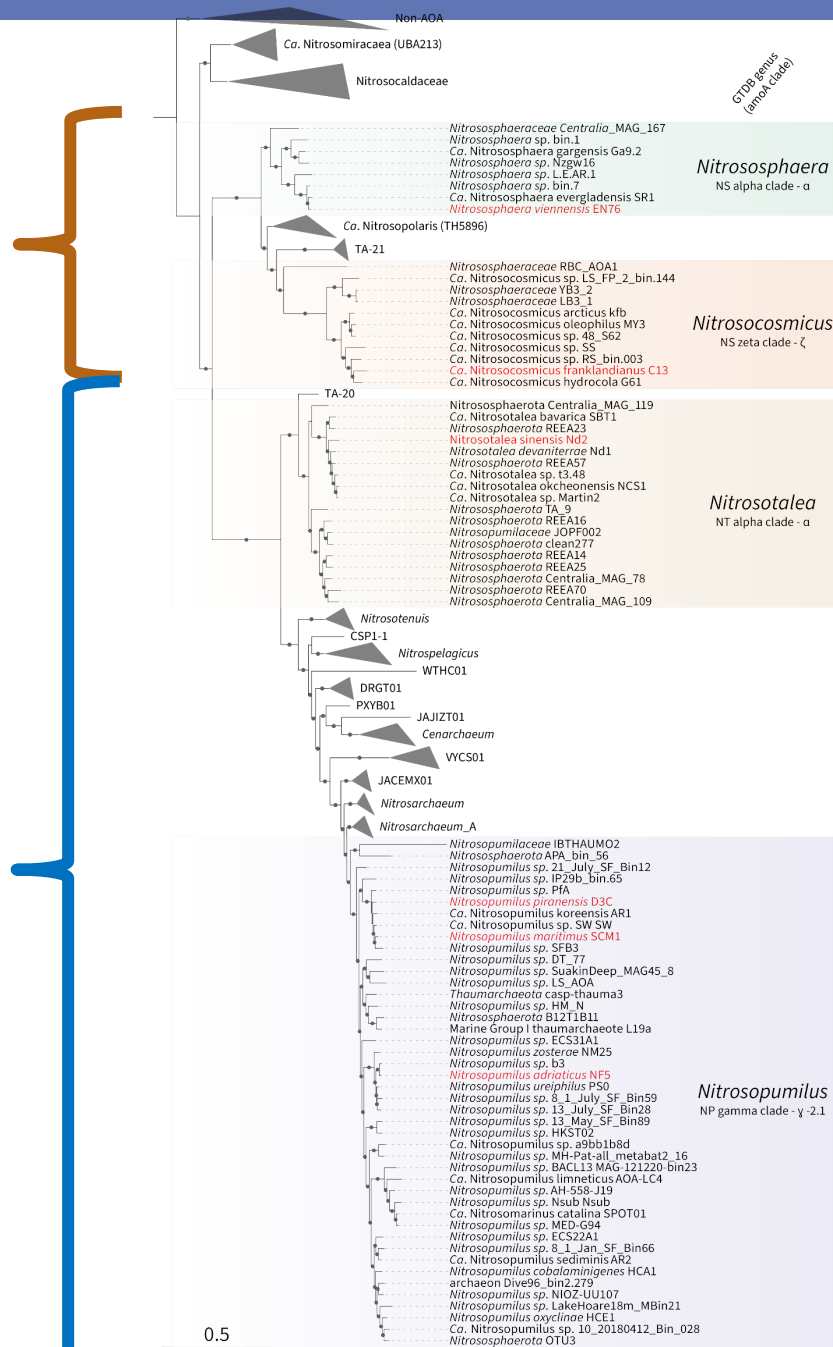
<https://gtdb.ecogenomic.org/>

Accession	NCBI organism name	NCBI taxonomy	GTDB taxonomy	GTDB species representative	NCBI type material
GCF_000698785.1	Nitrososphaera viennensis EN76	d__Archaea; p__Nitrososphaerota; c__Nitrososphaeria; o__Nitrososphaerales; f__Nitrososphaeraceae; g__Nitrososphaera; s__Nitrososphaera viennensis	d__Archaea; p__Thermoproteota; c__Nitrososphaeria; o__Nitrososphaerales; f__Nitrososphaeraceae; g__Nitrososphaera; s__Nitrososphaera viennensis	yes	yes

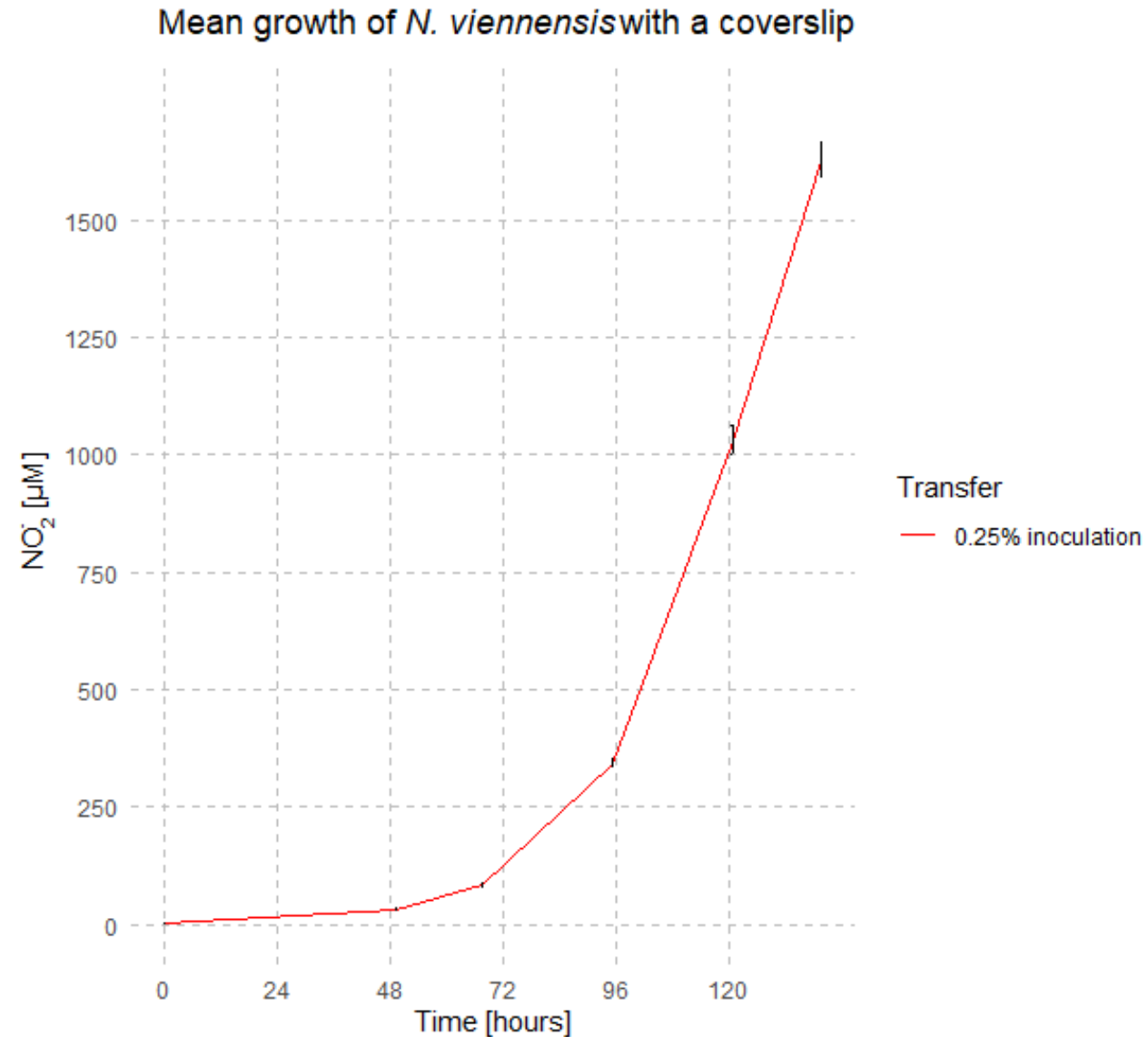
Accession	NCBI organism name ↑	NCBI taxonomy	GTDB taxonomy	GTDB species representative	NCBI type material
GCF_000018465.1	Nitrosopumilus maritimus SCM1	d__Archaea; p__Nitrososphaerota; c__Nitrososphaeria; o__Nitrosopumilales; f__Nitrosopumilaceae; g__Nitrosopumilus; s__Nitrosopumilus maritimus	d__Archaea; p__Thermoproteota; c__Nitrososphaeria; o__Nitrososphaerales; f__Nitrosopumilaceae; g__Nitrosopumilus; s__Nitrosopumilus maritimus	yes	yes

Nitrososphaeraceae

Nitrosopumilaceae

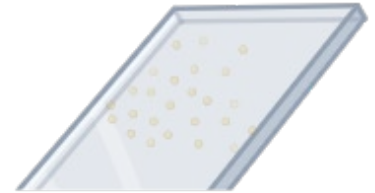
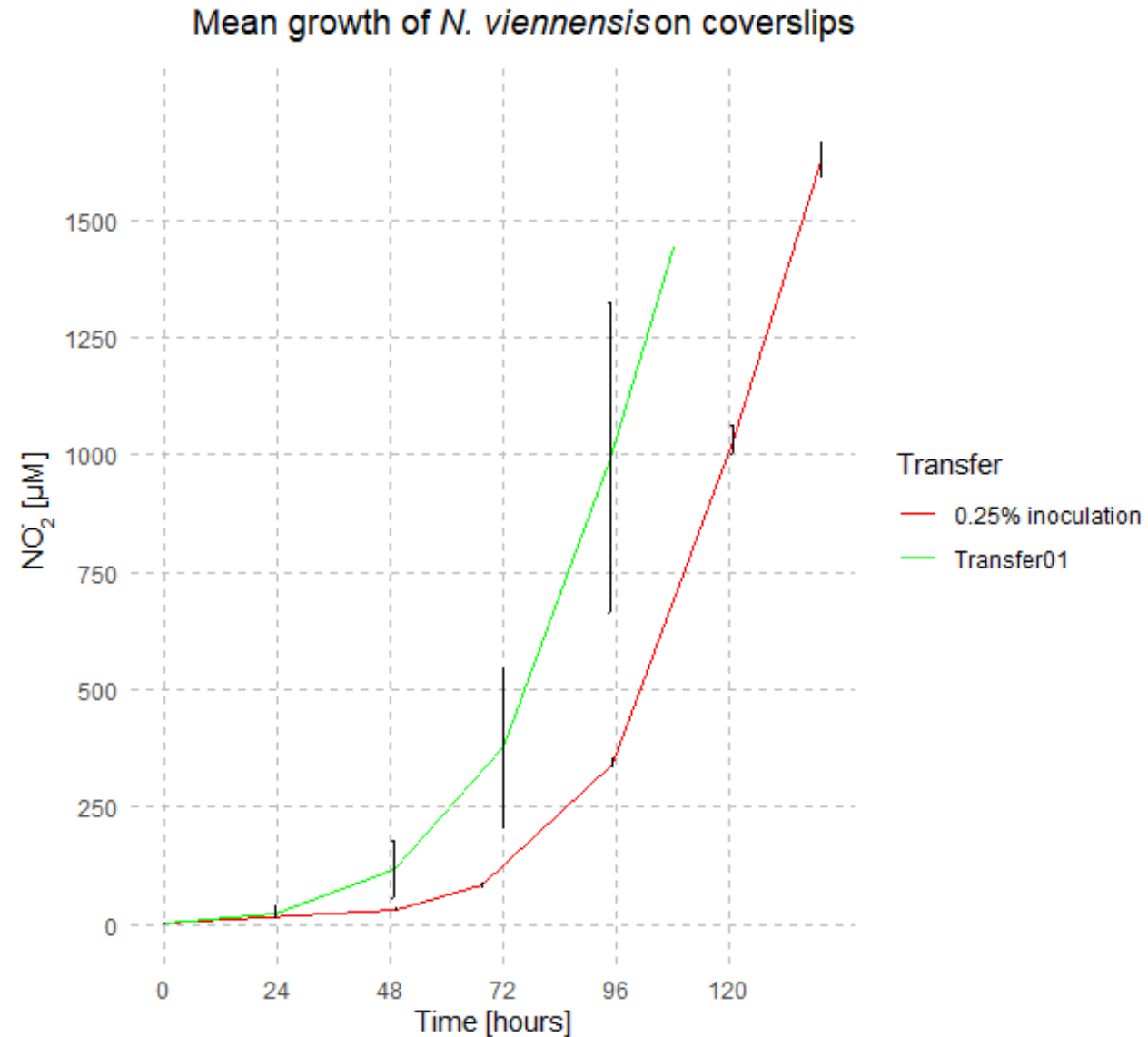


Initial inoculation – *N. viennensis*



Garden Soil

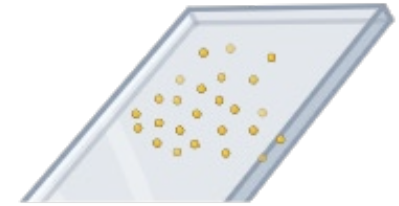
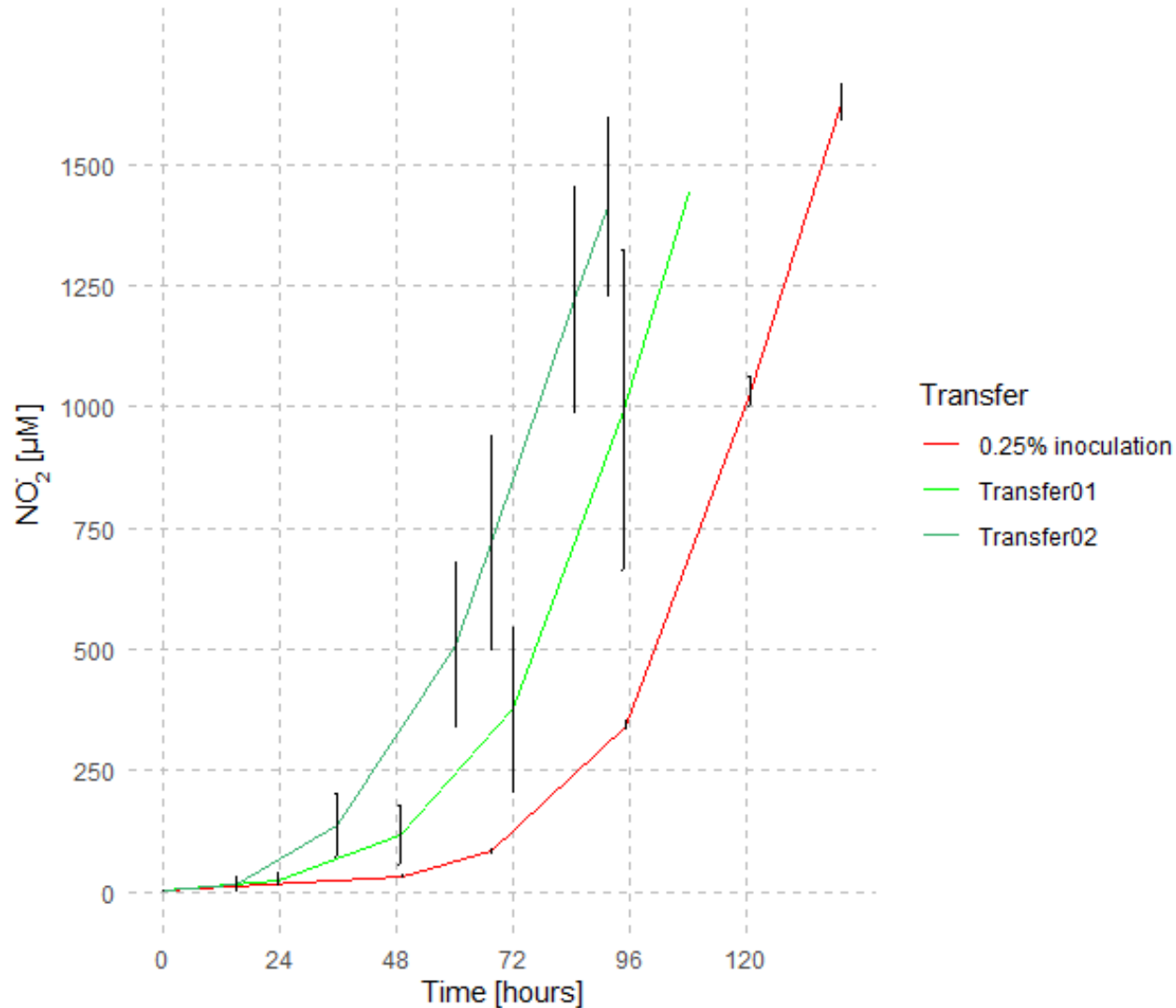
First transfer of coverslip



Garden Soil

Ammonia is oxidized faster – more cells in BF

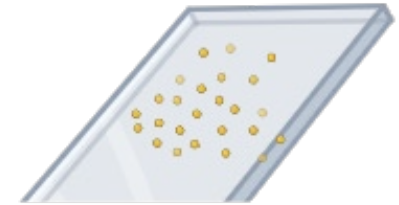
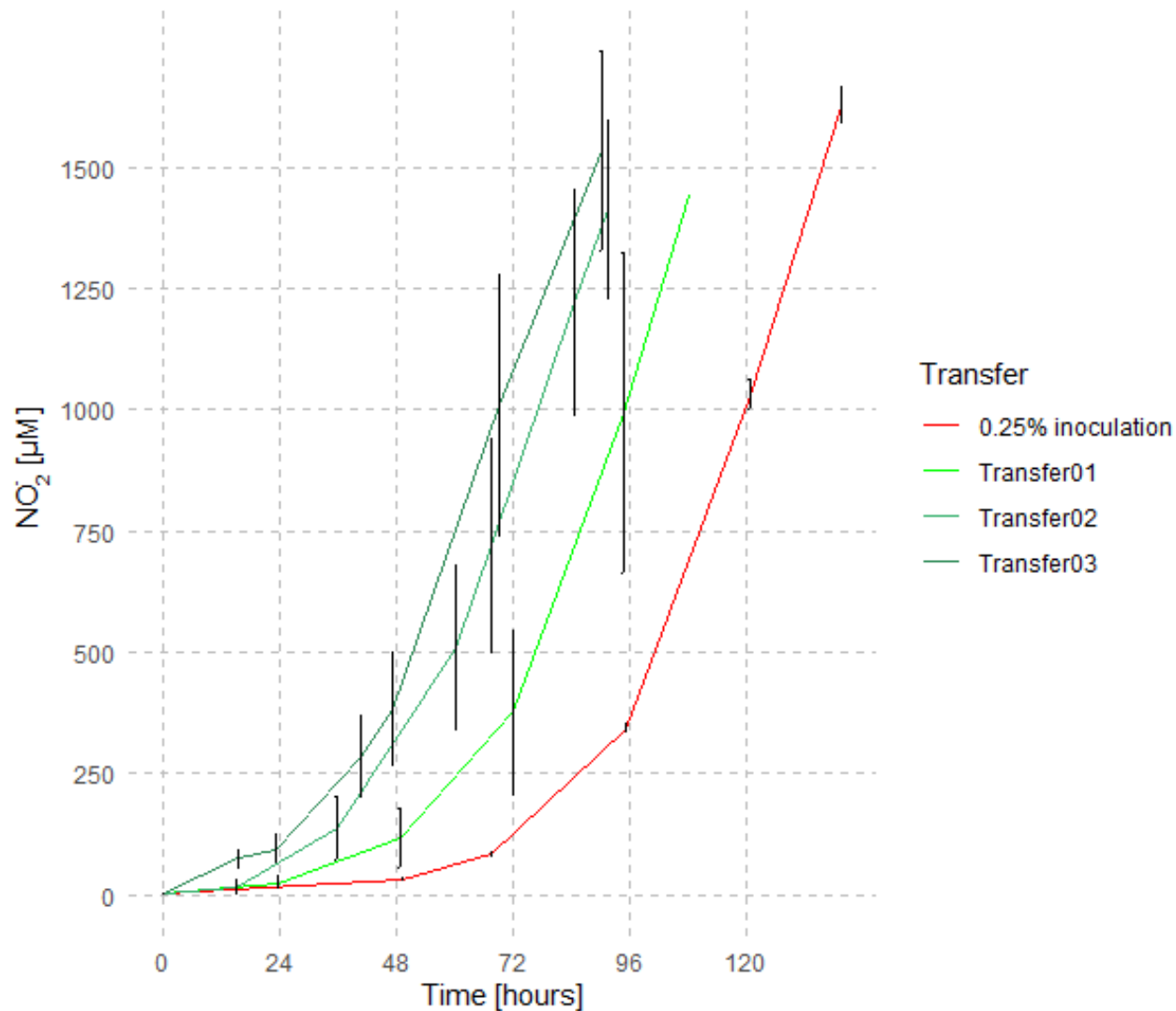
Mean growth of *N. viennensis* on coverslips



Garden Soil

Ammonia is oxidized faster – more cells in BF

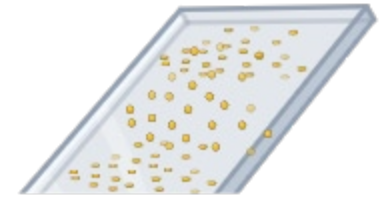
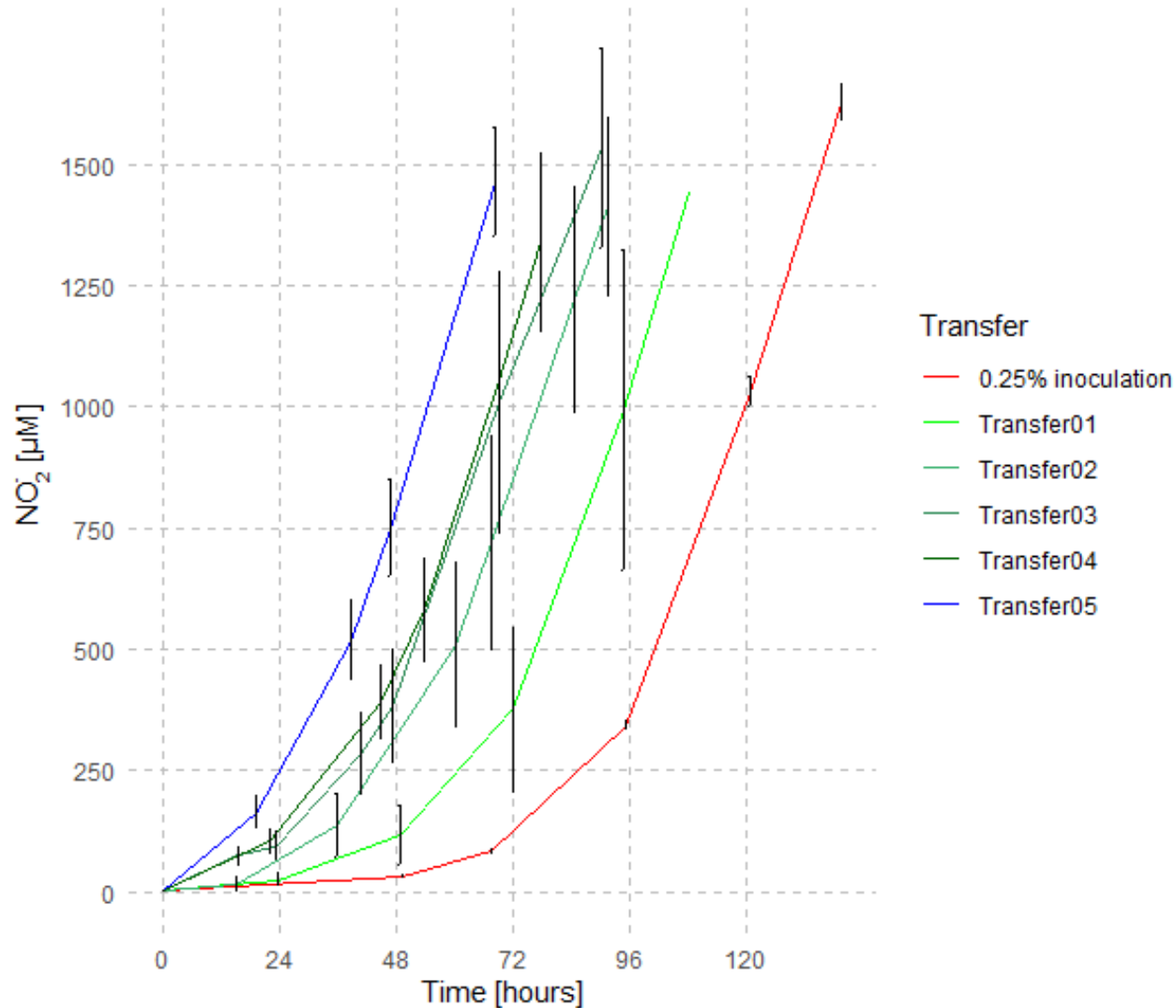
Mean growth of *N. viennensis* on coverslips



Garden Soil

Ammonia is oxidized faster – more cells in BF

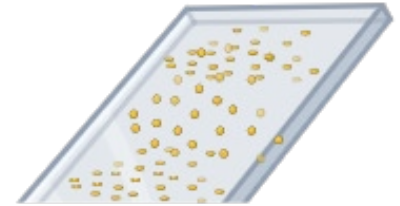
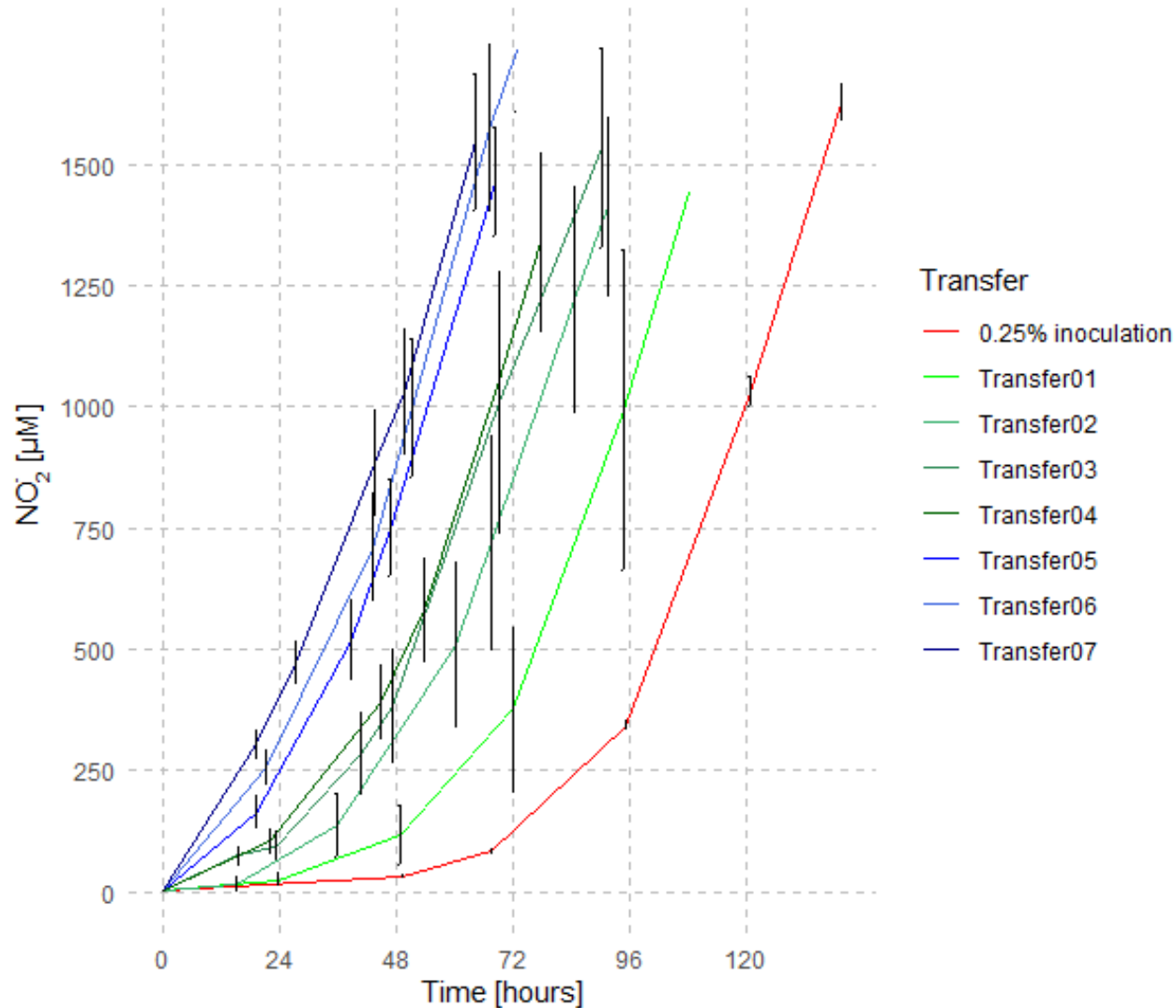
Mean growth of *N. viennensis* on coverslips



Garden Soil

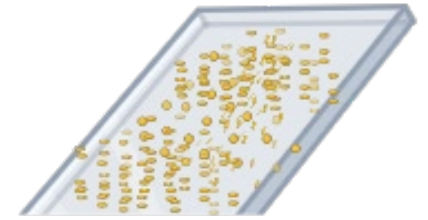
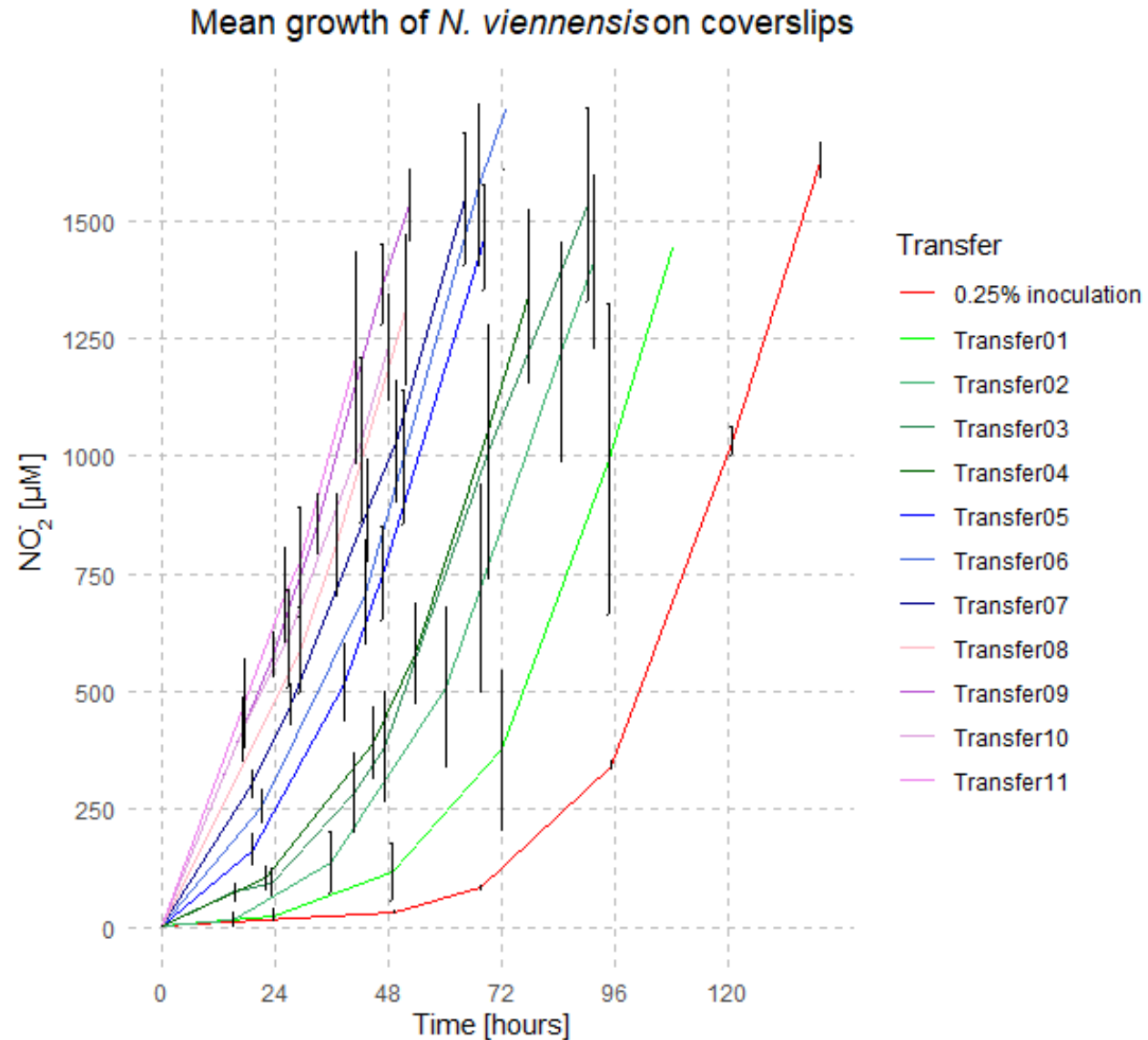
Ammonia is oxidized faster – more cells in BF

Mean growth of *N. viennensis* on coverslips



Garden Soil

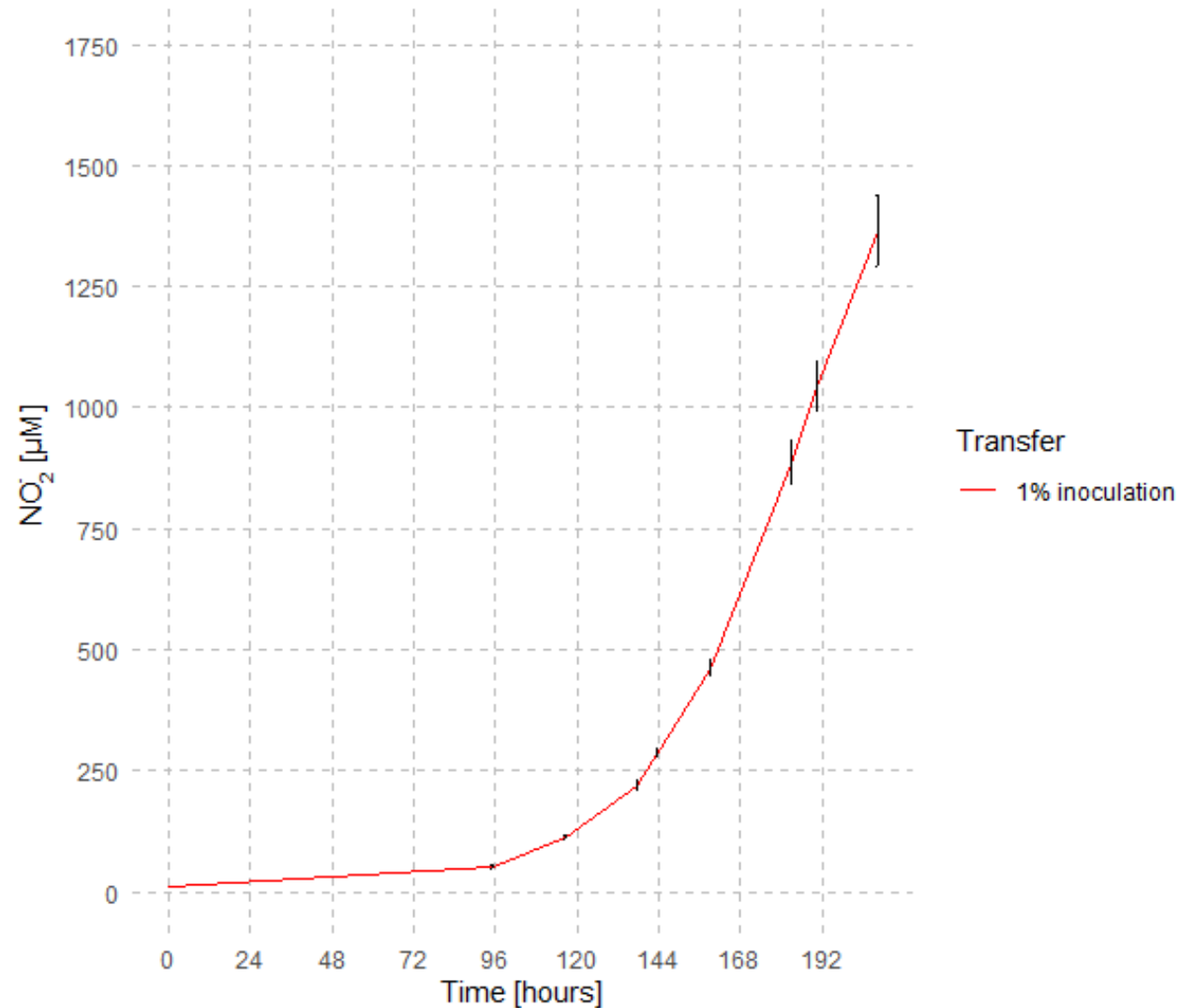
Maximum reached



Garden Soil

Initial inoculation - *N. franklandianus*

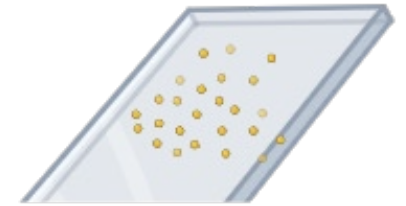
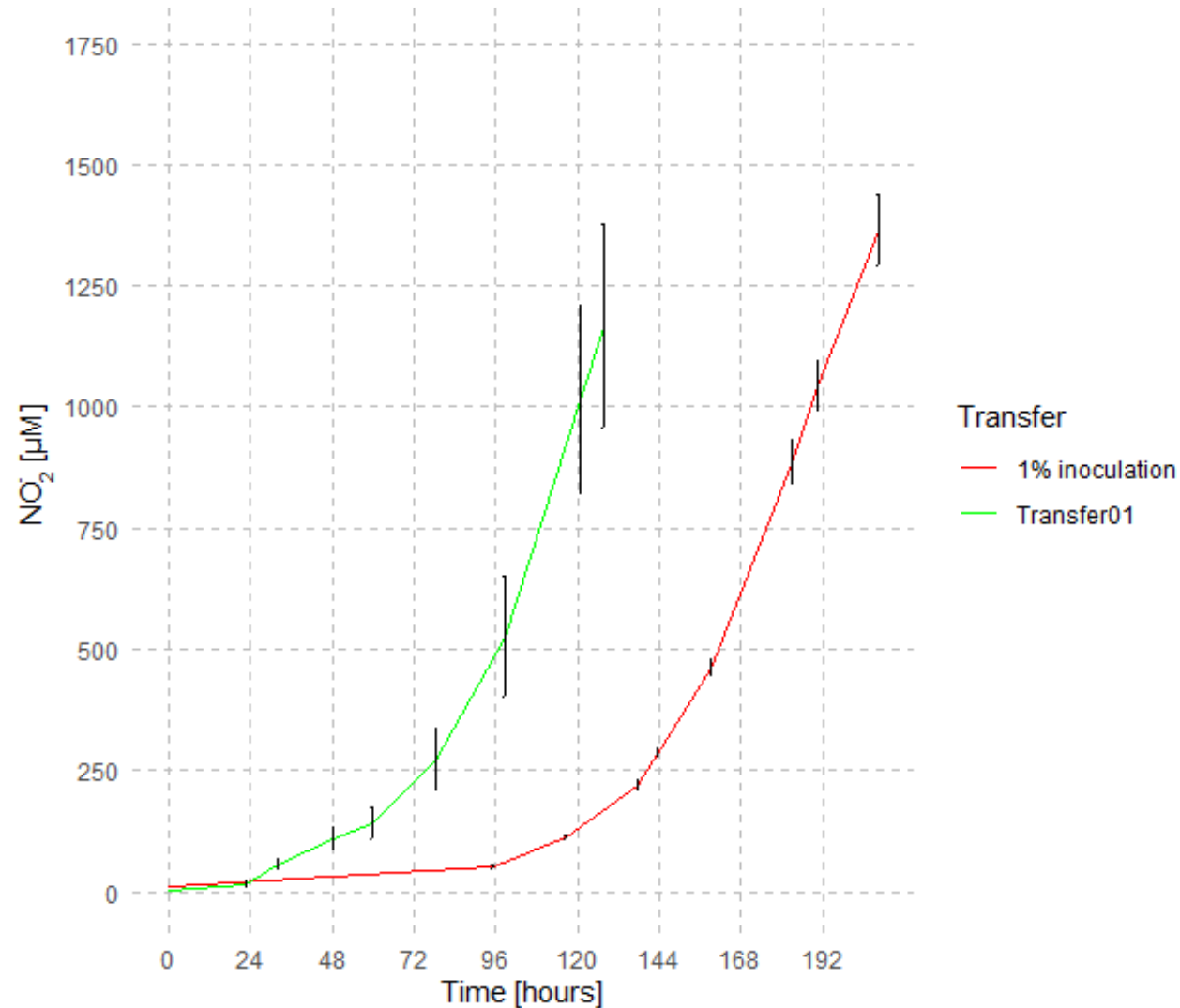
Mean growth of *N. franklandianus* with a coverslip



Agricultural Soil

Even faster acceleration than *N. viennensis*

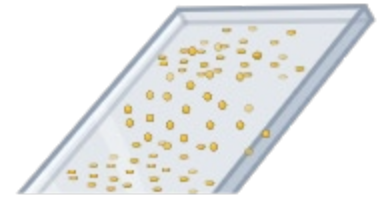
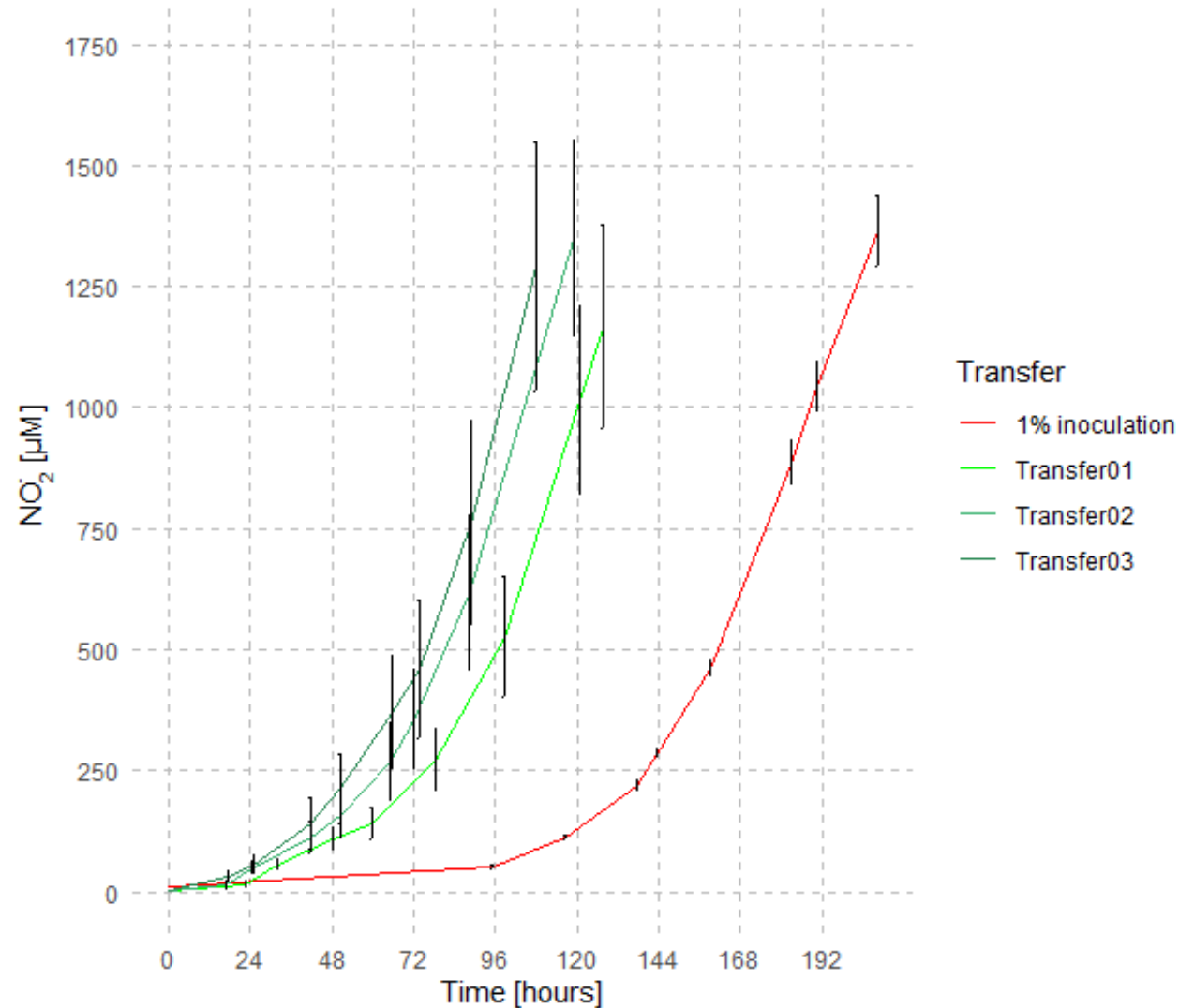
Mean growth of *N. franklandianus* with a coverslip



Agricultural Soil

Even faster acceleration than *N. viennensis*

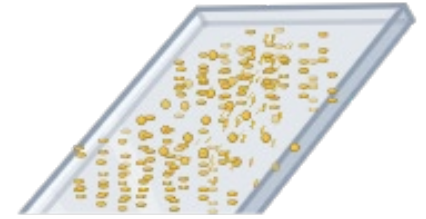
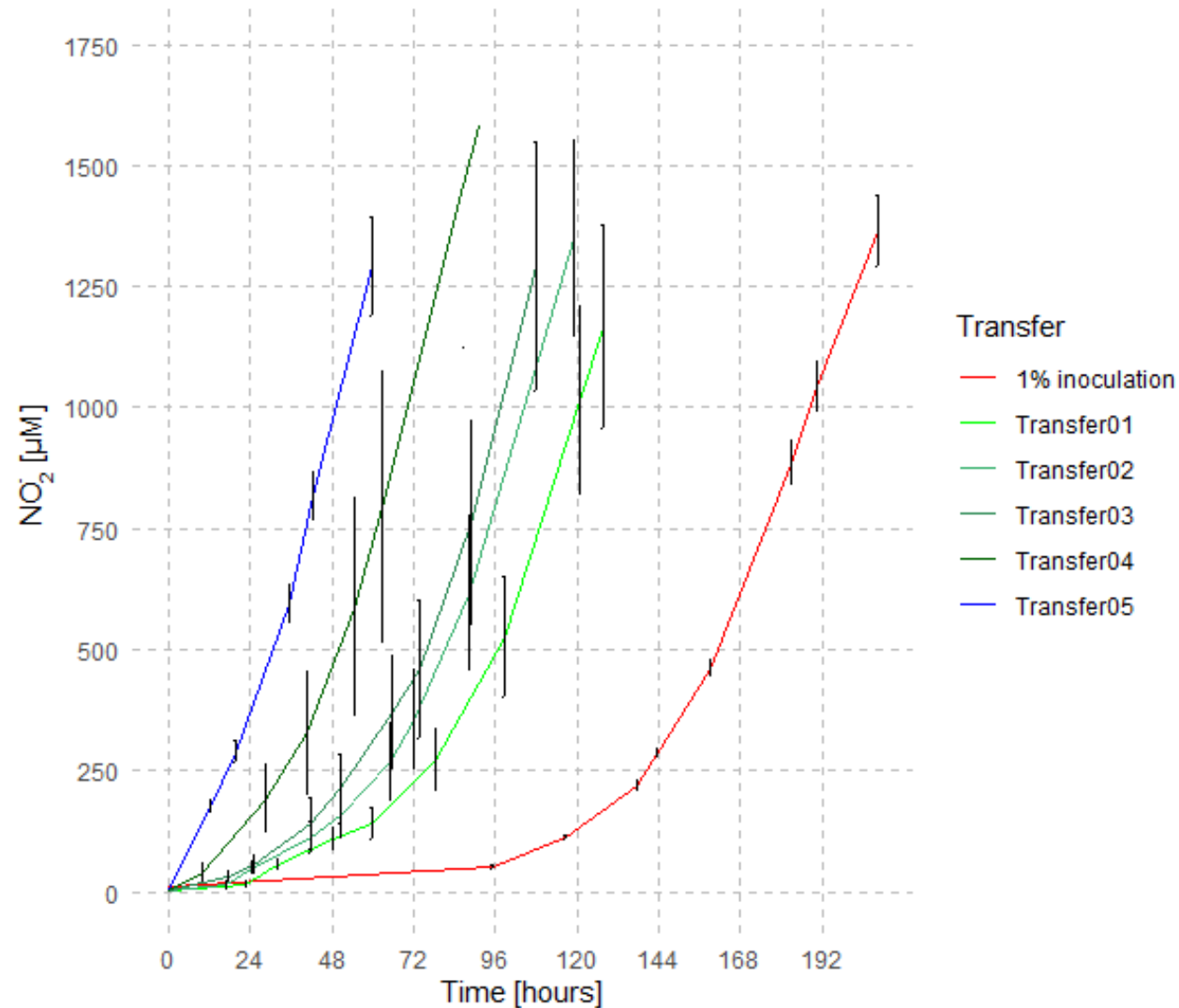
Mean growth of *N. franklandianus* with a coverslip



Agricultural Soil

Maximum reached faster

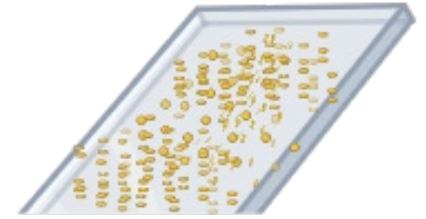
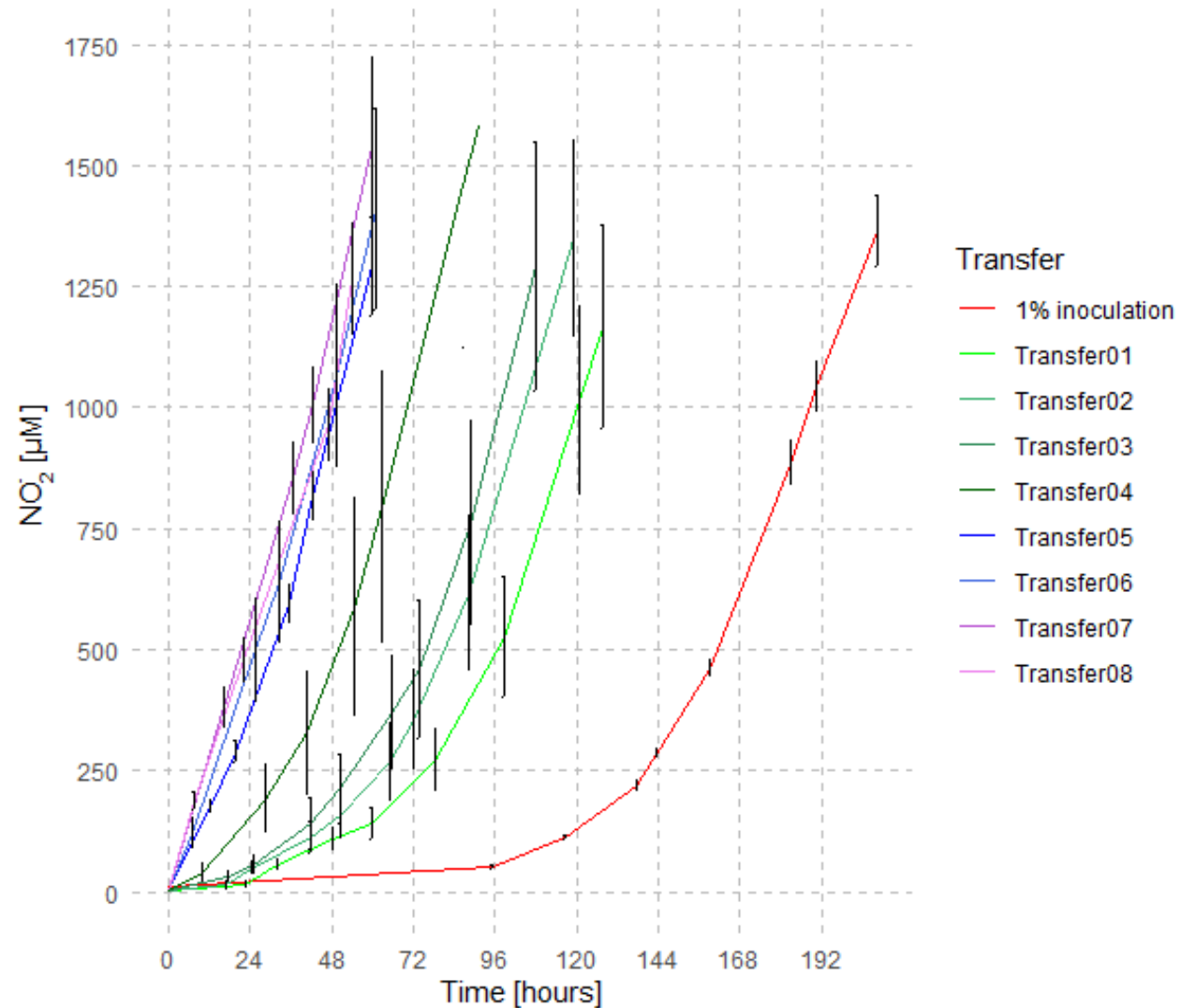
Mean growth of *N. franklandianus* with a coverslip



Agricultural Soil

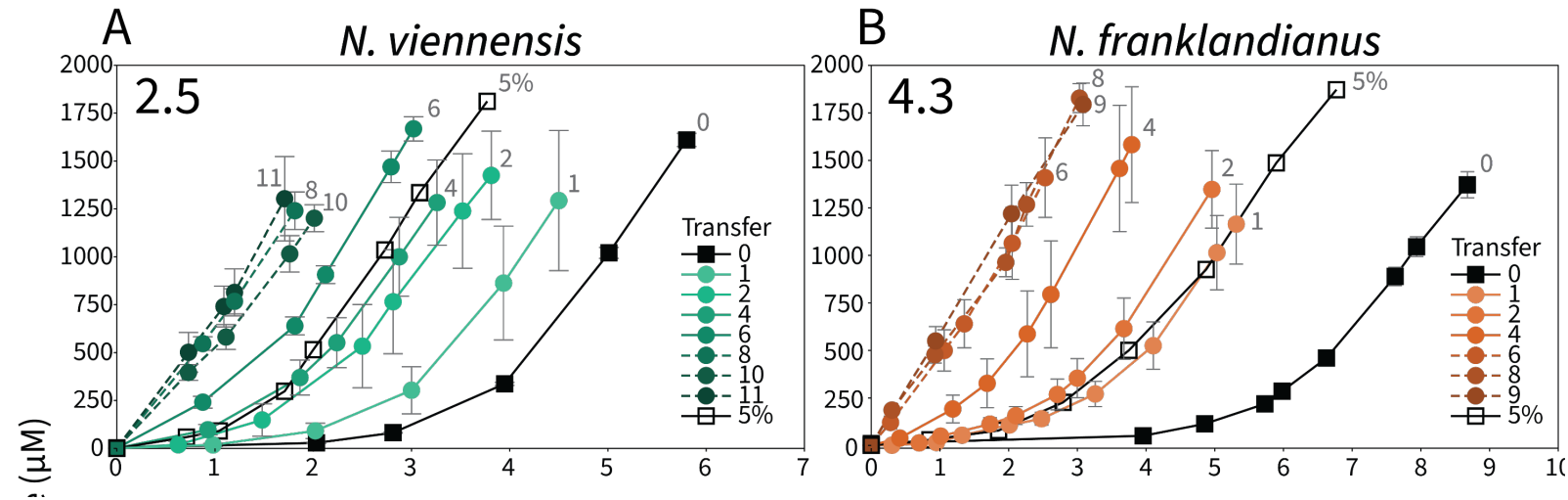
Stable maximum

Mean growth of *N. franklandianus* with a coverslip



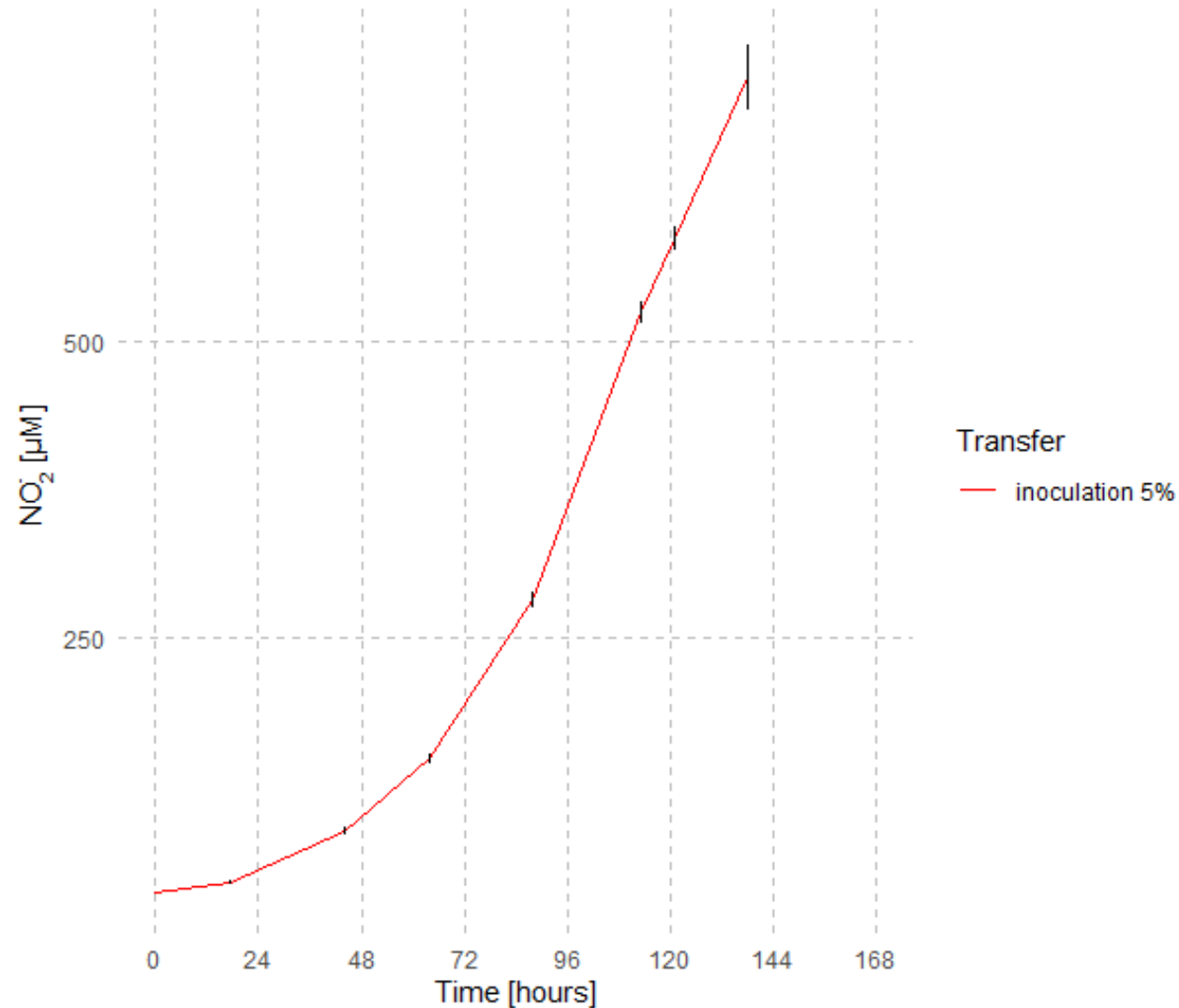
Agricultural Soil

AOA Growth as a Biofilm



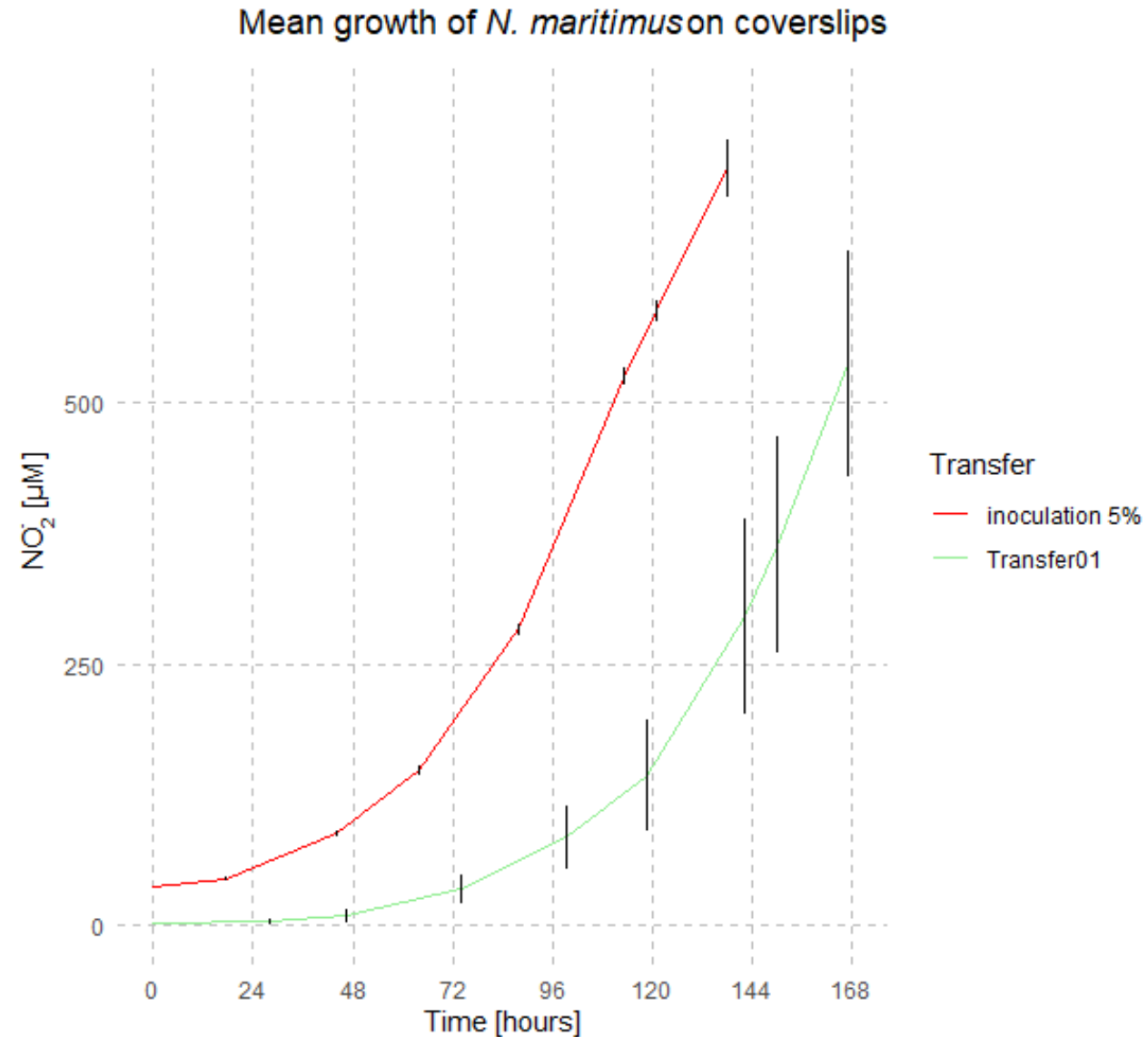
Initial inoculation - *N. maritimus*

Mean growth of *N. maritimus* on coverslips



Aquarium Gravel

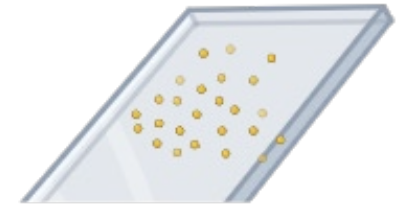
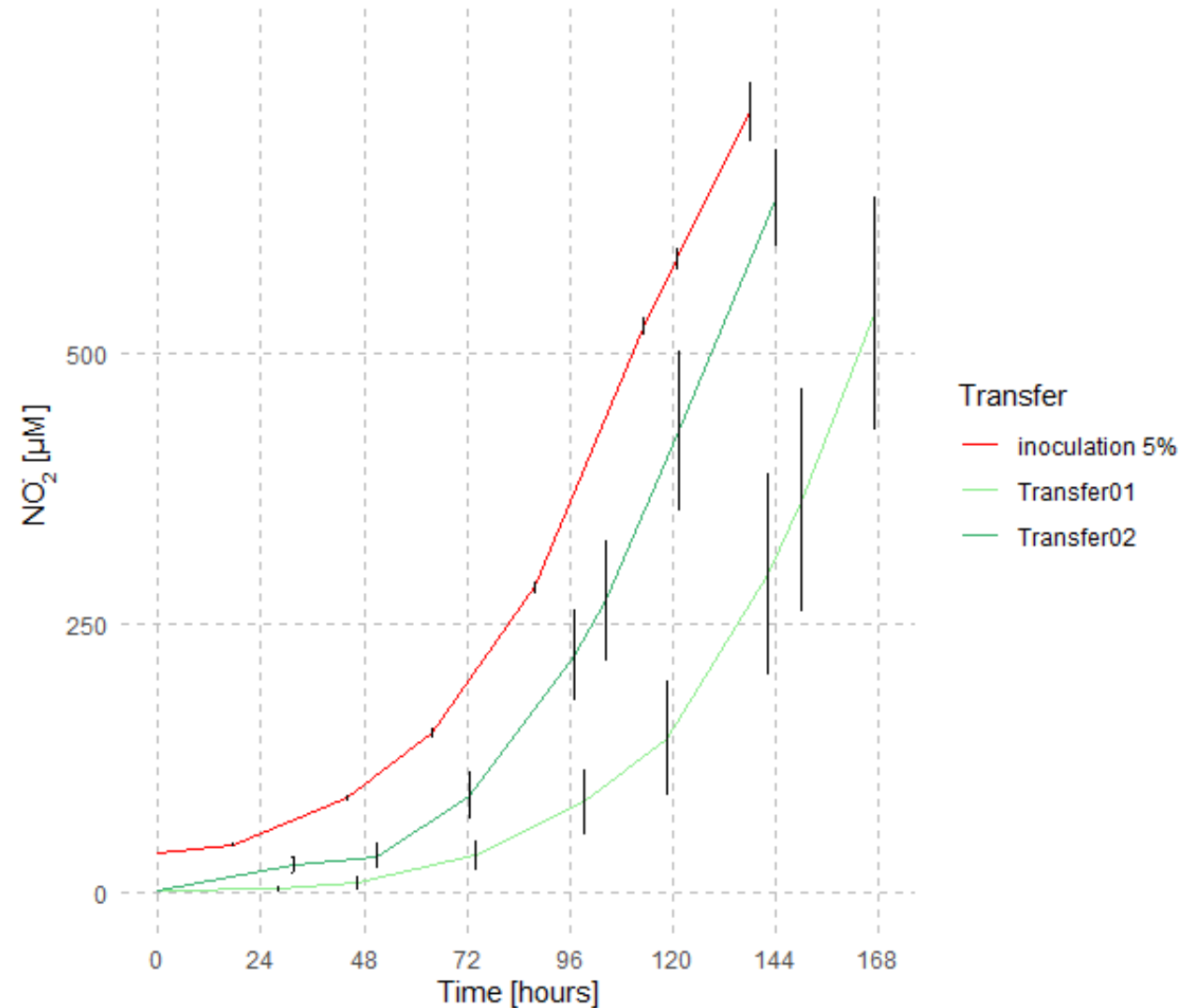
Longer lag phase



Aquarium Gravel

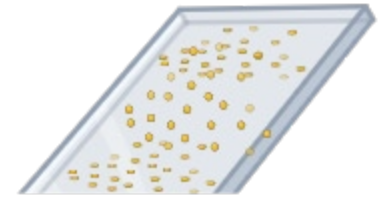
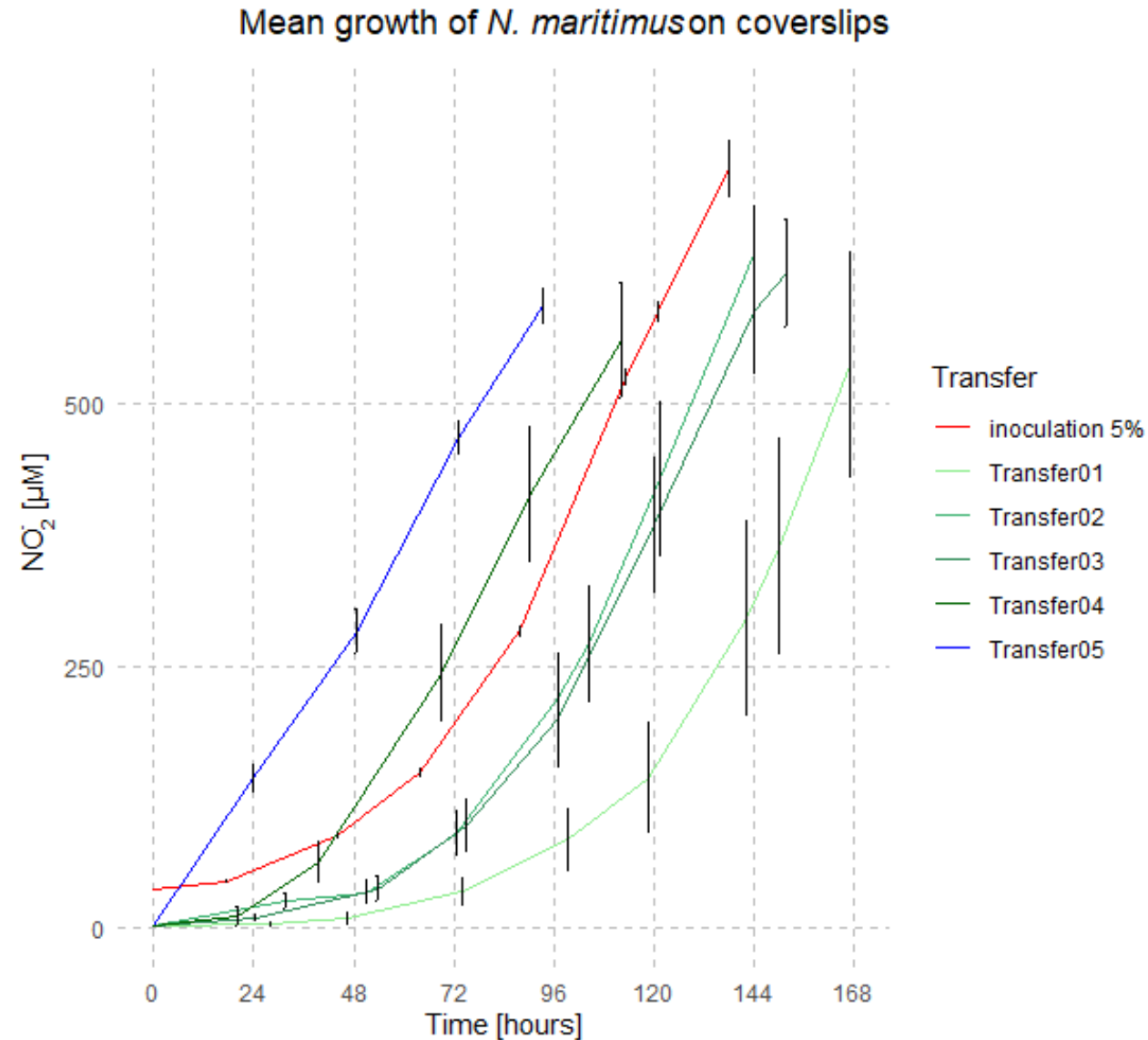
Biofilm is formed slowly

Mean growth of *N. maritimus* on coverslips



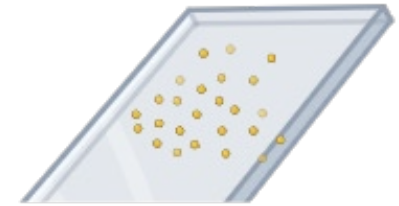
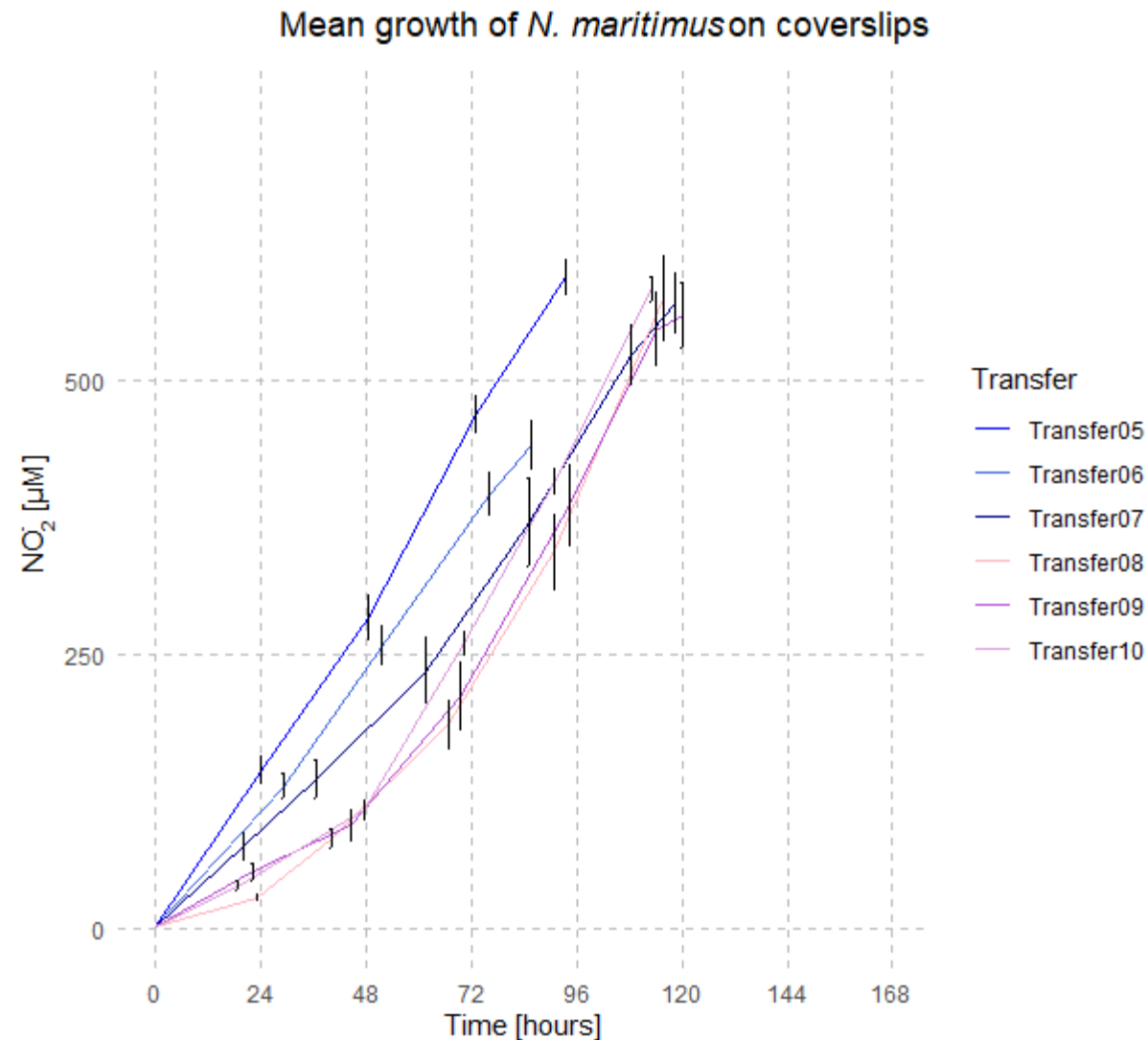
Aquarium Gravel

Maximum reached



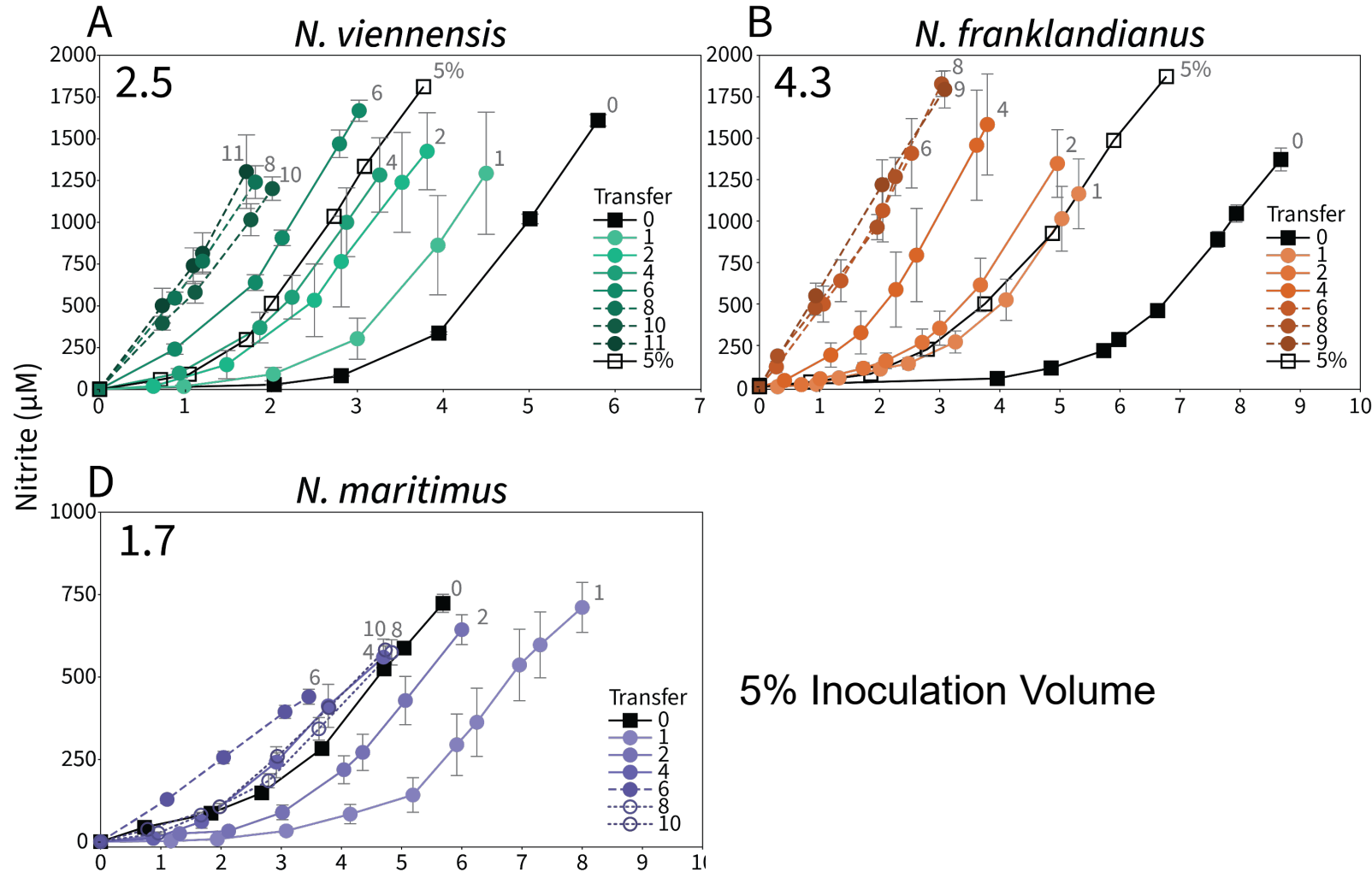
Aquarium Gravel

Unstable maximum



Aquarium Gravel

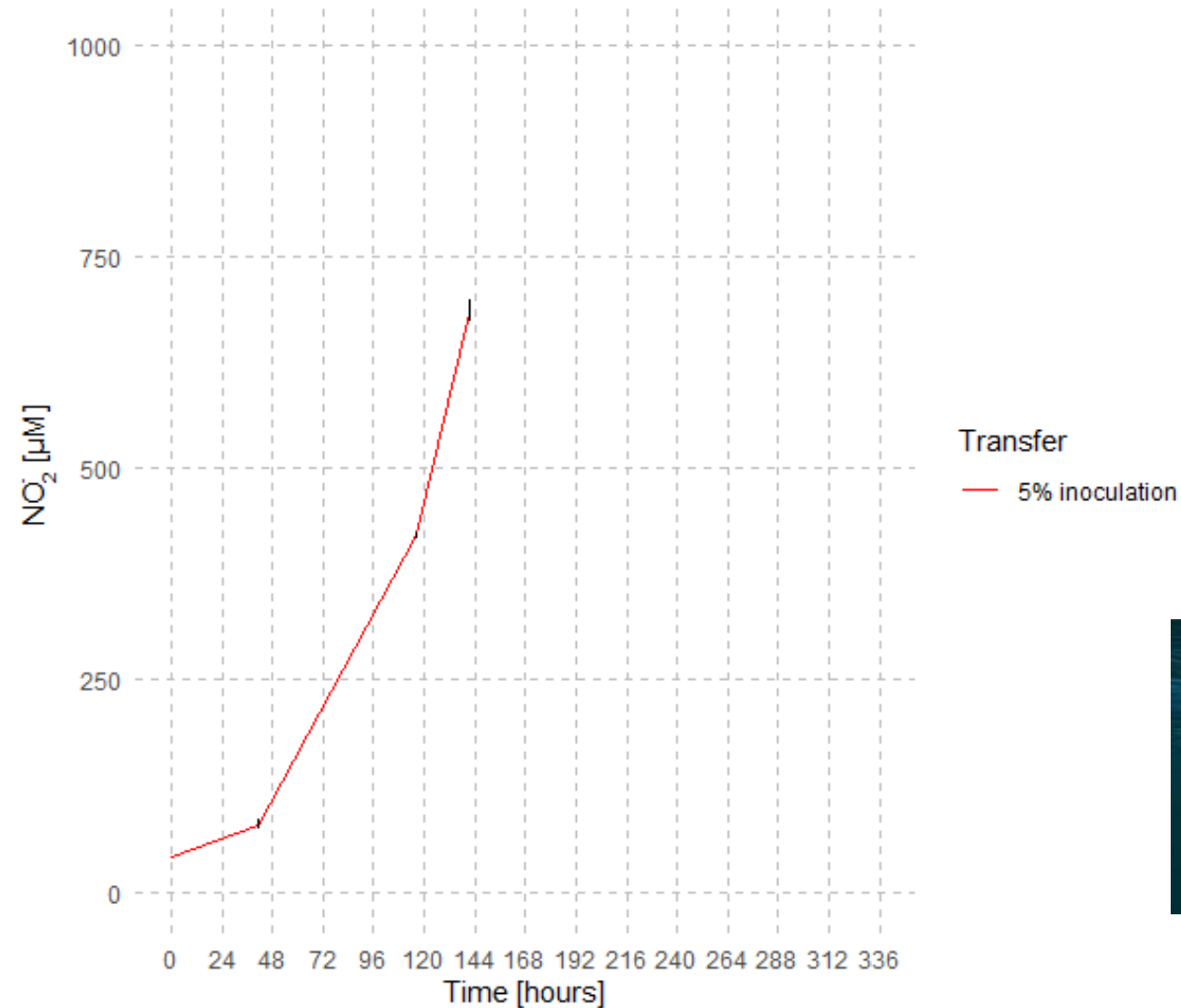
AOA Growth as a Biofilm



NV-0.25% Inoculation Volume
NF-1% Inoculation Volume

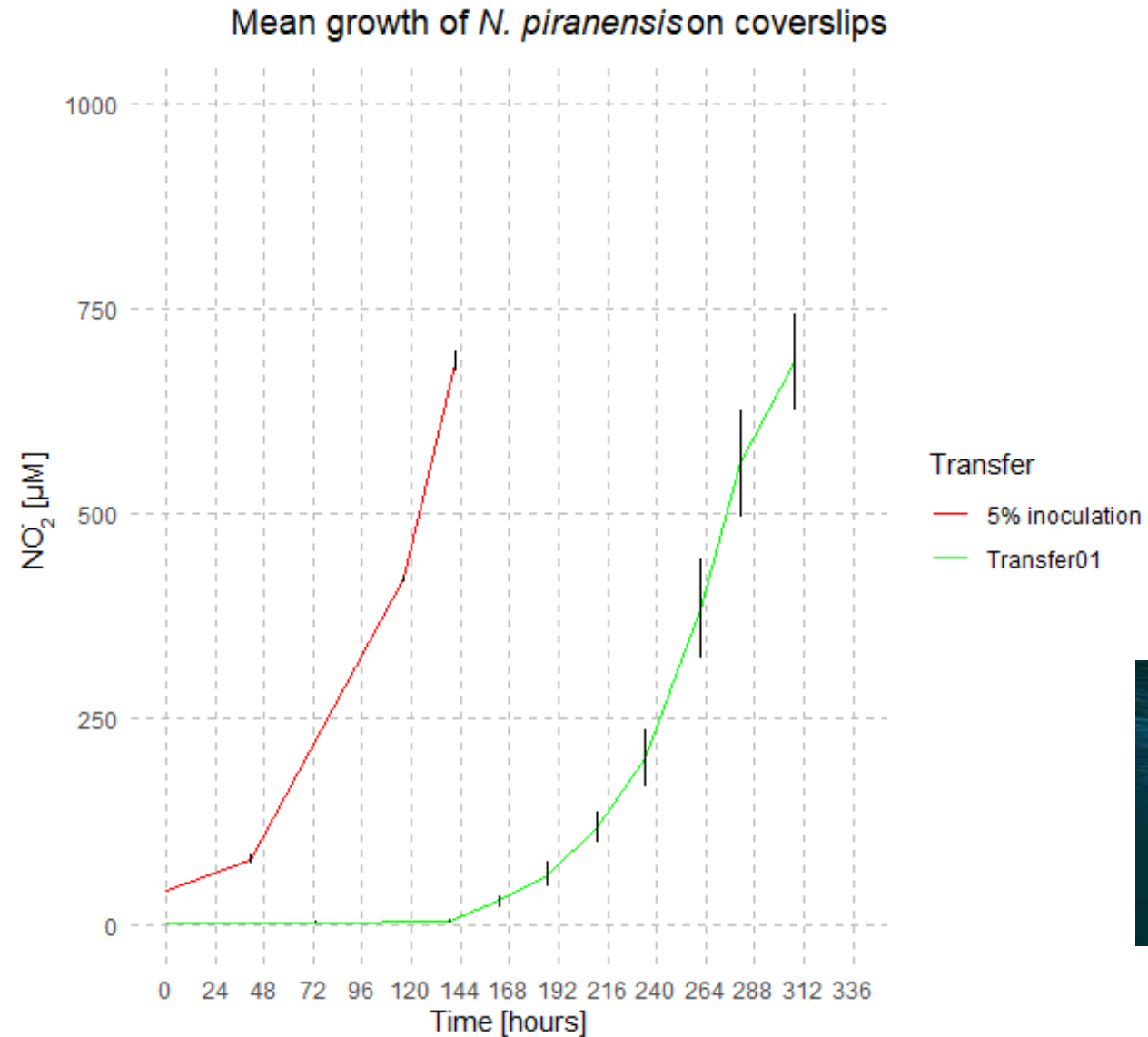
Initial inoculation - *N. piranensis*

Mean growth of *N. piranensis* with a coverslip



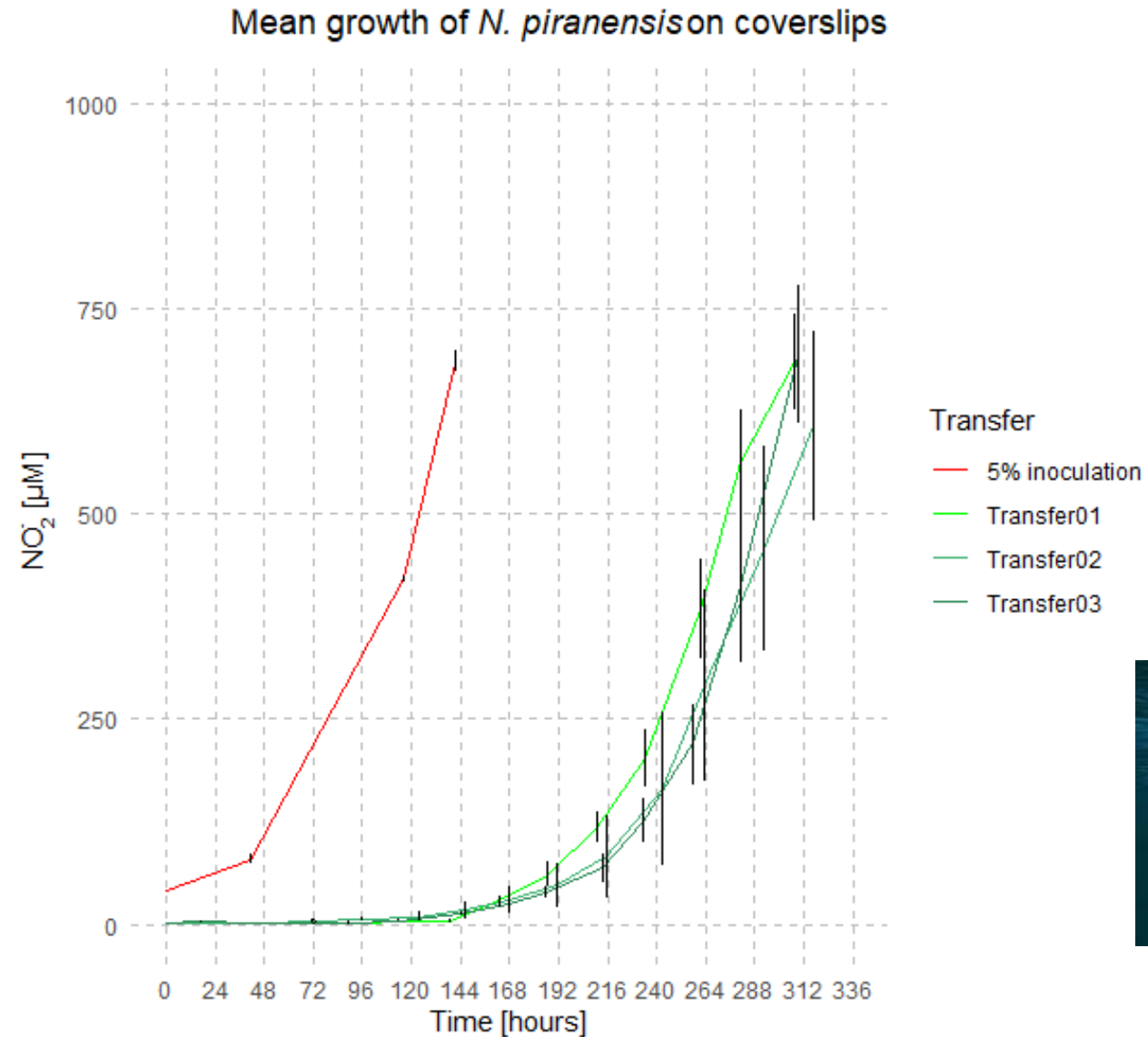
Coastal Surface Water

Very long initial lag phase



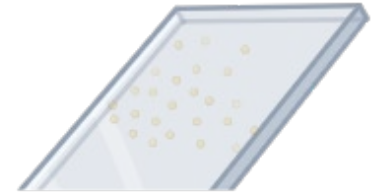
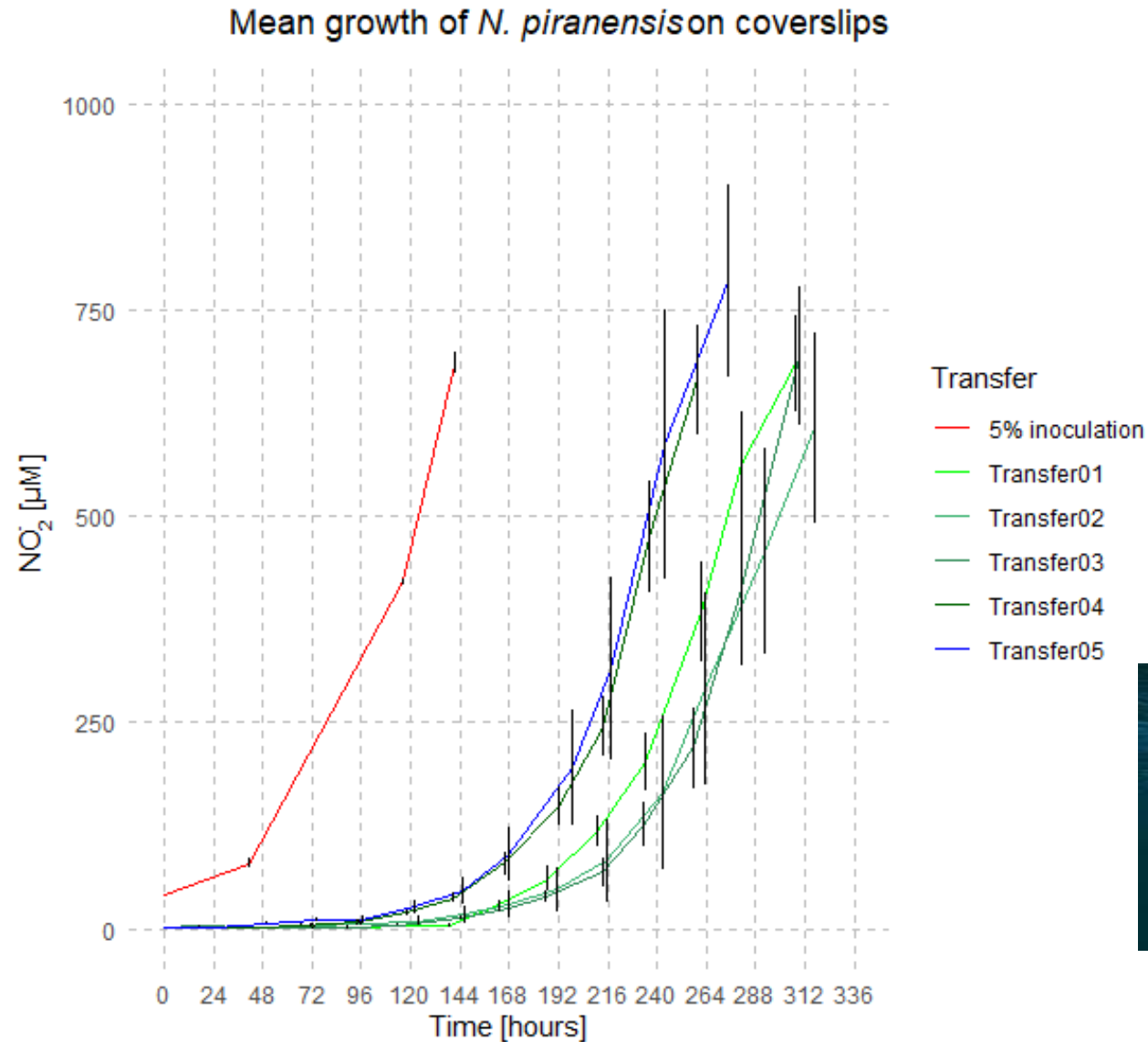
Coastal Surface Water

No acceleration



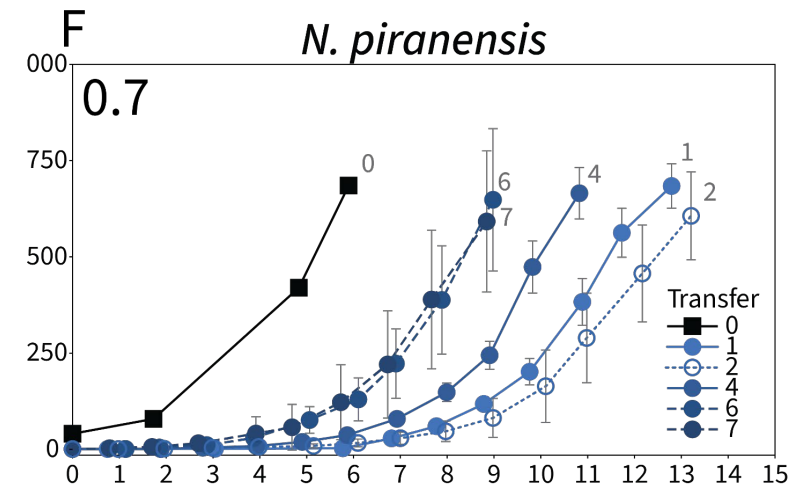
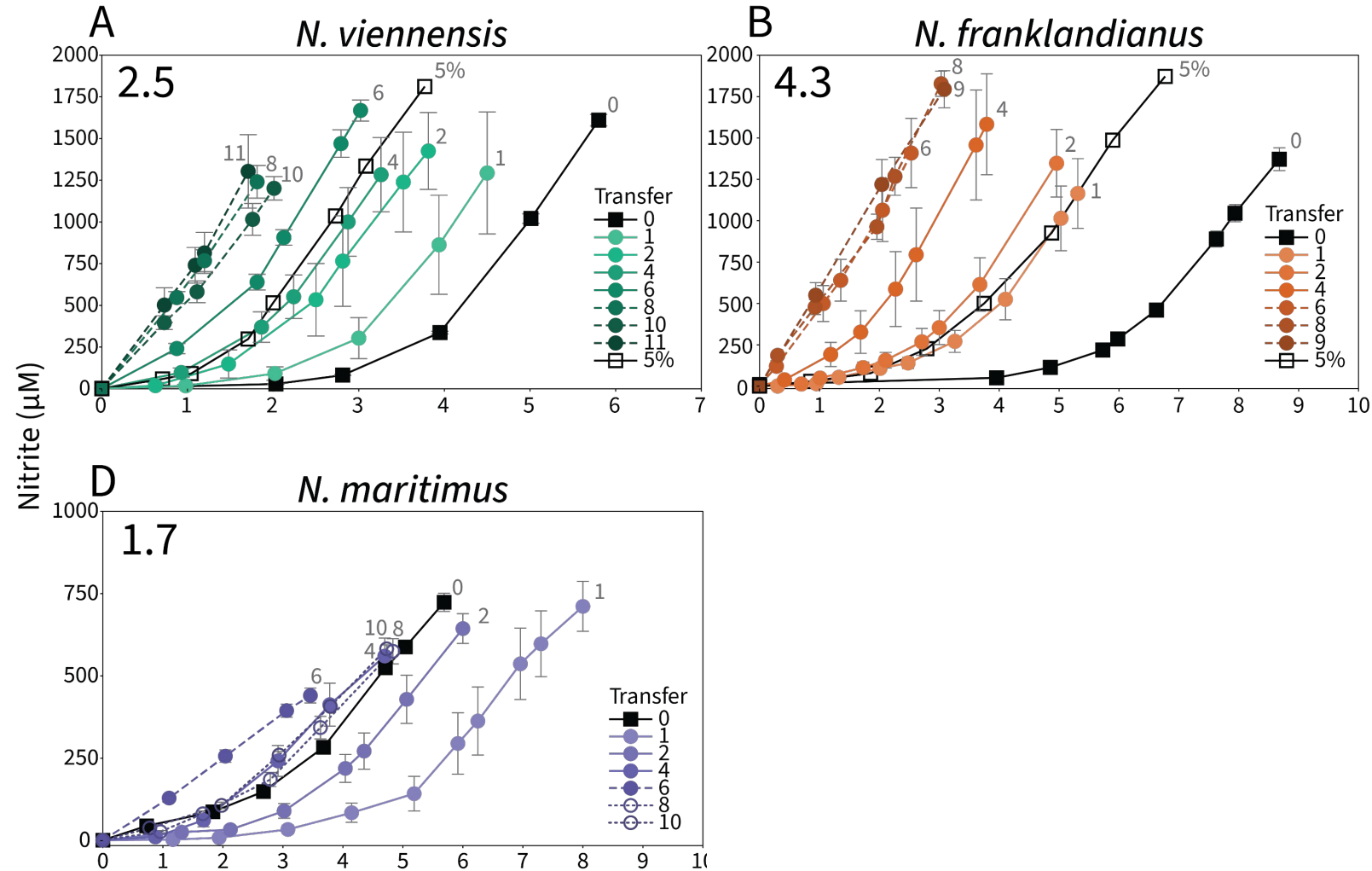
Coastal Surface Water

Minimal biofilm formation

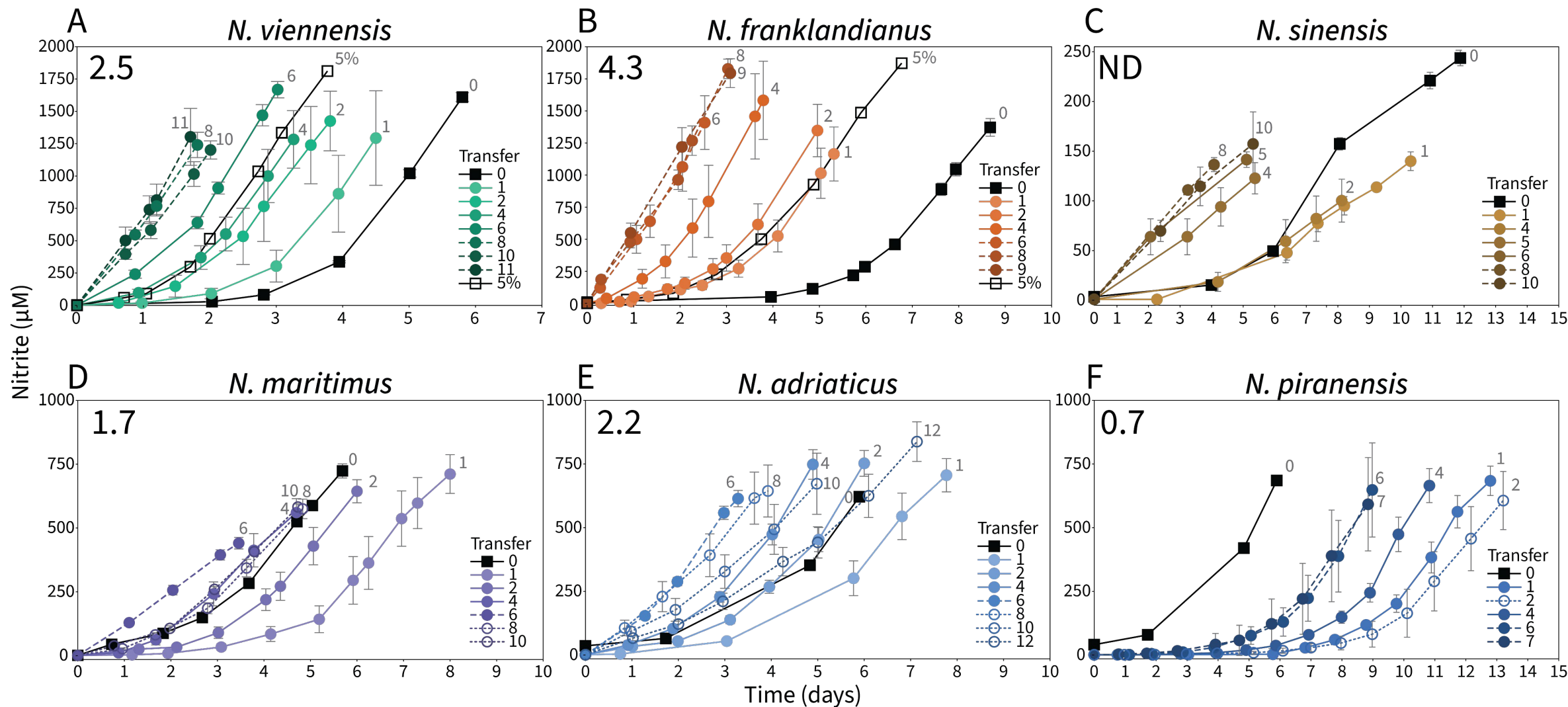


Coastal Surface Water

AOA Growth as a Biofilm



AOA Growth as a Biofilm

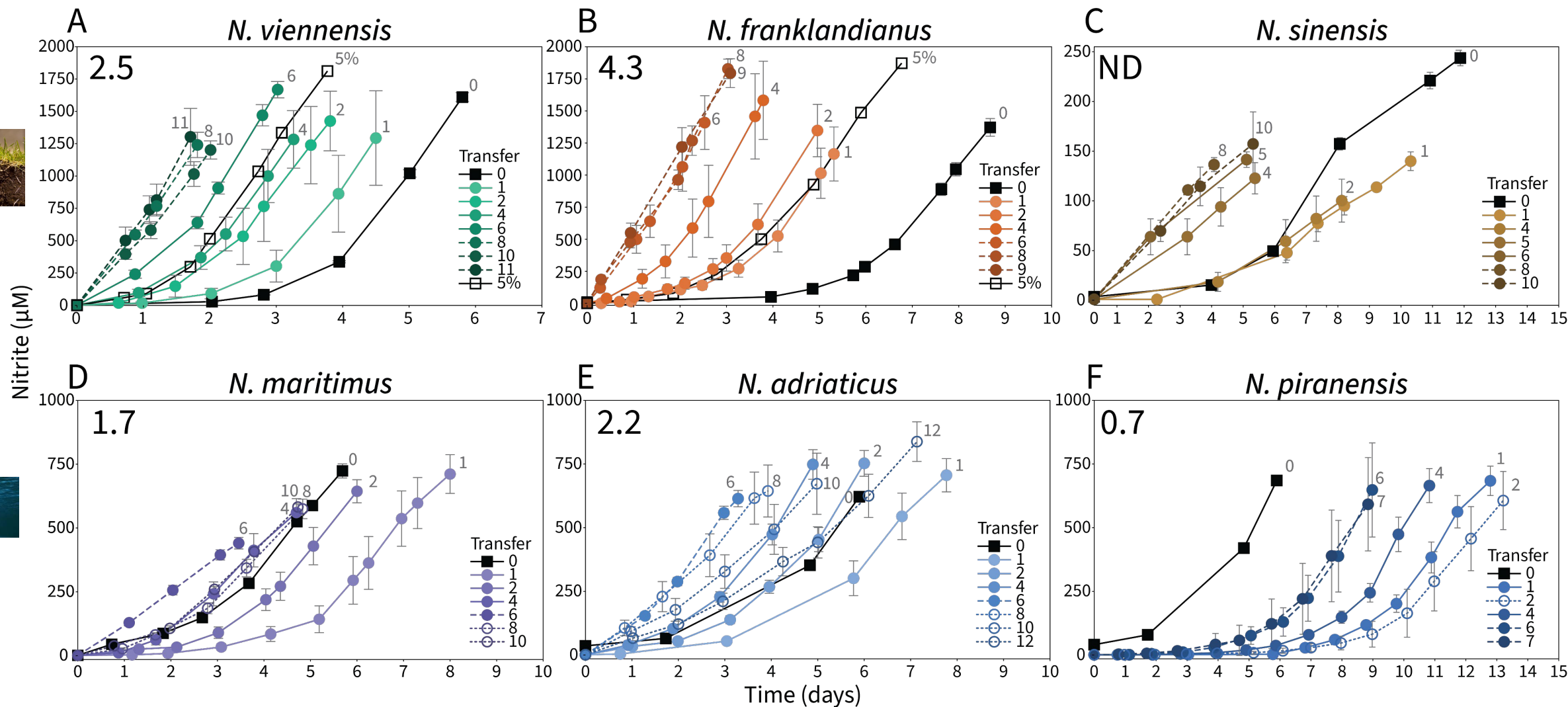


Biofilm Accumulation Rate – accounting for species specific generation times

- ST (Standard time) = time required to produce 500μM of NO₂ for a planktonic culture with a 5% inoculation volume
- BT (Biofilm time) = time required to produce 500μM of NO₂ for biofilms after every transfer

$$\text{Biofilm Accumulation Rate (BAR)} = \frac{ST}{BT_x}$$

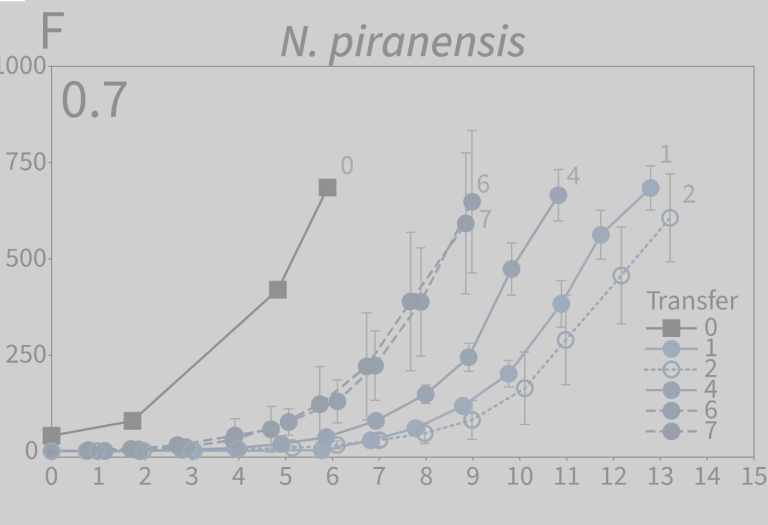
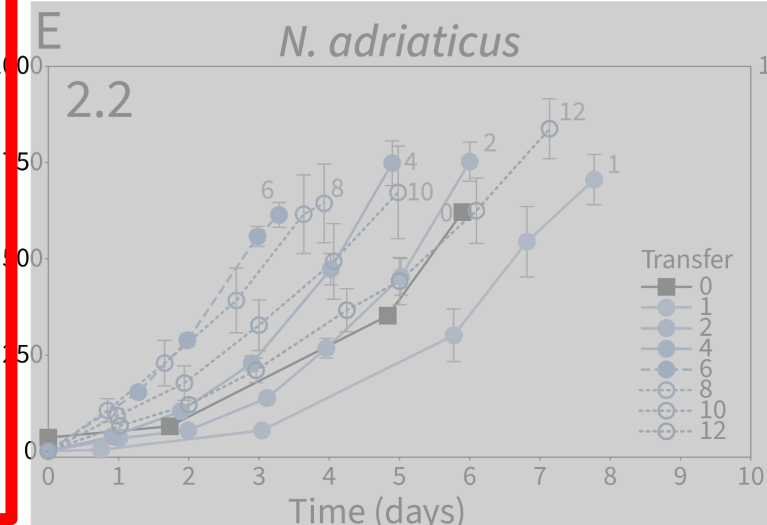
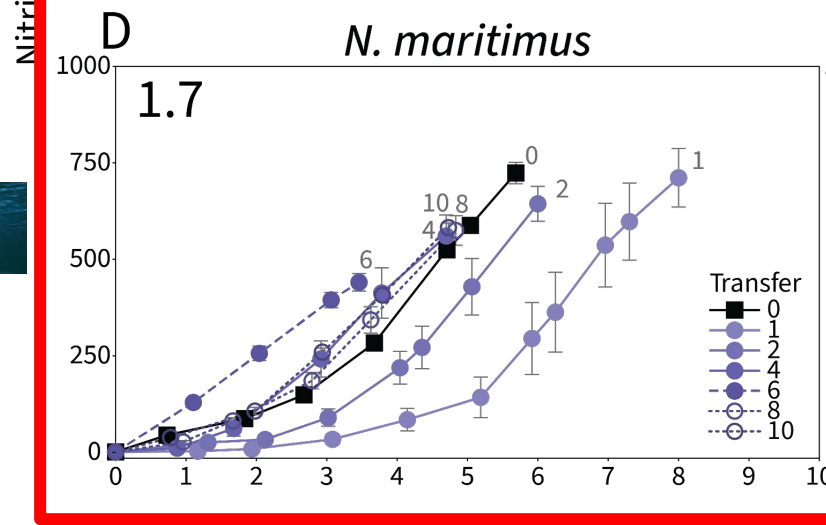
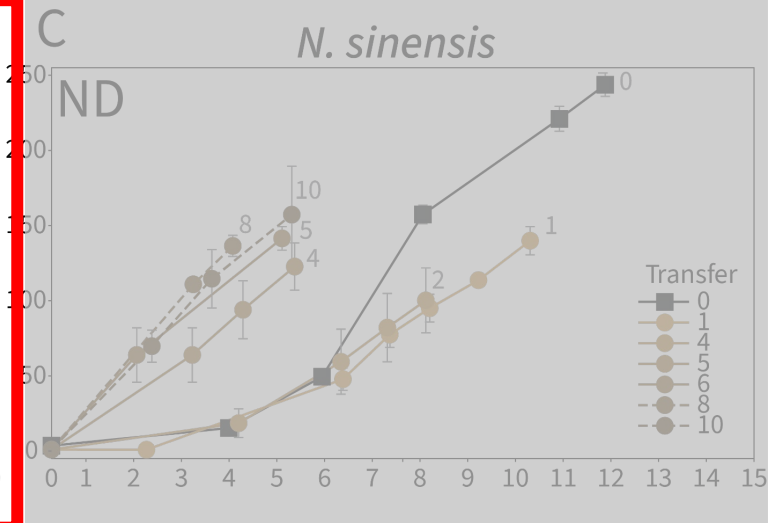
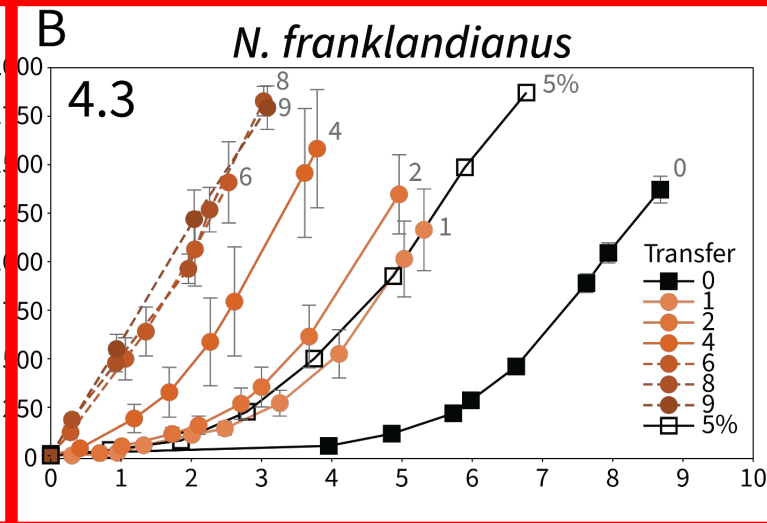
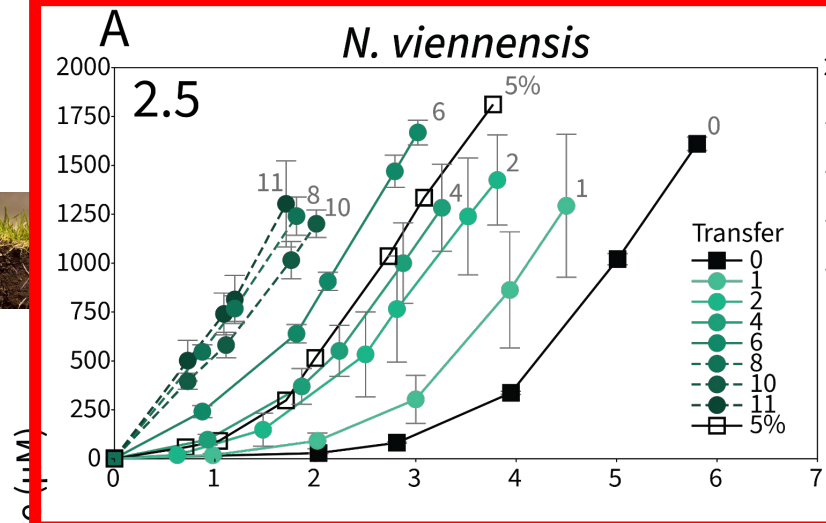
AOA Growth as a Biofilm



Questions

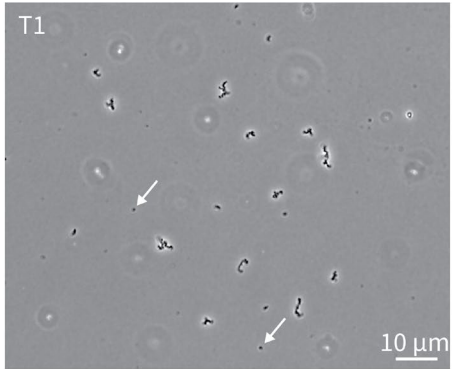
- Is biofilm formation a common trait of AOA? **YES**
- Are there physiological responses associated with biofilms?
- Does biofilm growth affect nitrification?

AOA Growth as a Biofilm

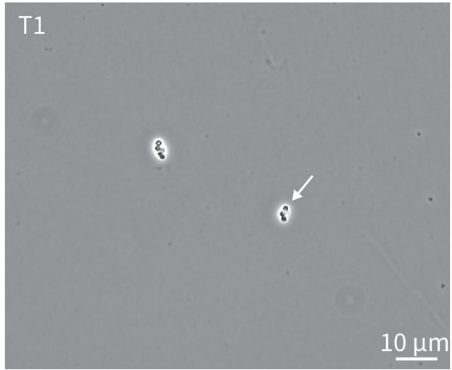


Growth Observed with Light Microscopy

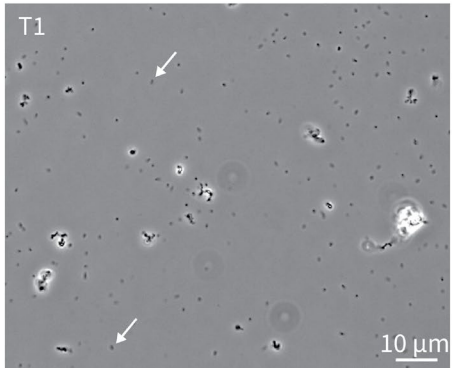
NV



NF

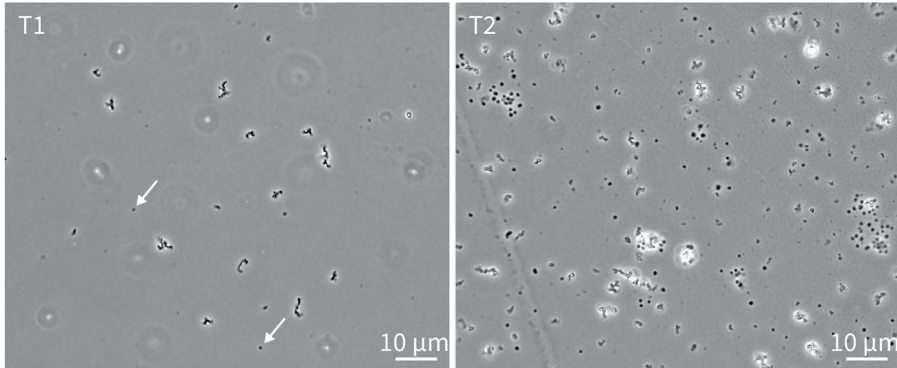


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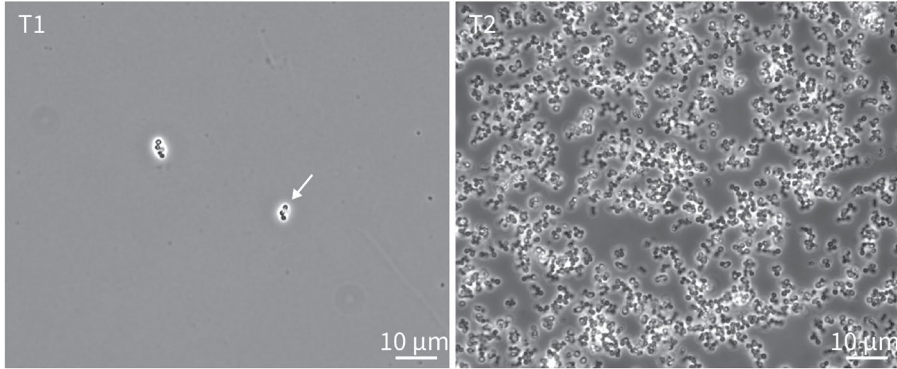


Growth Observed with Light Microscopy

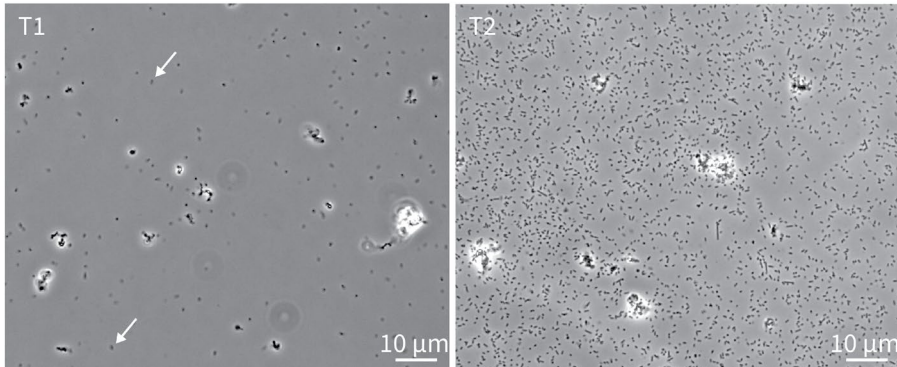
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NF

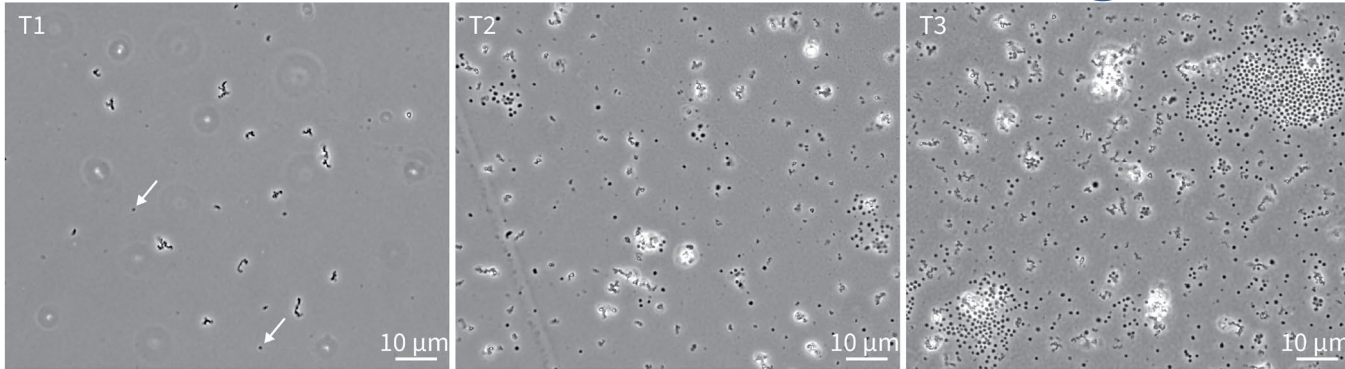


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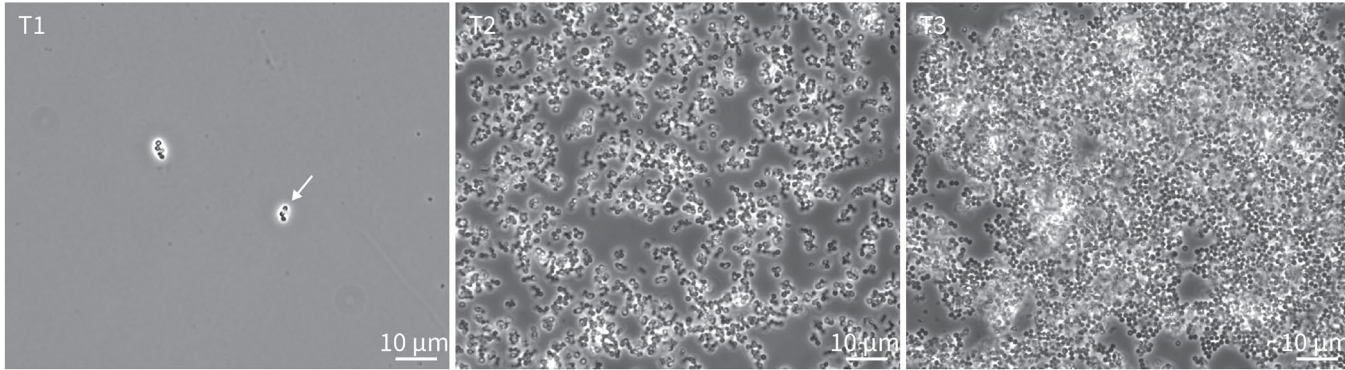


Growth Observed with Light Microscopy

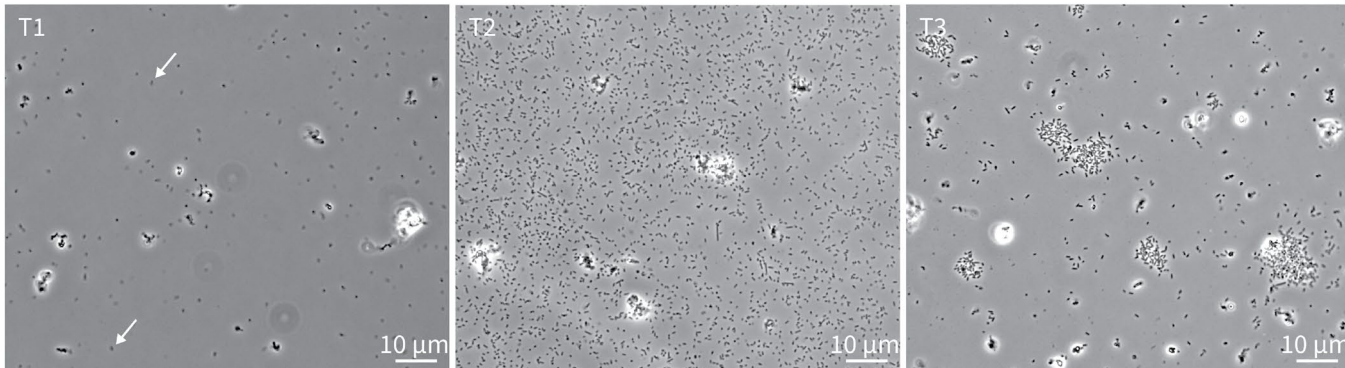
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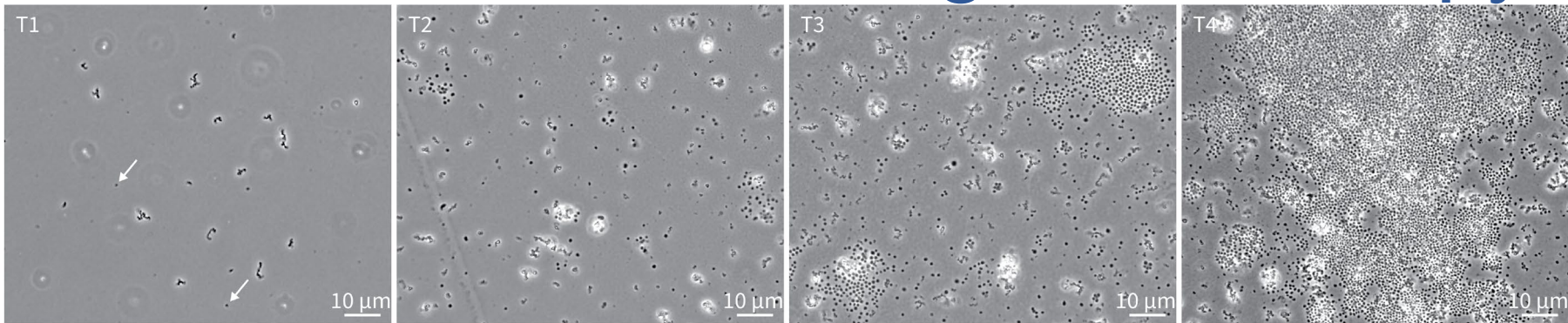


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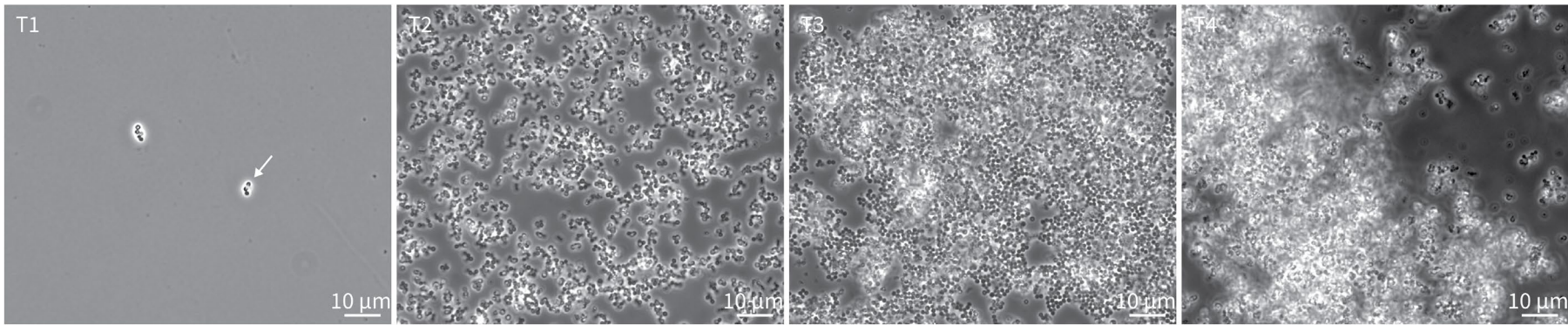


Growth Observed with Light Microscopy

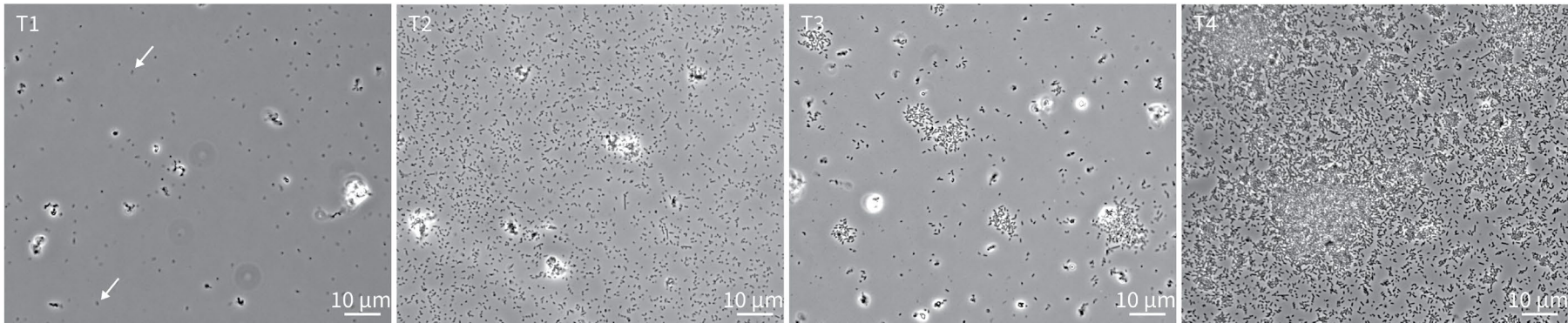
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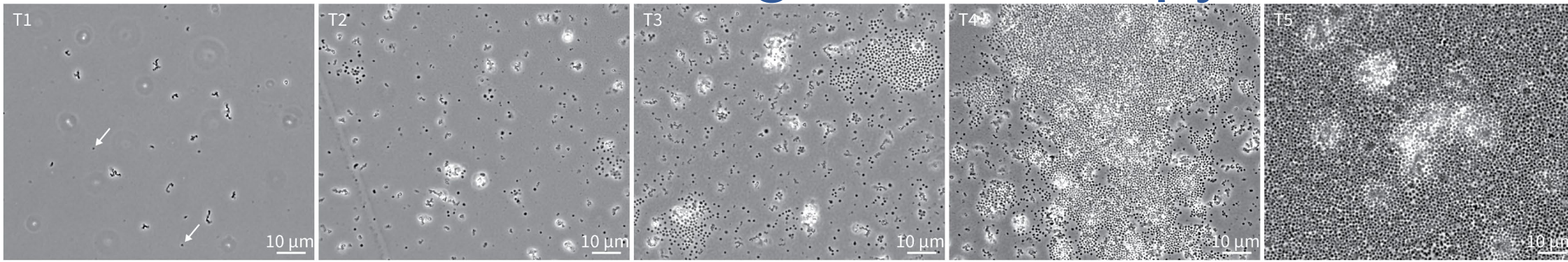


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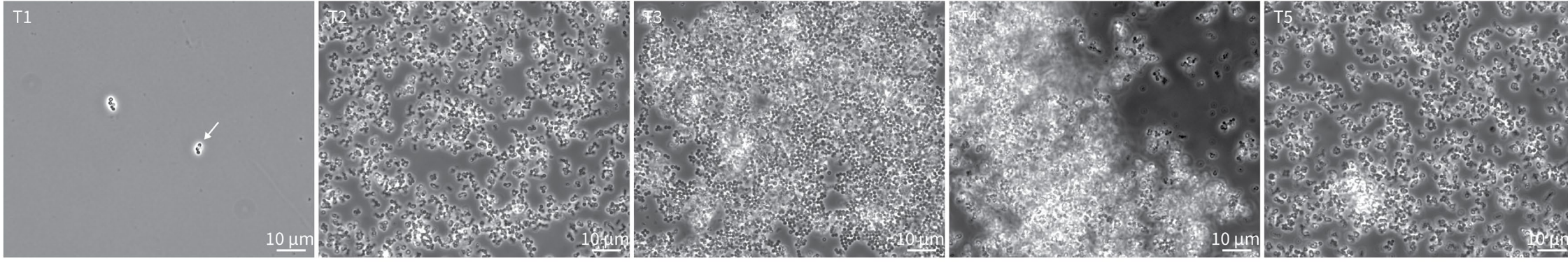


Growth Observed with Light Microscopy

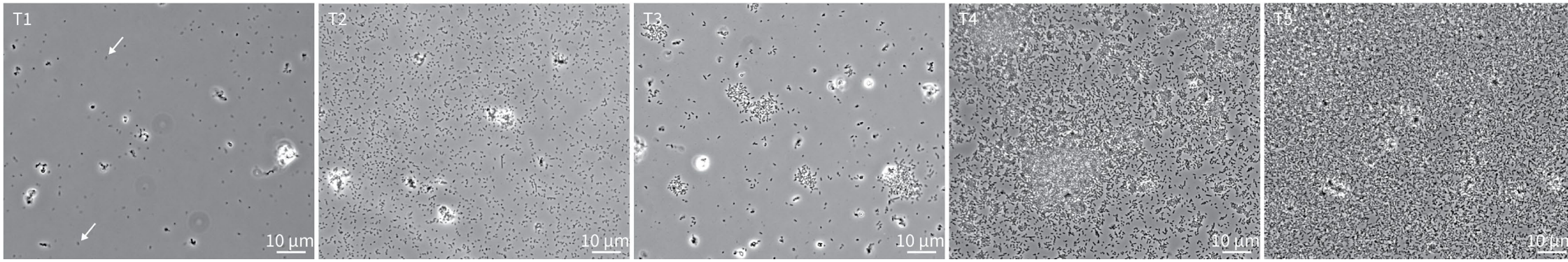
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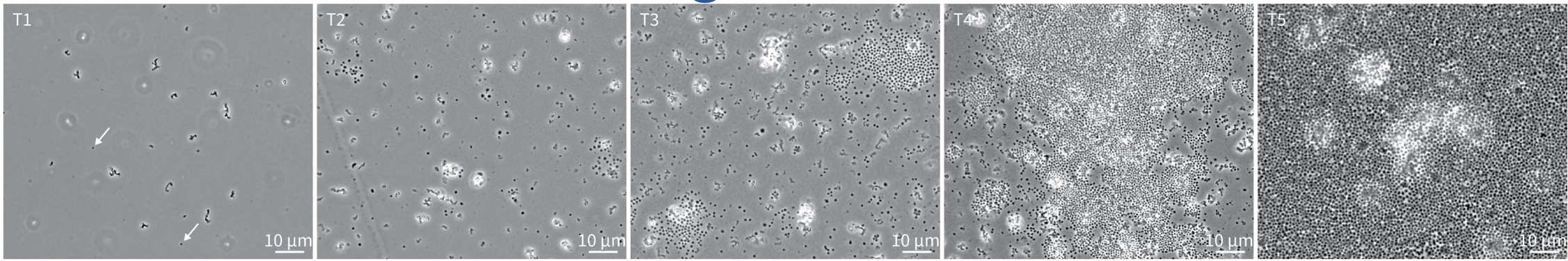


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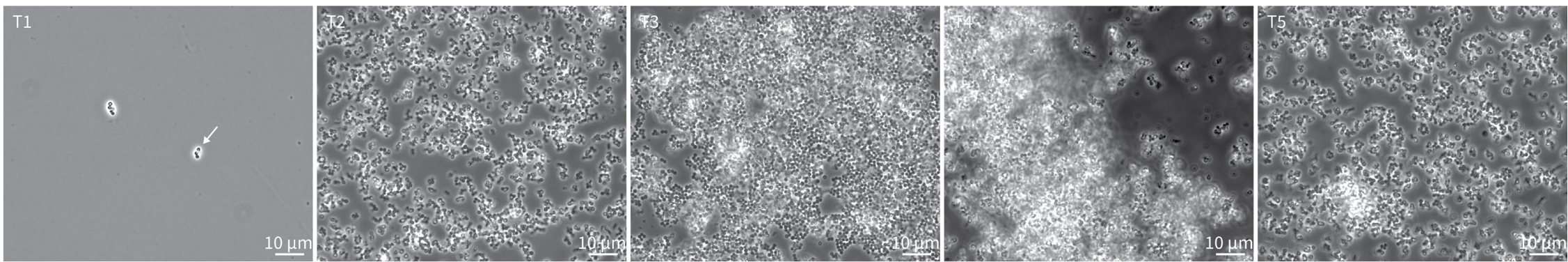
Two Attachment Strategies

NV



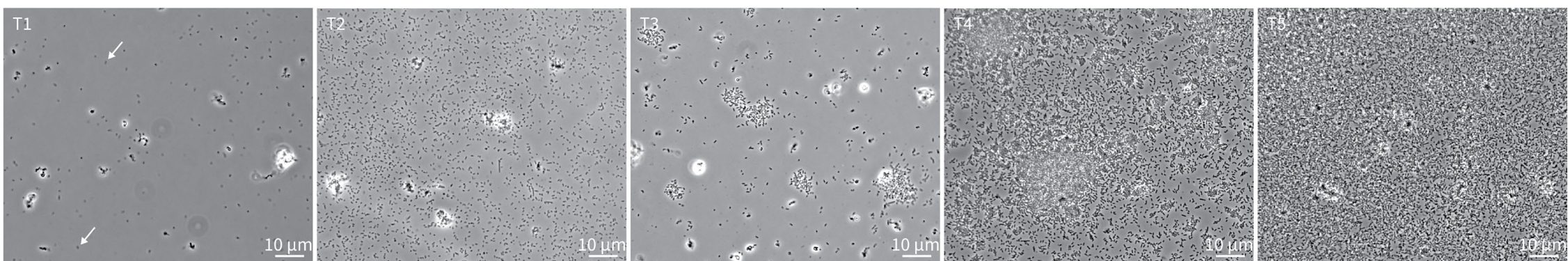
Single
Cell
Attachment

NF



Aggregate
Attachment

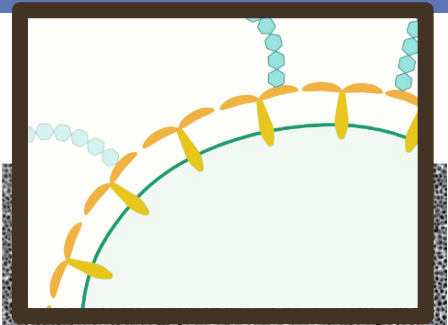
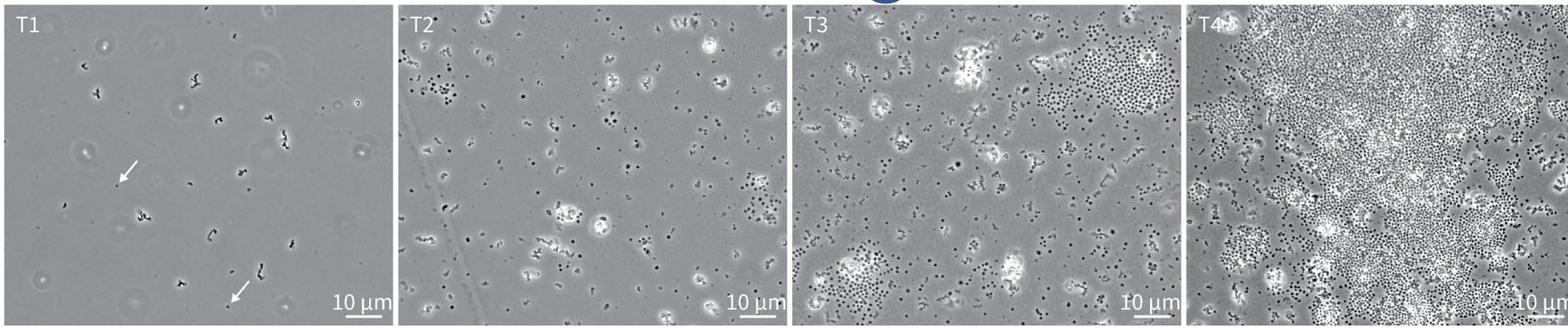
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Single
Cell
Attachment

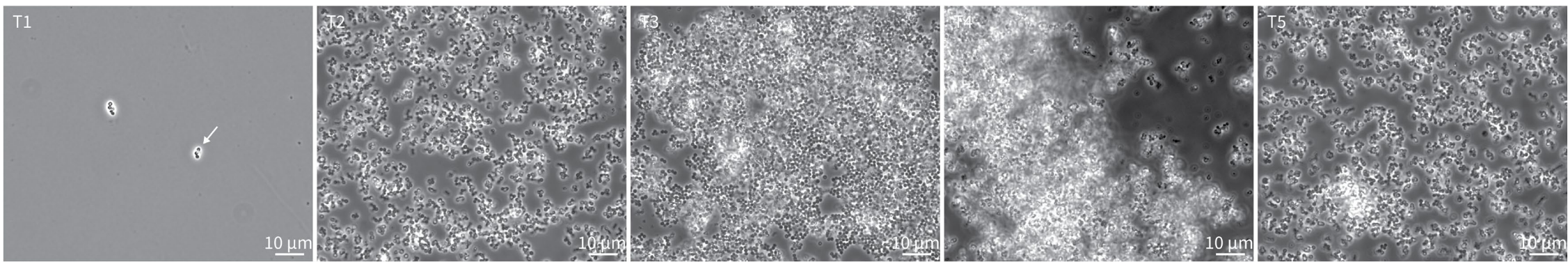
Two Attachment Strategies

NV



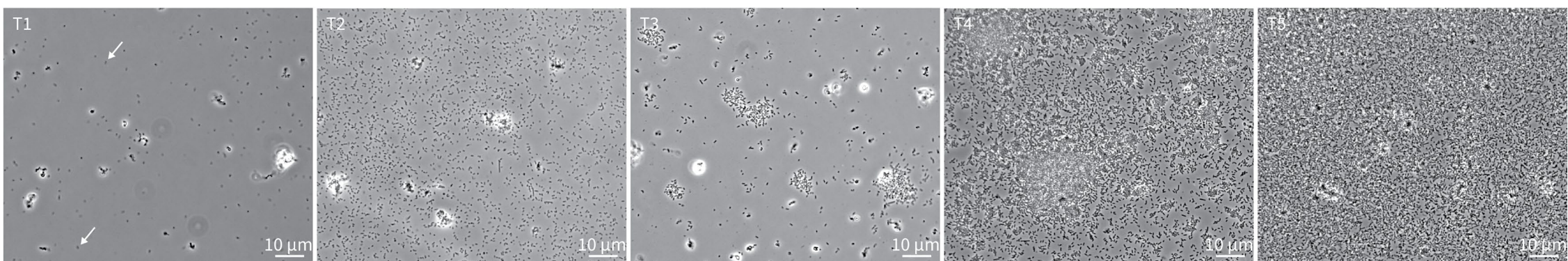
Single Cell Attachment (S-layer)

NF



Aggregate Attachment (no S-layer)

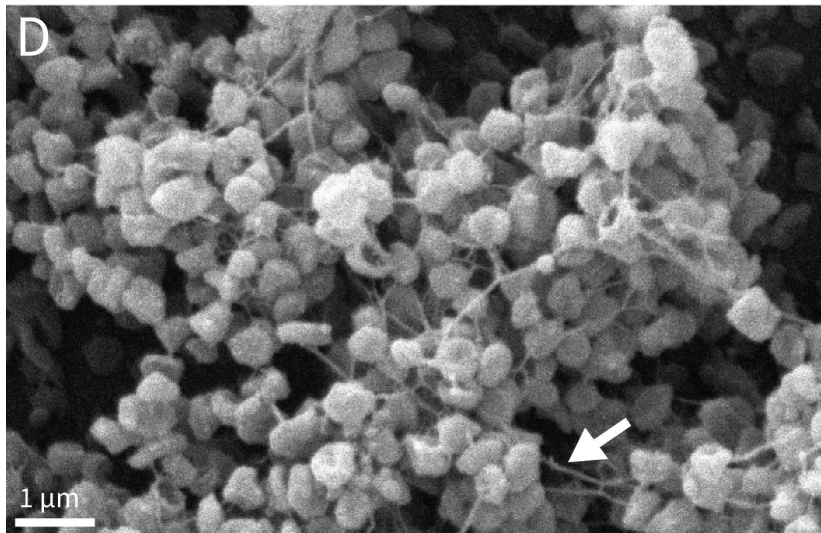
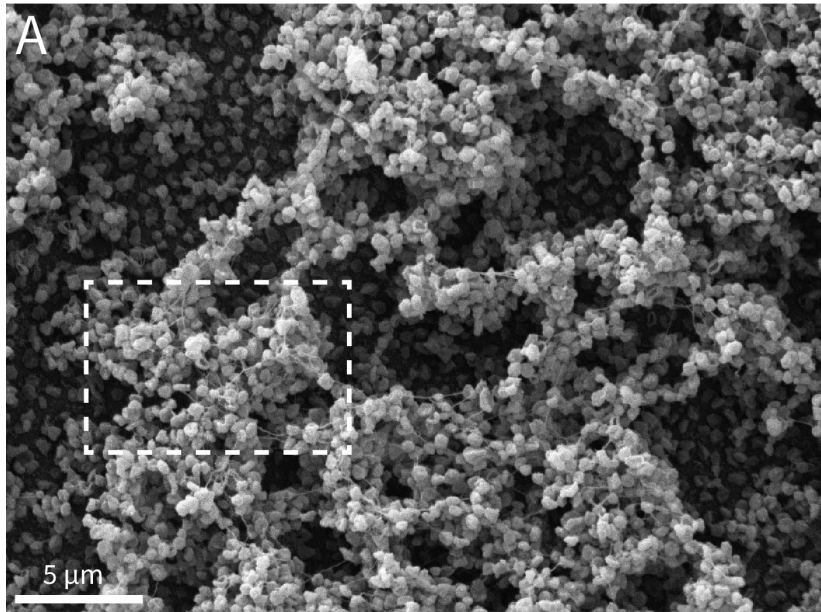
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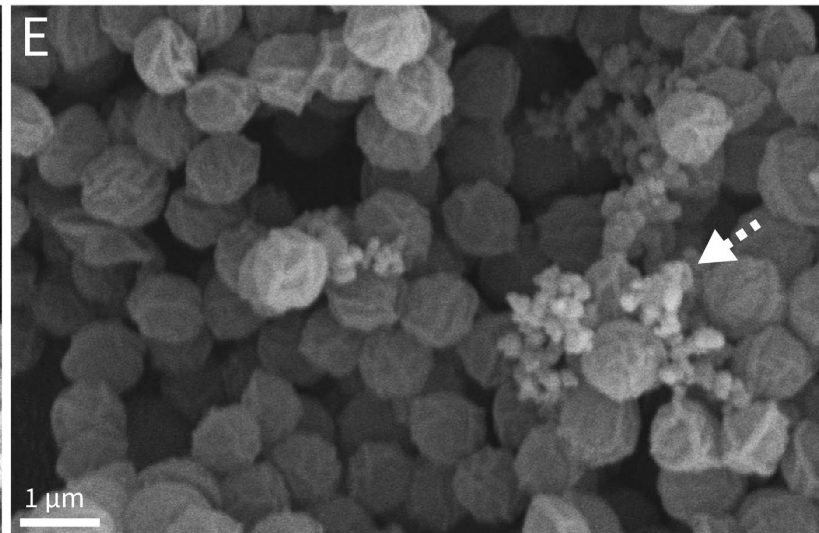
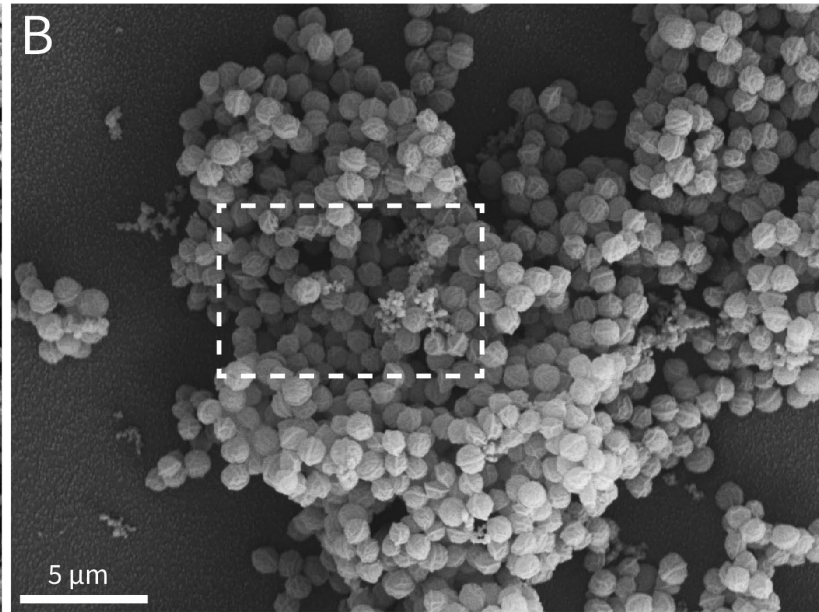
Single Cell Attachment (S-layer)

Scanning Electron Microscopy

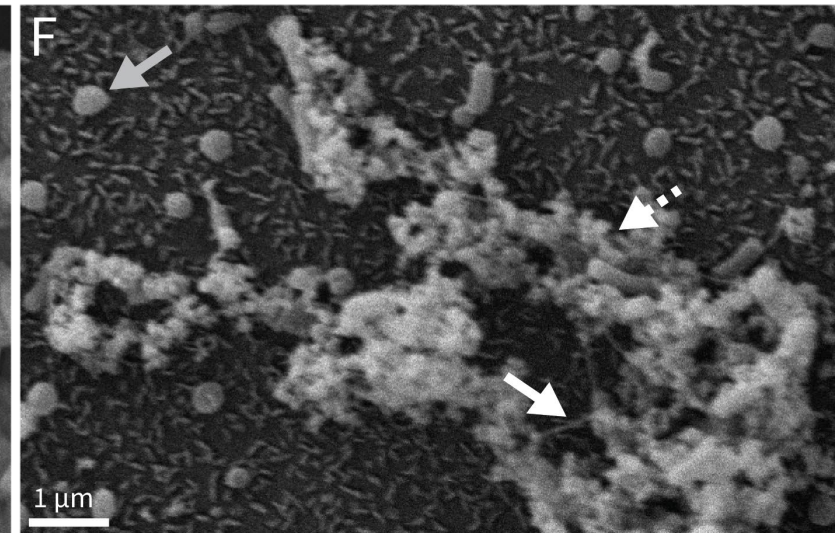
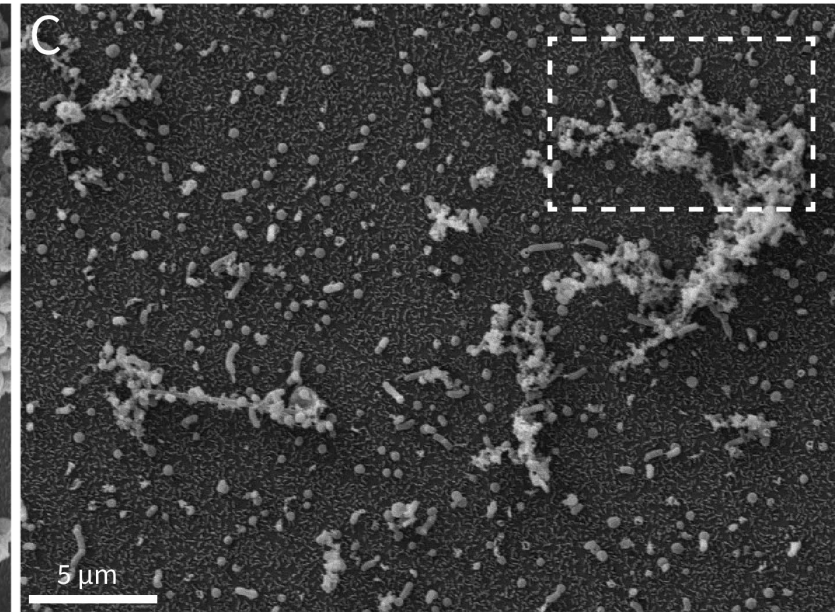
N. viennensis



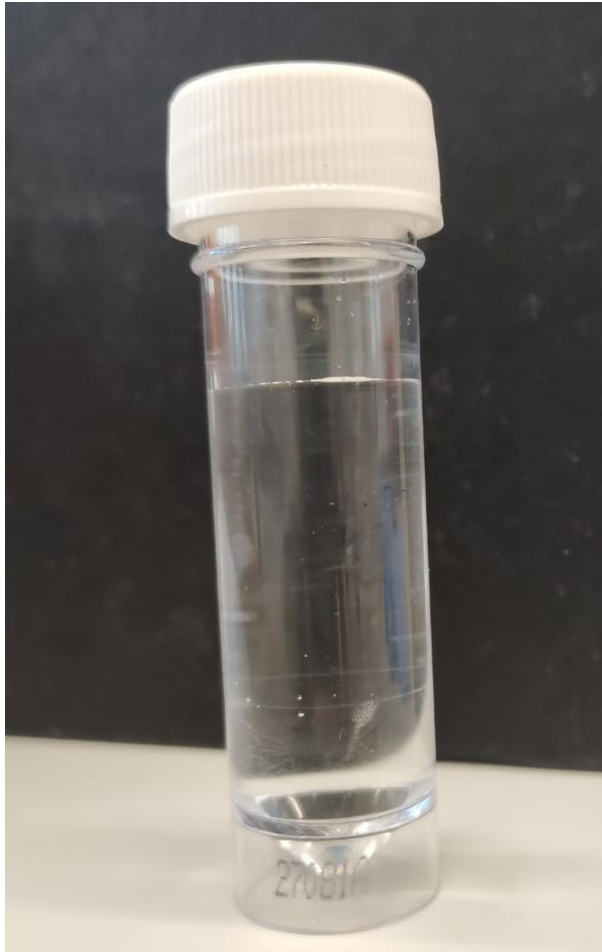
N. franklandianus



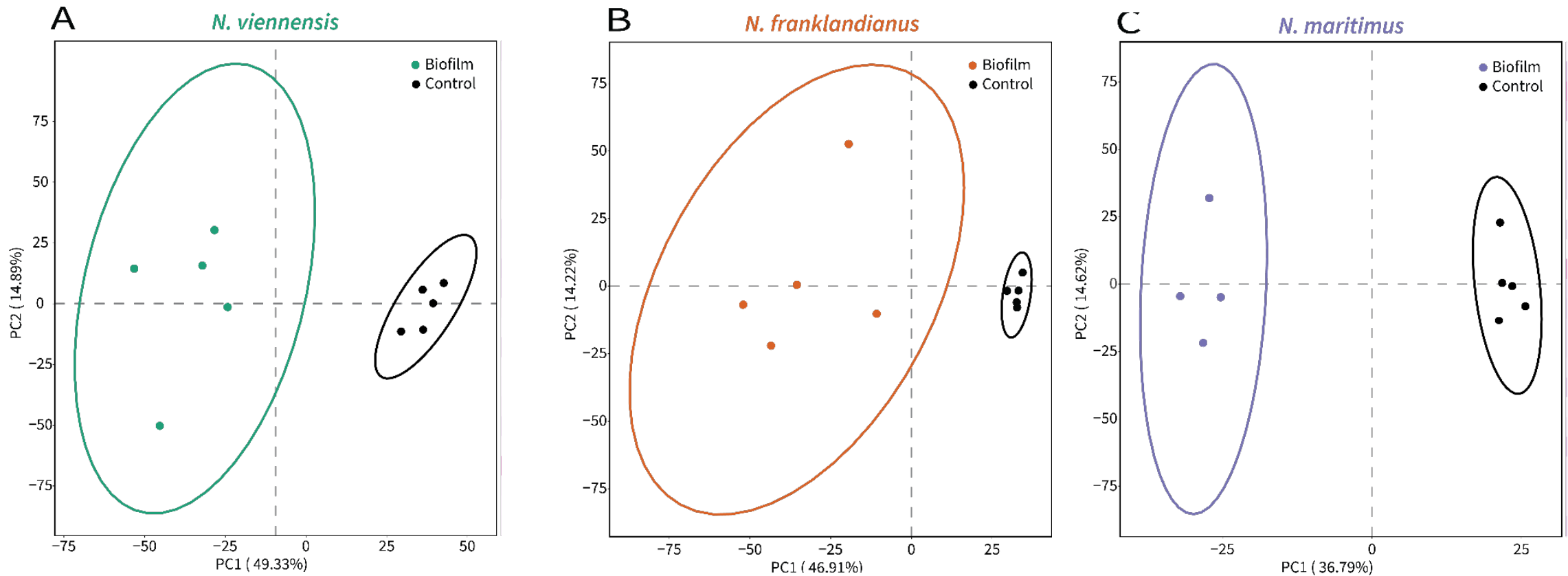
N. maritimus

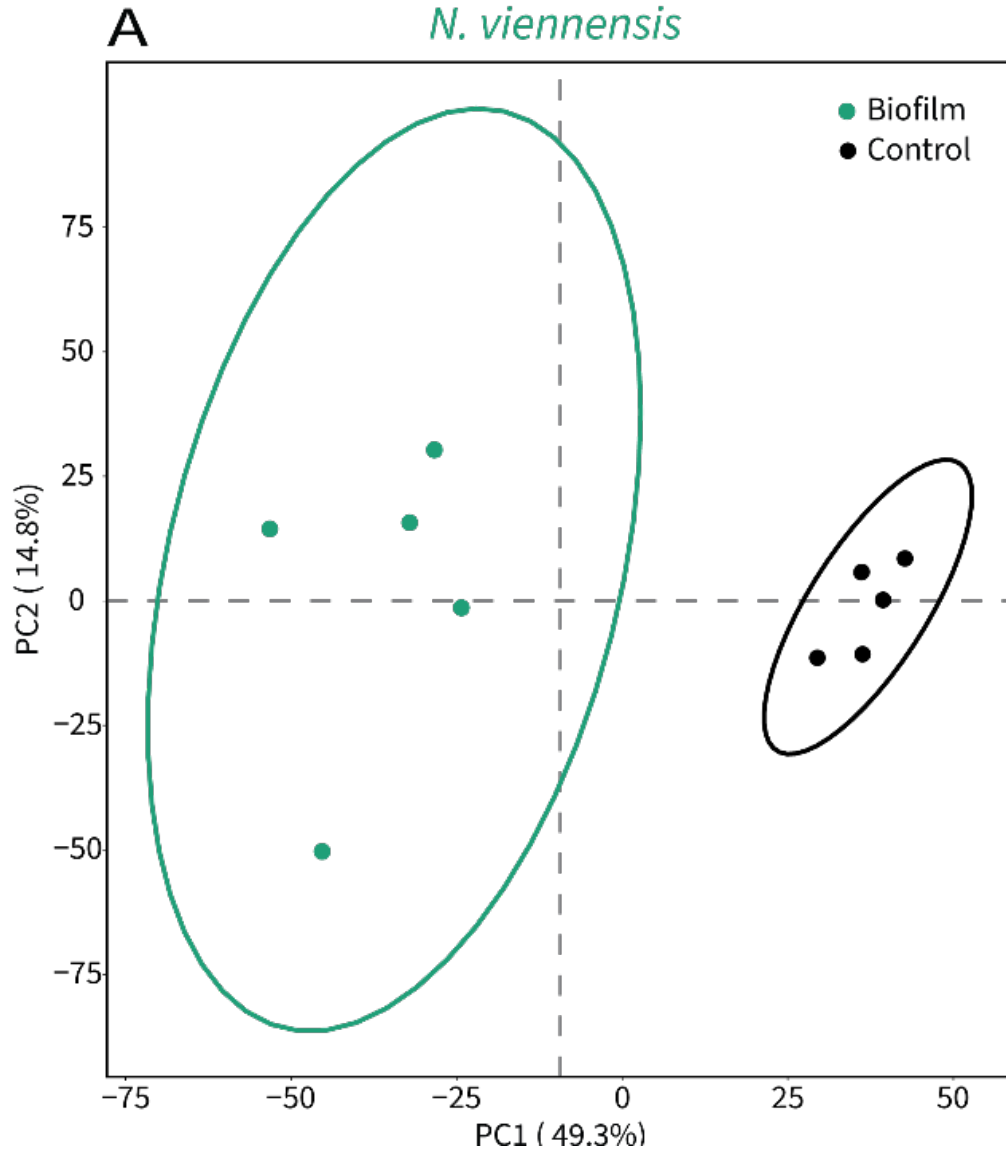
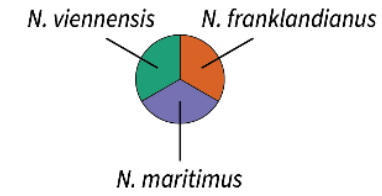


Physiology of Biofilms-Transcriptomics



Biofilms Exhibit Distinct Transcriptomic Responses

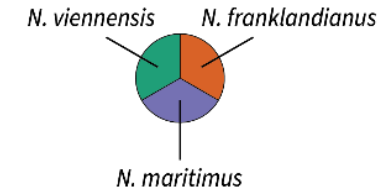




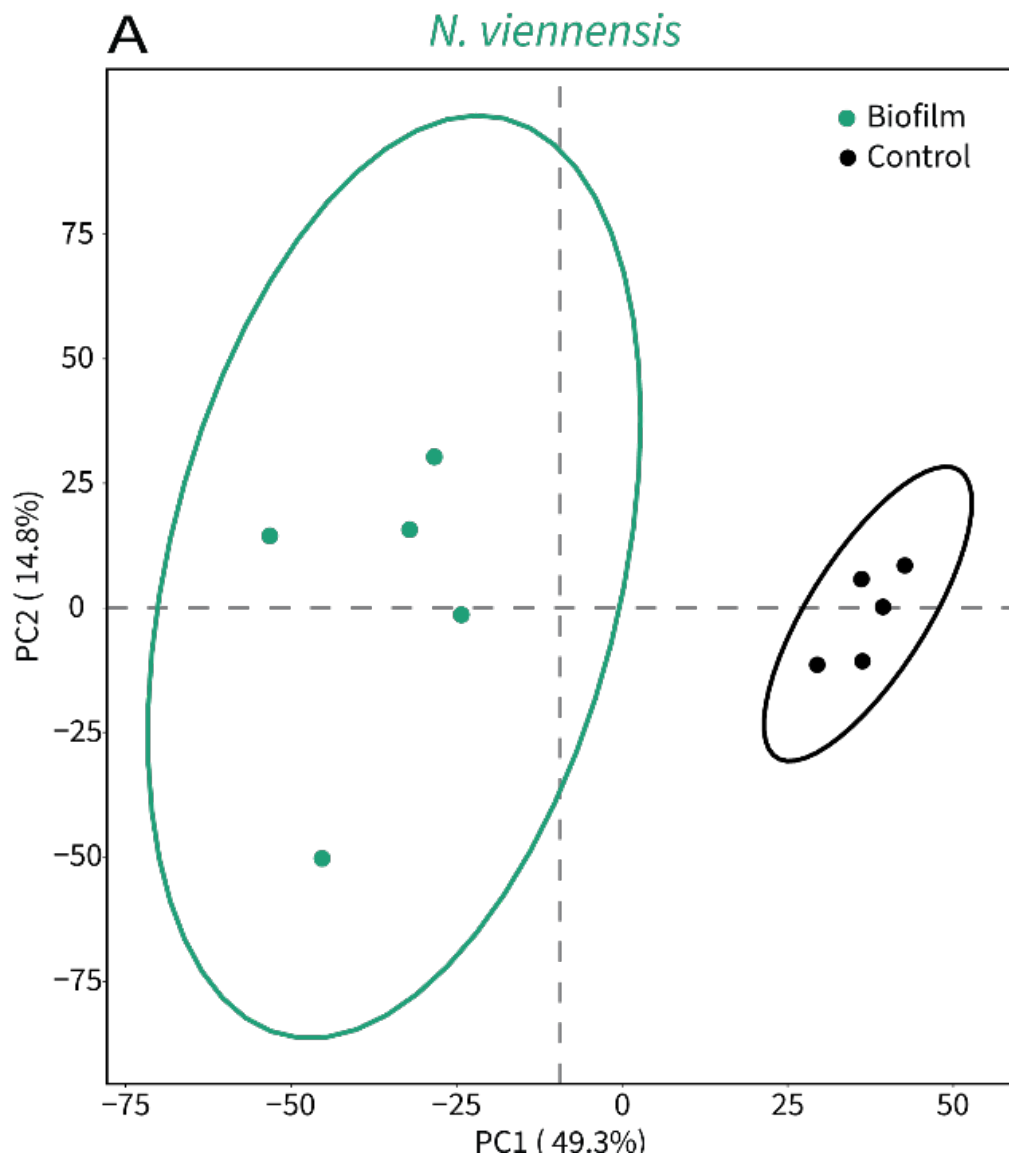
TPM		Log ₂ FC	Locus tag	
Ctrl	BF		NVIE_	
39	5453	7.45	019250	MCO4b
11	785	6.40	010050	protein of unknown function
6	383	6.21	003900	heat-shock protein Hsp20
10	575	6.09	019730	protein of unknown function
47	2255	5.88	000940	putative aggregation protein
20	946	5.82	019740	protein of unknown function
21	811	5.55	1444	hypothetical protein
27	806	5.22	001020	large adhesion protein
4	103	5.02	003890	protein of unknown function
50	1271	4.98	001000	putative surface-associated Ca ²⁺ -binding protein
29	748	4.97	003910	putative cupredoxin
248	6133	4.94	1457	exported protein of unknown function
107	2601	4.92	014300	Copper resistance protein CopC/CopD
7	156	4.80	014170	putative sialidase - neuraminidase family protein
3	73	4.74	004020	Universal stress protein YxiE
63	1318	4.69	001850	exported protein of unknown function
3	73	4.67	003950	protein of unknown function
5	90	4.52	004160	RDD family protein
8	157	4.51	004010	CBS domain-containing protein (modular protein)
48	844	4.47	018560	protein of unknown function
7	119	4.46	004000	CBS and zinc finger C2H2 domain-containing protein
1652	28590	4.41	000970	putative serine rich protein involved in cell adhesion
7	124	4.35	004170	hypothetical protein
5	77	4.35	012890	protein of unknown function
5	80	4.29	009530	molecular chaperone HSP90 family

Protein Family Categorization

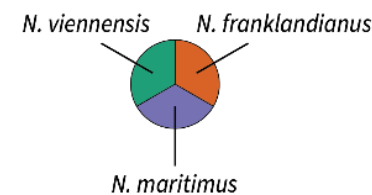
- ~25 complete or mostly complete genomes
- BLAST every amino acid sequence against each other
- Divide into protein families (35% identity, 70% coverage)

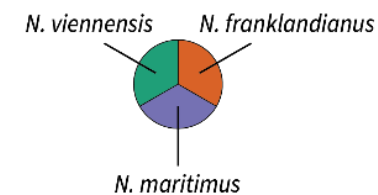
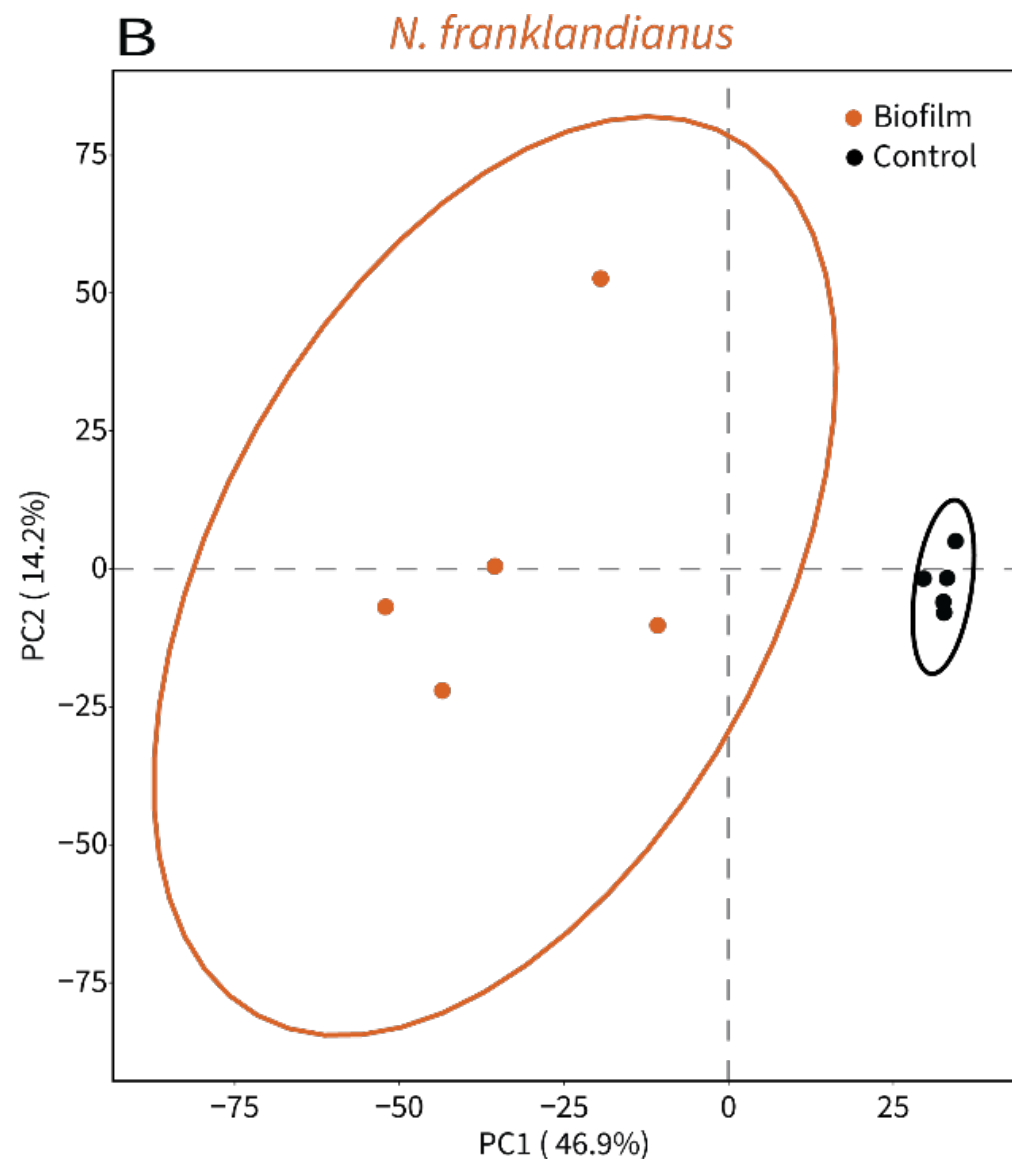


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NVIE_	
019250	MCO4b
010050	protein of unknown function
003900	heat-shock protein Hsp20
019730	protein of unknown function
000940	putative aggregation protein
019740	protein of unknown function
1444	hypothetical protein
001020	large adhesion protein
003890	protein of unknown function
001000	putative surface-associated Ca ²⁺ -binding protein
003910	putative cupredoxin
1457	exported protein of unknown function
014300	Copper resistance protein CopC/CopD
014170	putative sialidase - neuraminidase family protein
004020	Universal stress protein YxiE
001850	exported protein of unknown function
003950	protein of unknown function
004160	RDD family protein
004010	CBS domain-containing protein (modular protein)
018560	protein of unknown function
004000	CBS and zinc finger C2H2 domain-containing protein
000970	putative serine rich protein involved in cell adhesion
004170	hypothetical protein
012890	protein of unknown function
009530	molecular chaperone HSP90 family

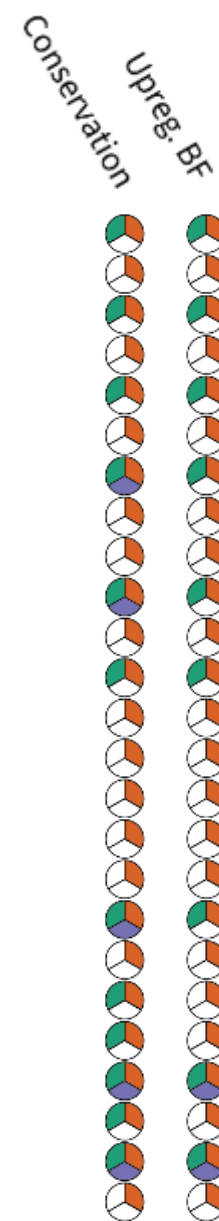


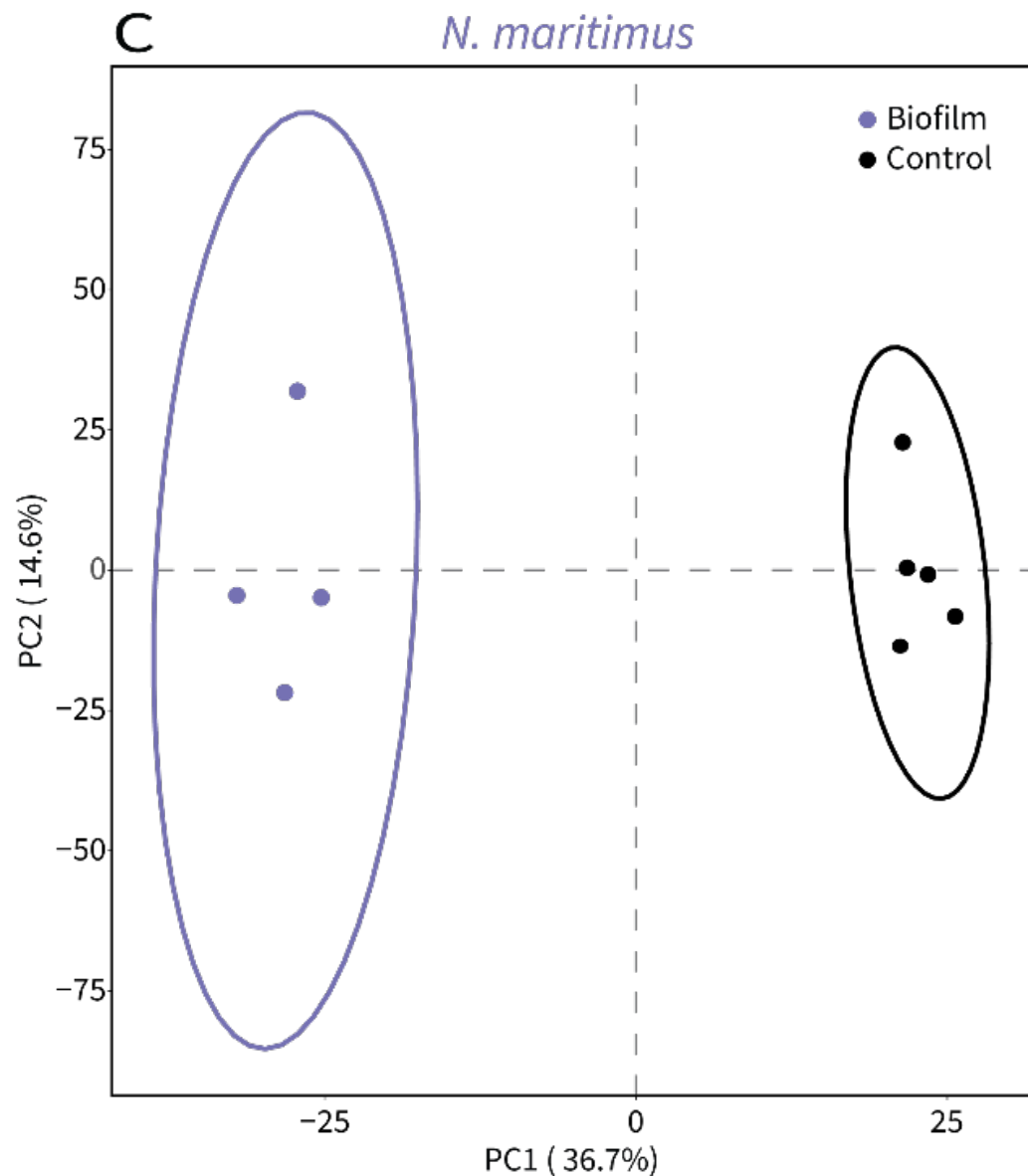
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6	383	6.21	003900	heat-shock protein Hsp20		
10	575	6.09	019730	protein of unknown function		
47	2255	5.88	000940	putative aggregation protein		
20	946	5.82	019740	protein of unknown function		
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27	806	5.22	001020	large adhesion protein		
4	103	5.02	003890	protein of unknown function		
50	1271	4.98	001000	putative surface-associated Ca ²⁺ -binding protein		
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3	73	4.67	003950	protein of unknown function		
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7	124	4.35	004170	hypothetical protein		
5	77	4.35	012890	protein of unknown function		
5	80	4.29	009530	molecular chaperone HSP90 family		



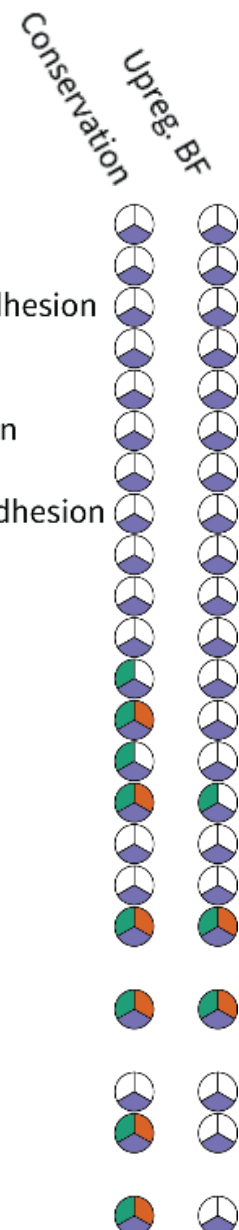
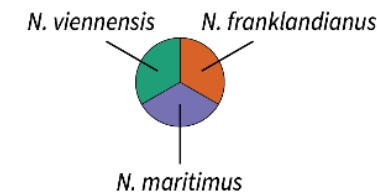


Ctrl	BF	Log ₂ FC	NFRAN_	
7	1090	7.8	1142	hypothetical protein
26	638	5.18	1218	SRPBCC family protein
65	1448	5.03	2155	cytochrome c biogenesis protein CcdA
165	3649	5.02	2154	sialidase family protein
83	1356	4.58	2146	sialidase family protein
2	28	4.46	RS08925	IS5 family transposase
32	393	4.16	RS02310	hypothetical protein
2	23	3.93	2152	sialidase family protein
53	539	3.9	1609	hypothetical protein
3	25	3.85	2058	response regulator
287	2444	3.64	1084	copper resistance protein CopC
601	4457	3.43	1083	hypothetical protein
10	63	3.28	RS10270	IS5 family transposase
785	4757	3.19	RS13965	hypothetical protein
1514	9353	3.17	2030	MCO3
2296	14073	3.16	2029	MCO3
1170	6995	3.13	2033	antibiotic biosynthesis monooxygenase
1539	8886	3.08	2032	ferredoxin family protein
64	352	3.01	1082	CopD family protein
57	310	3.01	1143	hypothetical protein
73	385	2.95	1144	winged HTH domain-containing protein
17	76	2.76	1611	TFB
46	200	2.66	2036	hypothetical protein
3803	16583	2.66	2792	MCO4b
2849	12045	2.64	RS13445	hypothetical protein

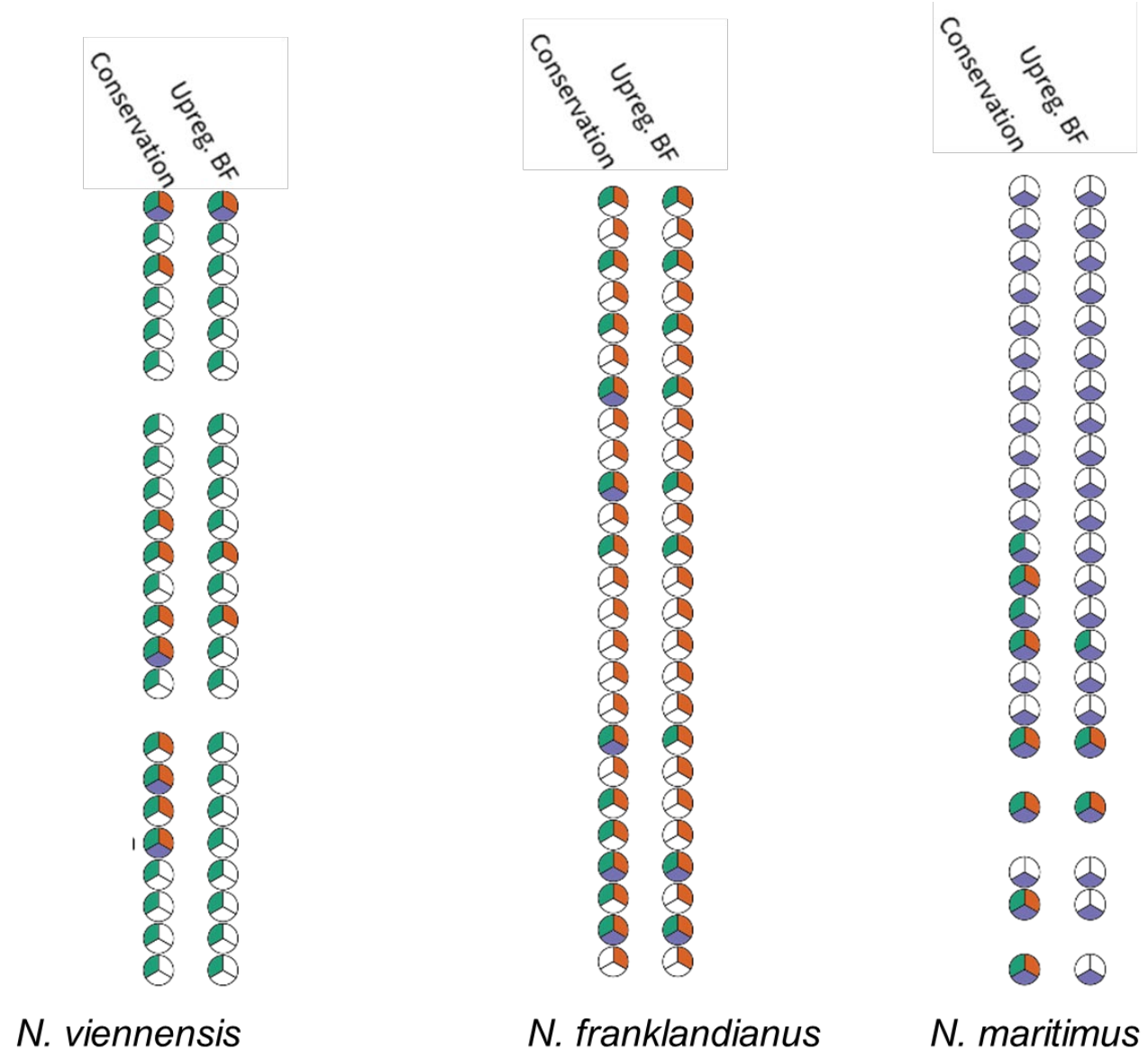
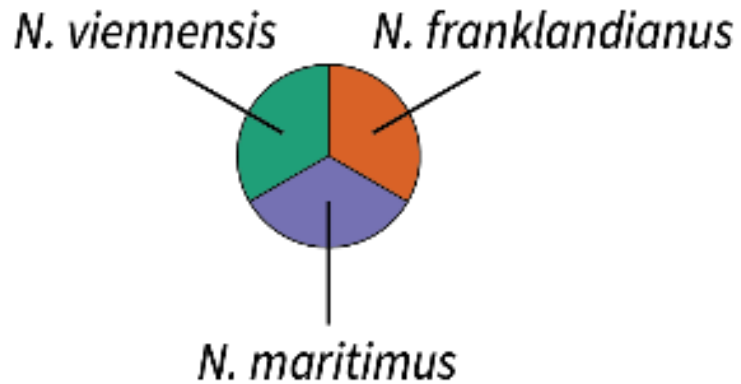




Ctrl	BF	Log ₂ FC	Nmar_	
6	227	6.04	0456	large adhesion protein
578	6629	4.13	1201	S-layer
2135	26172	4.11	0459	putative serine rich protein involved in cell adhesion
924	8057	3.62	1246	hypothetical protein
8	60	3.42	RS09750	hypothetical protein
12	69	3.31	1073	fibronectin type III domain-containing protein
70	429	3.15	RS05400	hypothetical protein
41	231	3.05	0455	hypothetical protein, putatively involved in adhesion
2	10	2.96	1347	hypothetical protein
66	346	2.92	0377	hypothetical protein
3	14	2.82	1346	diaminobutyrate acetyltransferase
1665	7969	2.72	0033	winged HTH domain-containing protein
91	400	2.62	0011	CDC48 family AAA ATPase
160	610	2.57	1351	hypothetical protein
66	272	2.56	1423	hypothetical protein
58	239	2.55	RS09755	hypothetical protein
30	131	2.49	0970	hypothetical protein
355	1349	2.44	0013	TFB
7	35	2.44	R0038	tRNA-Thr
18	68	2.43	1341	TFB
557	2000	2.41	1163	hypothetical protein
23	76	2.35	0905	hypothetical protein
14	51	2.35	RS04055	DUF1059 domain-containing protein
11	55	2.34	R0009	tRNA-Ser
195	703	2.34	0010	archaeal heat shock protein Hsp20

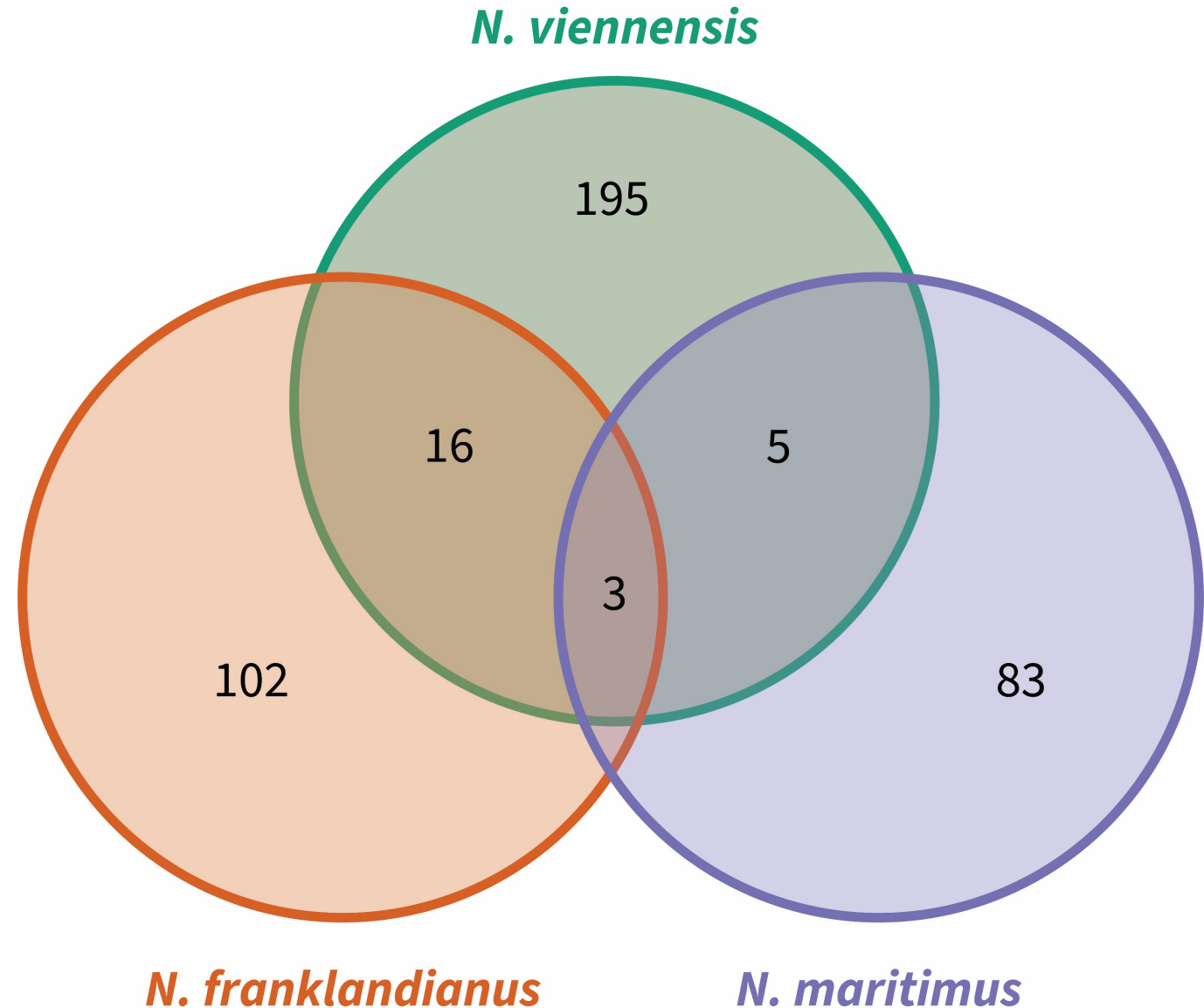


Species Specific Response in Up-Regulated Genes



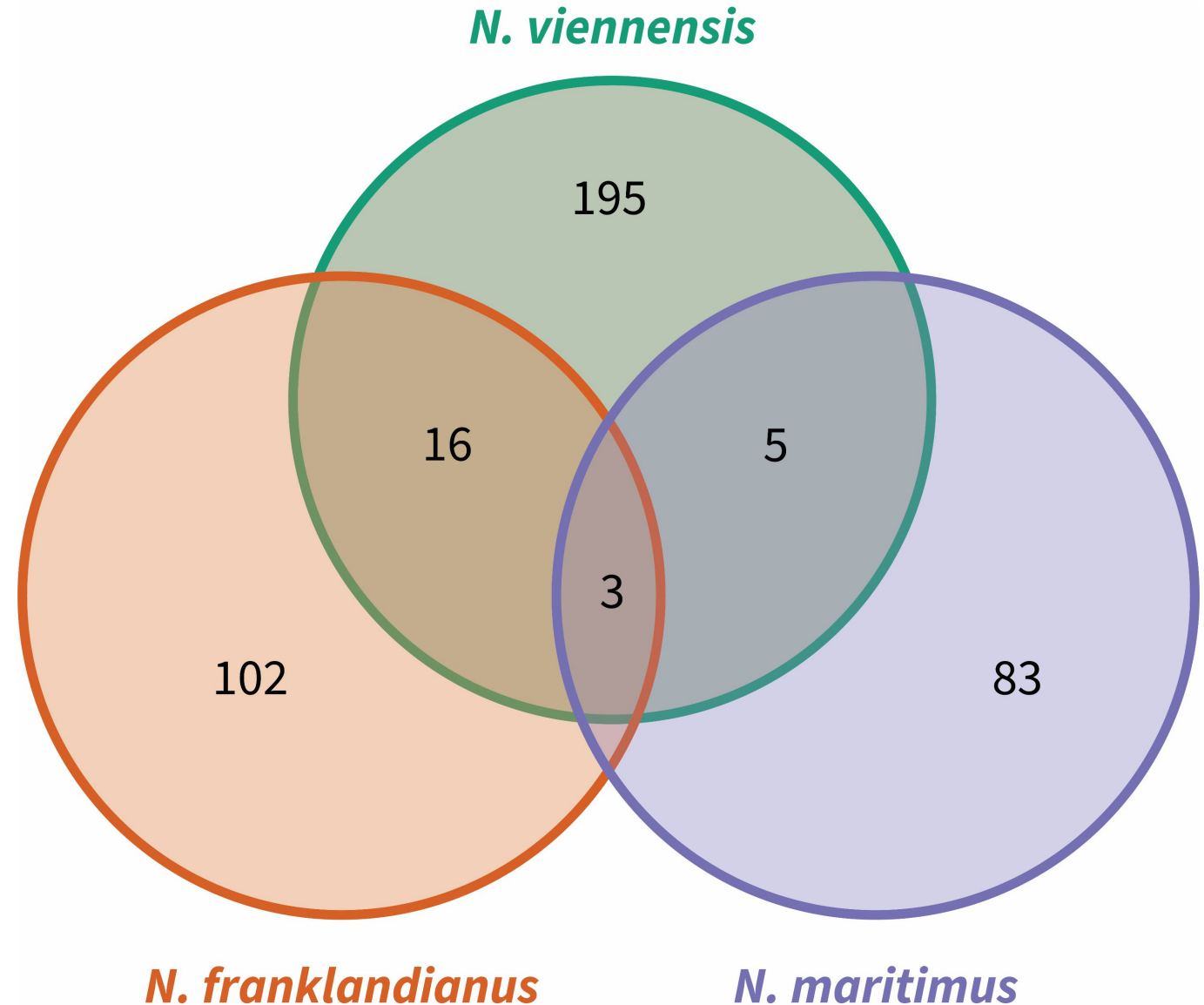
Common Up-regulated Protein Families

- Multicopper Oxidases (MCOs)
- Transcription factors (TFBs)
- Nitroso reductases



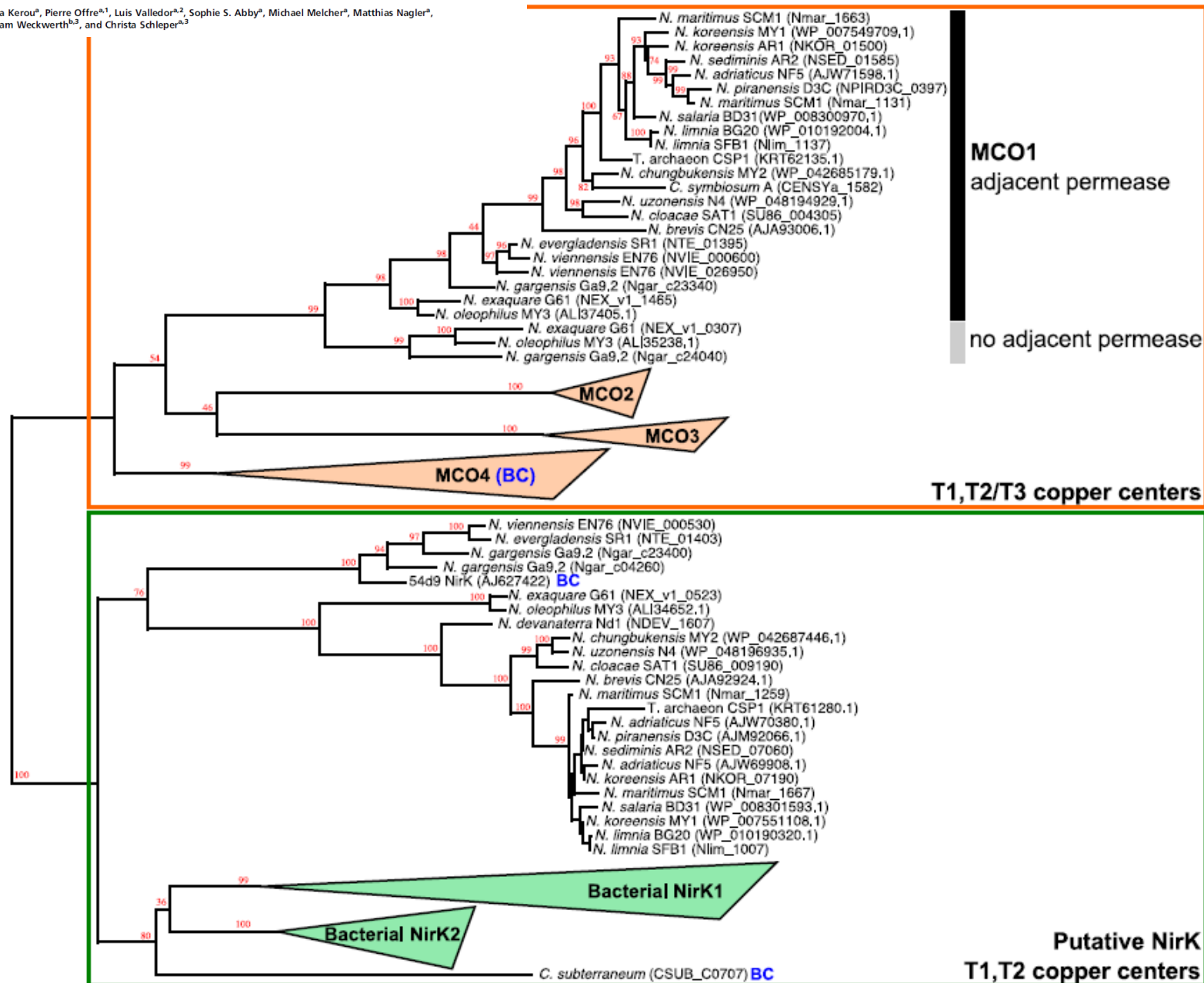
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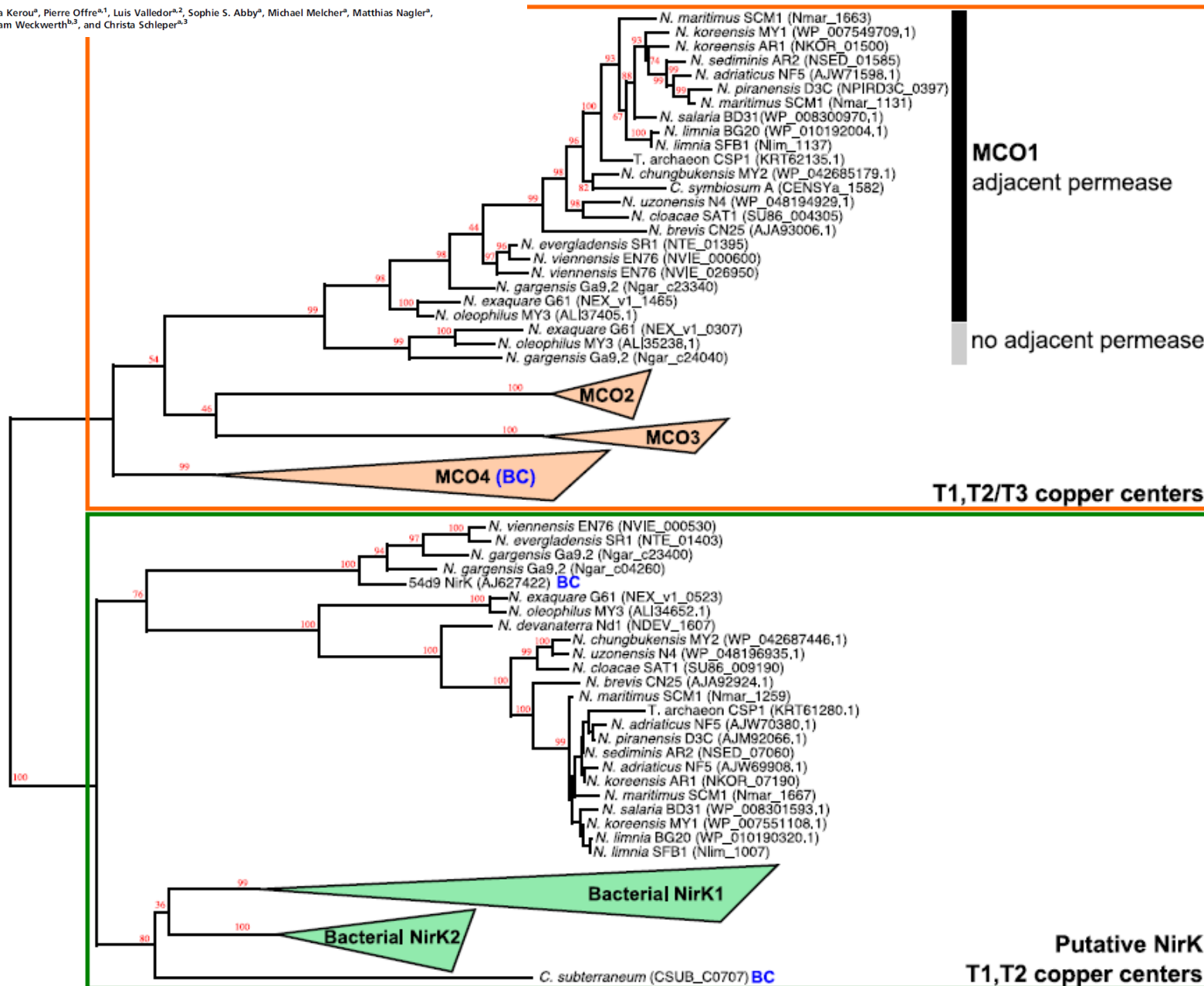
Proteomics and comparative genomics of *Nitrososphaera viennensis* reveal the core genome and adaptations of archaeal ammonia oxidizers

Melina Kerou^a, Pierre Offre^{a,1}, Luis Valledor^{a,2}, Sophie S. Abby^a, Michael Melcher^a, Matthias Nagler^a, Wolfram Weckwerth^{b,3}, and Christa Schleper^{a,3}



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Functions?

• Copper Acquisition

- MCO1
- MCO4?

Qin *et al.*, 2018
Reyes *et al.*, 2020

• N detoxification

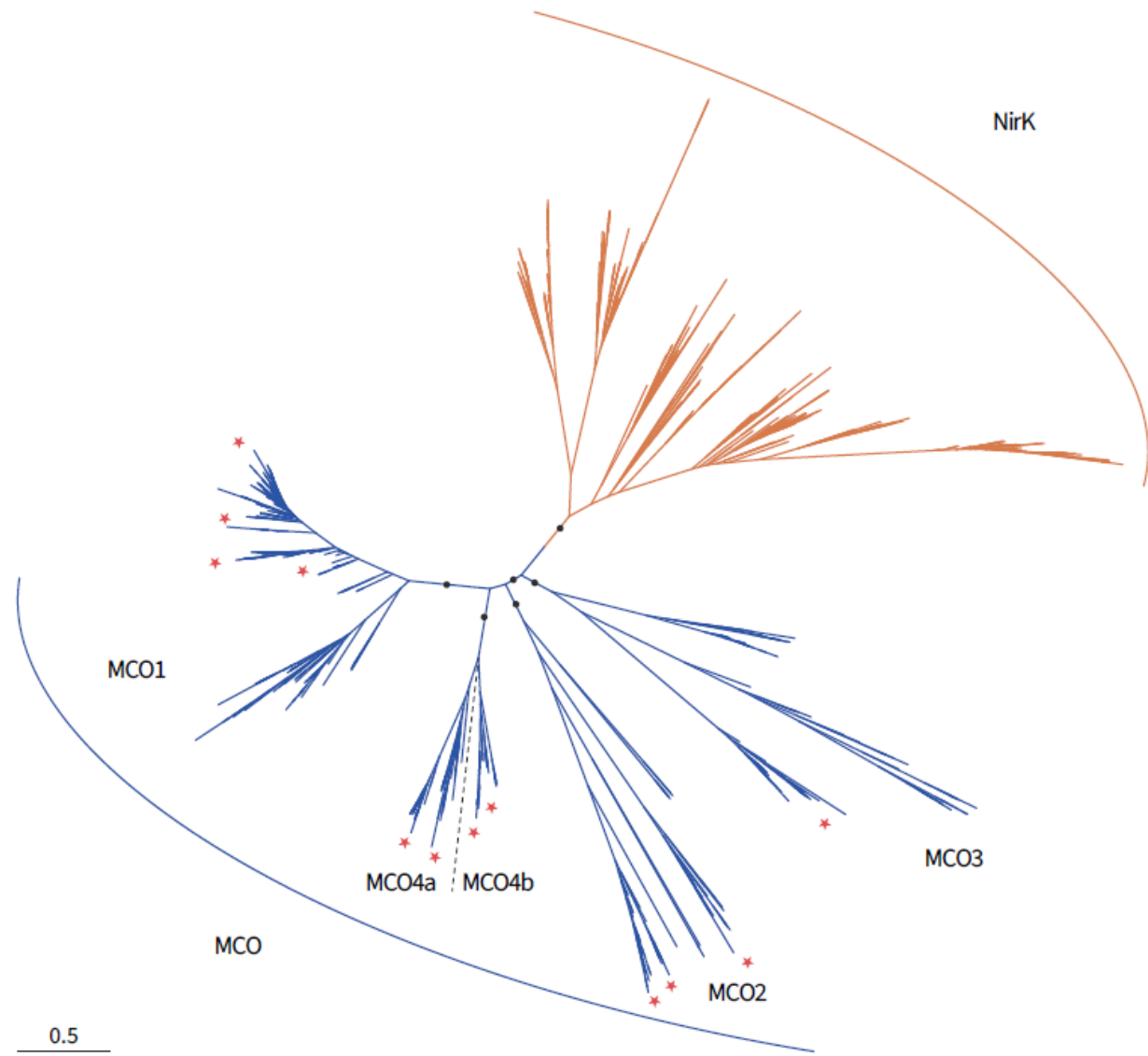
- MCO4

Voland *et al.*, 2025

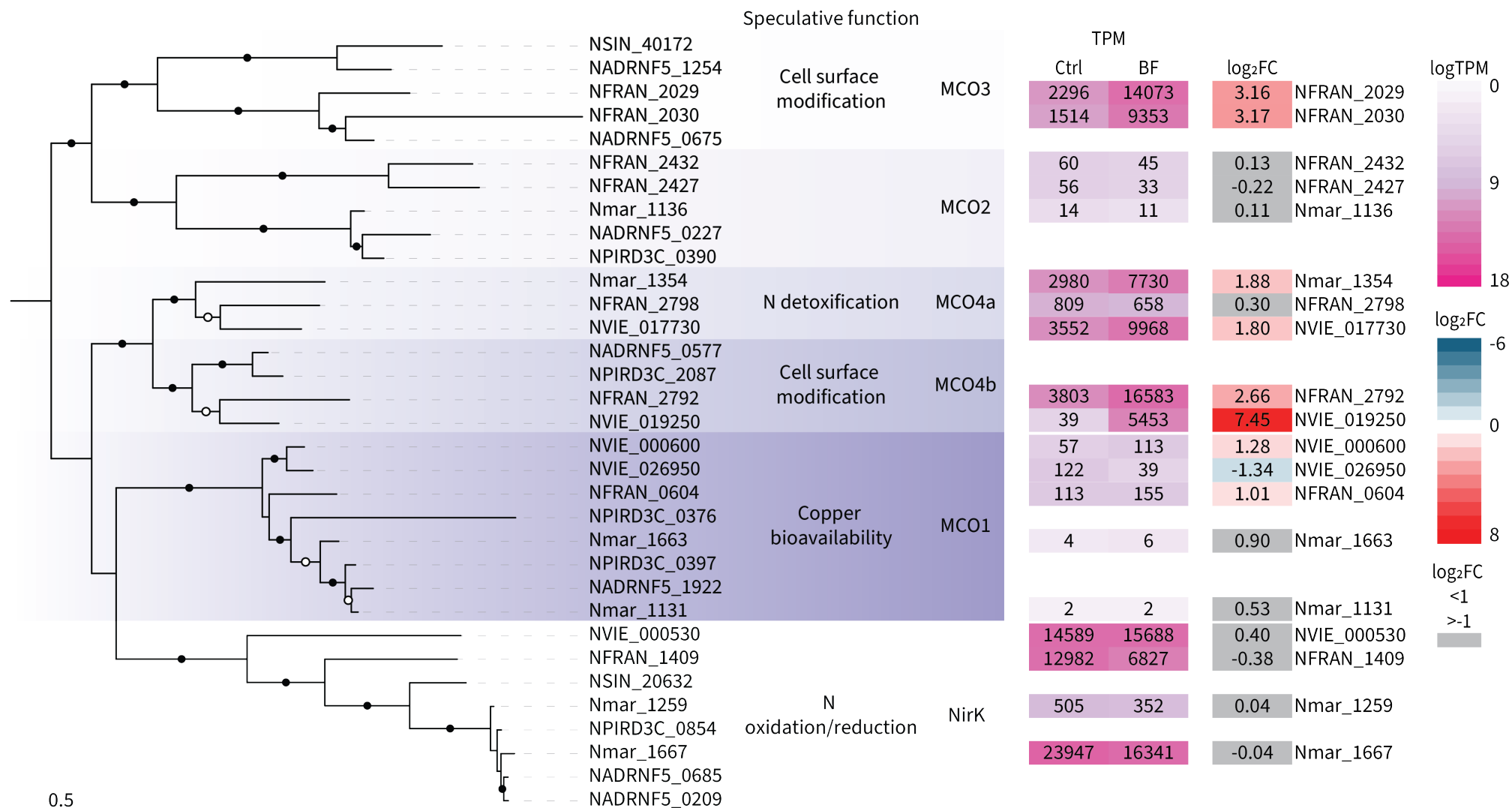
• Ammonia Oxidation

- NirK

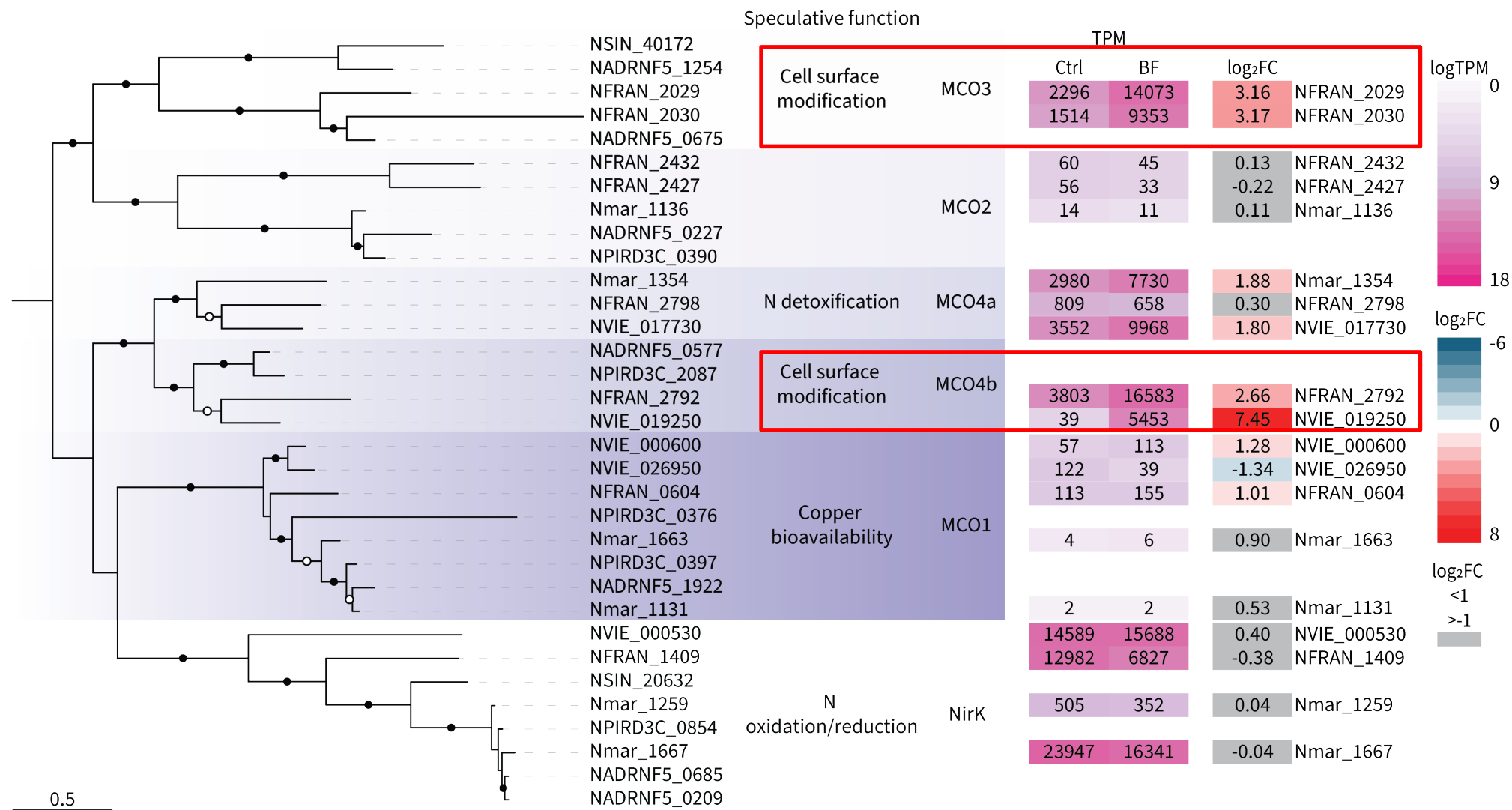
Kozlowski *et al.*, 2016



MCOs May Modify Cell surface of Biofilm Cells

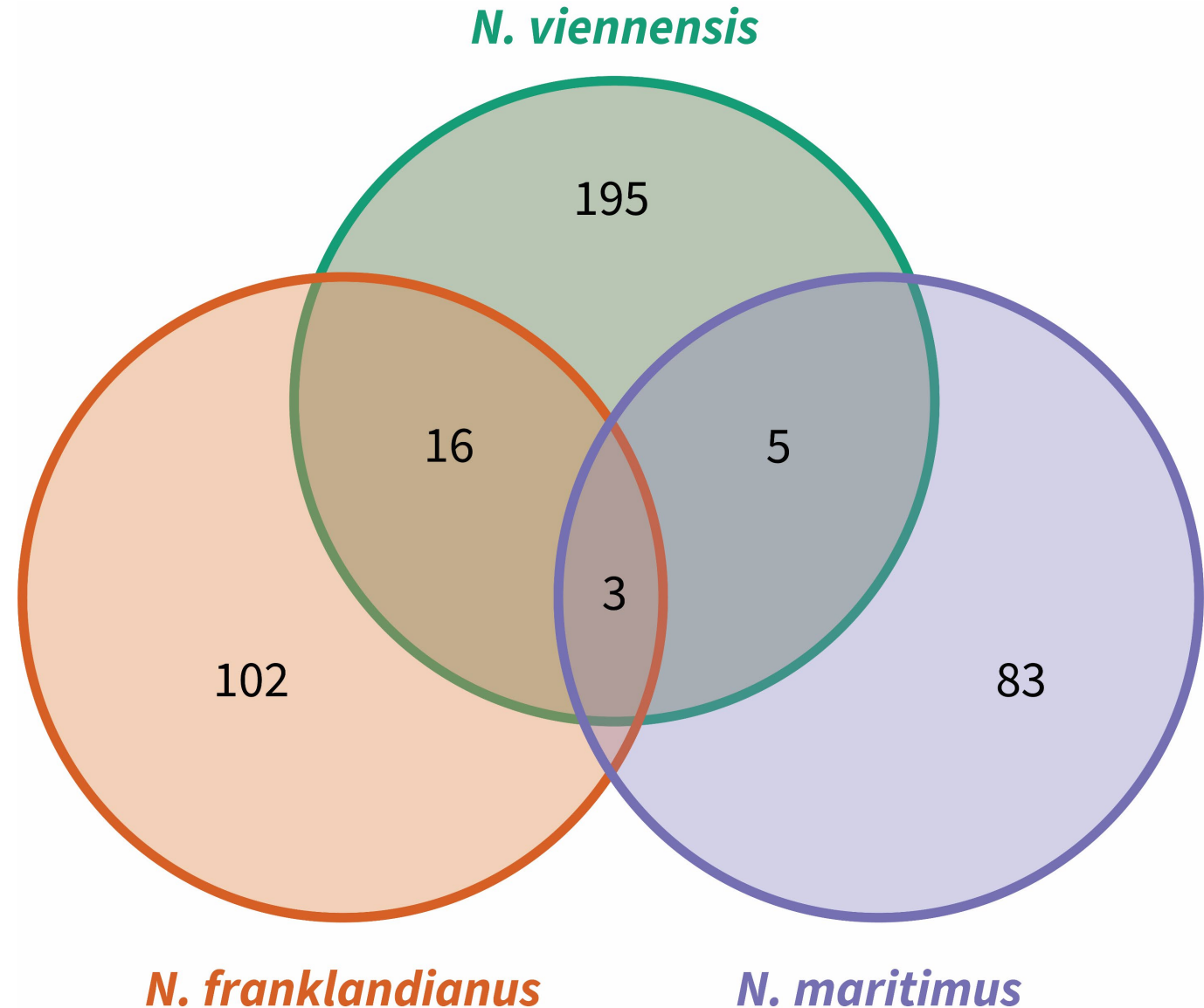


MCOs May Modify Cell surface of Biofilm Cells

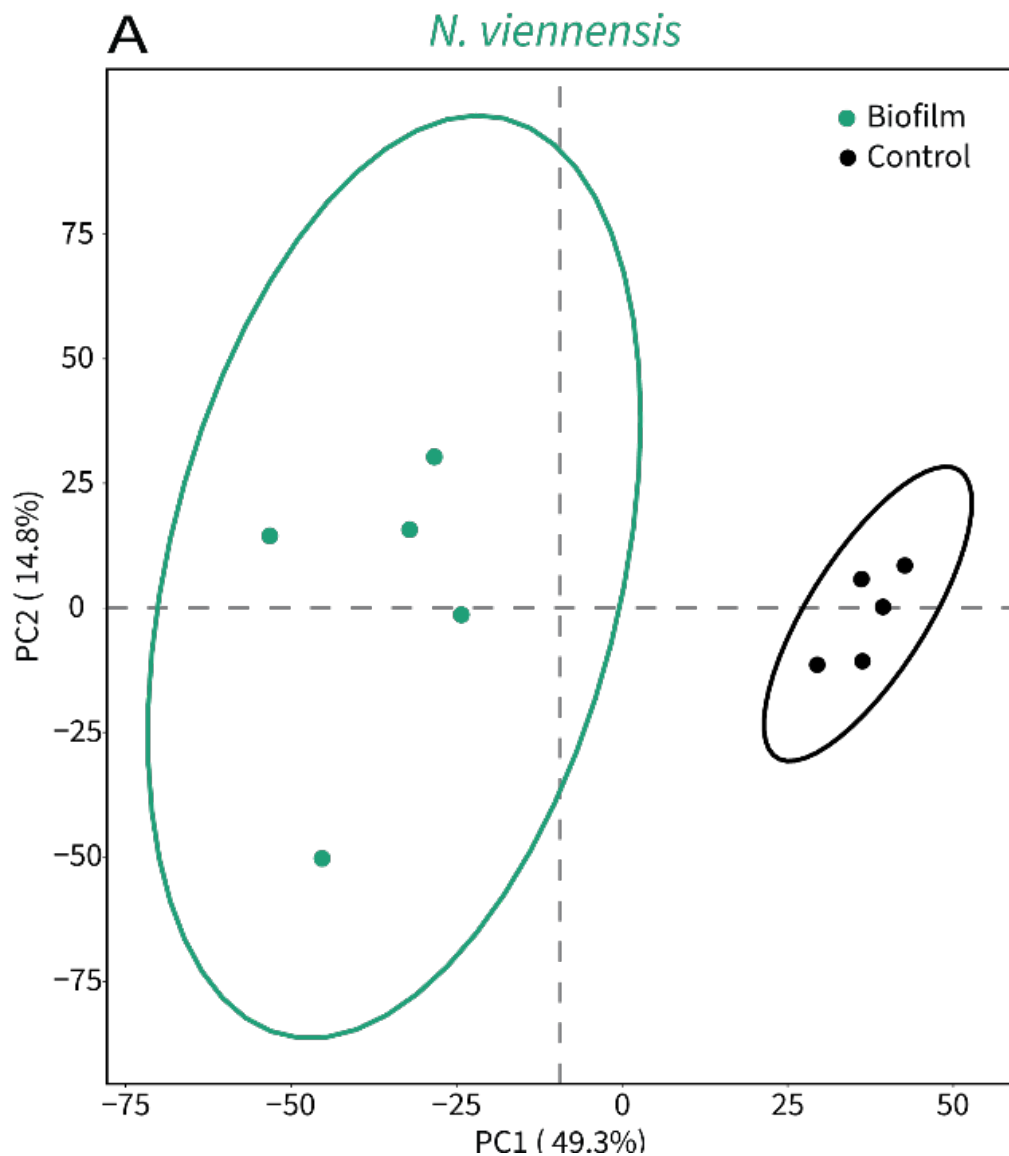


Common Up-regulated Protein Families

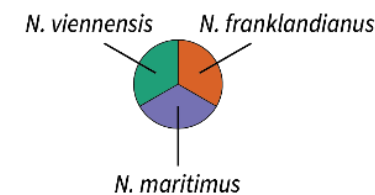
- Multicopper Oxidases (MCOs)
- Transcription factors (TFBs)
- Nitroso reductases



Identifying Biofilm Specific Genes in Each Species

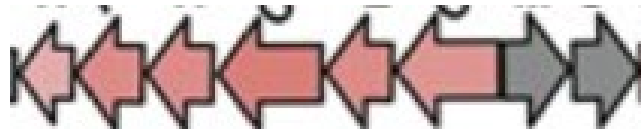


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11	785	6.40	010050	protein of unknown function		
6	383	6.21	003900	heat-shock protein Hsp20		
10	575	6.09	019730	protein of unknown function		
47	2255	5.88	000940	putative aggregation protein		
20	946	5.82	019740	protein of unknown function		
21	811	5.55	1444	hypothetical protein		
27	806	5.22	001020	large adhesion protein		
4	103	5.02	003890	protein of unknown function		
50	1271	4.98	001000	putative surface-associated Ca ²⁺ -binding protein		
29	748	4.97	003910	putative cupredoxin		
248	6133	4.94	1457	exported protein of unknown function		
107	2601	4.92	014300	Copper resistance protein CopC/CopD		
7	156	4.80	014170	putative sialidase - neuraminidase family protein		
3	73	4.74	004020	Universal stress protein YxiE		
63	1318	4.69	001850	exported protein of unknown function		
3	73	4.67	003950	protein of unknown function		
5	90	4.52	004160	RDD family protein		
8	157	4.51	004010	CBS domain-containing protein (modular protein)		
48	844	4.47	018560	protein of unknown function		
7	119	4.46	004000	CBS and zinc finger C2H2 domain-containing protein		
1652	28590	4.41	000970	putative serine rich protein involved in cell adhesion		
7	124	4.35	004170	hypothetical protein		
5	77	4.35	012890	protein of unknown function		
5	80	4.29	009530	molecular chaperone HSP90 family		



Identifying Biofilm Specific Genes in Each Species

- Differentially expressed
 - Within top 50 of up-regulated under biofilm conditions
- High Transcript Number
 - Within top 100 based on read count (transcript per million) in biofilm condition
- Syntenic with genes that meet the criteria
 - Syntenic=next to a gene in the genome



TPM		Log2 FC	Locus	Information	<i>N. viennensis</i>	Genomic region
Ctrl	BF					
47	2255	5.88	NVIE_000940	cell surface protein with DUF11 domain, putative aggregation protein	Adhesion	
1652	28590	4.41	NVIE_000970	putative serine rich protein involved in cell adhesion		
287	2405	3.36	NVIE_000990*	hypothetical protein, putative glycogen biosynthesis		
50	1271	4.98	NVIE_001000	putative surface-associated Ca ²⁺ -binding protein, Haemolysin-type		
27	806	5.22	NVIE_001020*	putative cell wall surface anchor family protein, large adhesion protein		
63	1318	4.69	NVIE_001850	exported protein of unknown function		
1174	9330	3.30	NVIE_014250	exported protein of unknown function	copC/copD	
538	2865	2.72	NVIE_014290*	hypothetical protein, putative cation channel protein		
107	2601	4.92	NVIE_014300	CopC/CopD		
248	6133	4.94	NVIE_1457	exported protein of unknown function, inbetween copC/copD		
355	1352	2.24	NVIE_014310*	CopC/CopD		
3552	9968	1.8	NVIE_017730	MCO4a	MCO4a	
430	1825	2.38	NVIE_017740*	antibiotic biosynthesis monooxygenase		
39	5453	7.45	NVIE_019250	MCO4b	MCO4b	

TPM		Log2 FC	Locus	Information	<i>N. viennensis</i>	Genomic region
Ctrl	BF					
47	2255	5.88	NVIE_000940	cell surface protein with DUF11 domain, putative aggregation protein		
1652	28590	4.41	NVIE_000970	putative serine rich protein involved in cell adhesion		
287	2405	3.36	NVIE_000990*	hypothetical protein, putative glycogen biosynthesis		Adhesion
50	1271	4.98	NVIE_001000	putative surface-associated Ca2+-binding protein, Haemolysin-type		
27	806	5.22	NVIE_001020*	putative cell wall surface anchor family protein, large adhesion protein		
63	1318	4.69	NVIE_001850	exported protein of unknown function		
1174	9330	3.30	NVIE_014250	exported protein of unknown function		
538	2865	2.72	NVIE_014290*	hypothetical protein, putative cation channel protein		copC/copD
107	2601	4.92	NVIE_014300	CopC/CopD		
248	6133	4.94	NVIE_1457	exported protein of unknown function, inbetween copC/copD		
355	1352	2.24	NVIE_014310*	CopC/CopD		
3552	9968	1.8	NVIE_017730	MCO4a		MCO4a
430	1825	2.38	NVIE_017740*	antibiotic biosynthesis monooxygenase		
39	5453	7.45	NVIE_019250	MCO4b		MCO4b

N. franklandianus

64	352	3.01	NFRAN_1082*	CopD		
601	4457	3.43	NFRAN_1083	exported protein of unknown function, inbetween copC/copD		copC/copD
287	2444	3.64	NFRAN_1084	CopC		
2296	14073	3.16	NFRAN_2029	MCO3		
1514	9353	3.17	NFRAN_2030	MCO3		MCO
1539	8886	3.08	NFRAN_2032	ferredoxin family protein		
1170	6995	3.13	NFRAN_2033	antibiotic biosynthesis monooxygenase		
837	2333	2.02	NFRAN_2077	hypothetical protein		
83	1356	4.58	NFRAN_2146	sialidase family protein		
165	3649	5.02	NFRAN_2154	sialidase family protein		Sialidases
65	1448	5.03	NFRAN_2155	cytochrome c biogenesis protein CcdA		
3803	16583	2.66	NFRAN_2792	MCO4b		MCO
658	809	0.30	NFRAN_2798*	MCO4a		
2849	12045	2.64	NFRAN_RS13445	hypothetical protein		
785	4757	3.19	NFRAN_RS13965	hypothetical protein		

N. maritimus

195	703	2.34	Nmar_0010	archaeal heat shock protein Hsp20		
355	1349	2.44	Nmar_0013	TFB		TFB
1665	7969	2.72	Nmar_0033	winged HTH domain-containing protein		
741	2357	2.21	Nmar_0034	TmrB family transcriptional regulator		
1297	3717	2.09	Nmar_0063	hypothetical protein		
41	231	3.05	Nmar_0455	hypothetical protein, putatively involved in adhesion		
6	227	6.04	Nmar_0456	putative cell wall surface anchor family protein, large adhesion protein		Adhesion
2135	26172	4.11	Nmar_0459	putative serine rich protein involved in cell adhesion		
70	429	3.15	NMAR_RS05400	hypothetical protein		
578	6629	4.13	Nmar_1201	S-Layer		S-layer
924	8057	3.62	Nmar_1246	hypothetical protein		
184	445	1.83	Nmar_1340	TFB		
154	469	2.15	Nmar_1353	hemerythrin domain-containing protein		MCO
2980	7730	1.88	Nmar_1354*	MCO4a		

TPM		Log2 FC	Locus	Information	<i>N. viennensis</i>	Genomic region
Ctrl	BF					
47	2255	5.88	NVIE_000940	cell surface protein with DUF11 domain, putative aggregation protein		
1652	28590	4.41	NVIE_000970	putative serine rich protein involved in cell adhesion		
287	2405	3.36	NVIE_000990*	hypothetical protein, putative glycogen biosynthesis		Adhesion
50	1271	4.98	NVIE_001000	putative surface-associated Ca2+-binding protein, Haemolysin-type		
27	806	5.22	NVIE_001020*	putative cell wall surface anchor family protein, large adhesion protein		
63	1318	4.69	NVIE_001850	exported protein of unknown function		
1174	9330	3.30	NVIE_014250	exported protein of unknown function		
538	2865	2.72	NVIE_014290*	hypothetical protein, putative cation channel protein		copC/copD
107	2601	4.92	NVIE_014300	CopC/CopD		
248	6133	4.94	NVIE_1457	exported protein of unknown function, inbetween copC/copD		
355	1352	2.24	NVIE_014310*	CopC/CopD		
3552	9968	1.8	NVIE_017730	MCO4a		MCO4a
430	1825	2.38	NVIE_017740*	antibiotic biosynthesis monooxygenase		
39	5453	7.45	NVIE_019250	MCO4b		MCO4b

		Log2 FC	Locus	Information	<i>N. franklandianus</i>	Genomic region
Ctrl	BF					
64	352	3.01	NFRAN_1082*	CopD		
601	4457	3.43	NFRAN_1083	exported protein of unknown function, inbetween copC/copD		copC/copD
287	2444	3.64	NFRAN_1084	CopC		
2296	14073	3.16	NFRAN_2029	MCO3		
1514	9353	3.17	NFRAN_2030	MCO3		MCO
1539	8886	3.08	NFRAN_2032	ferredoxin family protein		
1170	6995	3.13	NFRAN_2033	antibiotic biosynthesis monooxygenase		
837	2333	2.02	NFRAN_2077	hypothetical protein		
83	1356	4.58	NFRAN_2146	sialidase family protein		
165	3649	5.02	NFRAN_2154	sialidase family protein		Sialidases
65	1448	5.03	NFRAN_2155	cytochrome c biogenesis protein CcdA		
3803	16583	2.66	NFRAN_2792	MCO4b		MCO
658	809	0.30	NFRAN_2798*	MCO4a		
2849	12045	2.64	NFRAN_RS13445	hypothetical protein		
785	4757	3.19	NFRAN_RS13965	hypothetical protein		

		Log2 FC	Locus	Information	<i>N. maritimus</i>	Genomic region
Ctrl	BF					
195	703	2.34	Nmar_0010	archaeal heat shock protein Hsp20		
355	1349	2.44	Nmar_0013	TFB		TFB
1665	7969	2.72	Nmar_0033	winged HTH domain-containing protein		
741	2357	2.21	Nmar_0034	TmrB family transcriptional regulator		
1297	3717	2.09	Nmar_0063	hypothetical protein		
41	231	3.05	Nmar_0455	hypothetical protein, putatively involved in adhesion		
6	227	6.04	Nmar_0456	putative cell wall surface anchor family protein, large adhesion protein		Adhesion
2135	26172	4.11	Nmar_0459	putative serine rich protein involved in cell adhesion		
70	429	3.15	NMAR_RS05400	hypothetical protein		
578	6629	4.13	Nmar_1201	S-Layer		S-layer
924	8057	3.62	Nmar_1246	hypothetical protein		
184	445	1.83	Nmar_1340	TFB		
154	469	2.15	Nmar_1353	hemerythrin domain-containing protein		MCO
2980	7730	1.88	Nmar_1354*	MCO4a		

Adhesion protein

Sialidases MCO3

Adhesion protein

TPM		Log2 FC	Locus	Information	<i>N. viennensis</i>	Genomic region
Ctrl	BF					
47	2255	5.88	NVIE_000940	cell surface protein with DUF11 domain, putative aggregation protein		
1652	28590	4.41	NVIE_000970	putative serine rich protein involved in cell adhesion		
287	2405	3.36	NVIE_000990*	hypothetical protein, putative glycogen biosynthesis		Adhesion
50	1271	4.98	NVIE_001000	putative surface-associated Ca2+-binding protein, Haemolysin-type		
27	806	5.22	NVIE_001020*	putative cell wall surface anchor family protein, large adhesion protein		
63	1318	4.69	NVIE_001850	exported protein of unknown function		
1174	9330	3.30	NVIE_014250	exported protein of unknown function		
538	2865	2.72	NVIE_014290*	hypothetical protein, putative cation channel protein		copC/copD
107	2601	4.92	NVIE_014300	CopC/CopD		
248	6133	4.94	NVIE_1457	exported protein of unknown function, inbetween copC/copD		
355	1352	2.24	NVIE_014310*	CopC/CopD		
3552	9968	1.8	NVIE_017730	MCO4a		MCO4a
430	1825	2.38	NVIE_017740*	antibiotic biosynthesis monooxygenase		
39	5453	7.45	NVIE_019250	MCO4b		MCO4b

		Log2 FC	Locus	Information	<i>N. franklandianus</i>	Genomic region
Ctrl	BF					
64	352	3.01	NFRAN_1082*	CopD		
601	4457	3.43	NFRAN_1083	exported protein of unknown function, inbetween copC/copD		copC/copD
287	2444	3.64	NFRAN_1084	CopC		
2296	14073	3.16	NFRAN_2029	MCO3		
1514	9353	3.17	NFRAN_2030	MCO3		MCO
1539	8886	3.08	NFRAN_2032	ferredoxin family protein		
1170	6995	3.13	NFRAN_2033	antibiotic biosynthesis monooxygenase		
837	2333	2.02	NFRAN_2077	hypothetical protein		
83	1356	4.58	NFRAN_2146	sialidase family protein		
165	3649	5.02	NFRAN_2154	sialidase family protein		Sialidases
65	1448	5.03	NFRAN_2155	cytochrome c biogenesis protein CcdA		
3803	16583	2.66	NFRAN_2792	MCO4b		MCO
658	809	0.30	NFRAN_2798*	MCO4a		
2849	12045	2.64	NFRAN_RS13445	hypothetical protein		
785	4757	3.19	NFRAN_RS13965	hypothetical protein		

		Log2 FC	Locus	Information	<i>N. maritimus</i>	Genomic region
Ctrl	BF					
195	703	2.34	Nmar_0010	archaeal heat shock protein Hsp20		
355	1349	2.44	Nmar_0013	TFB		TFB
1665	7969	2.72	Nmar_0033	winged HTH domain-containing protein		
741	2357	2.21	Nmar_0034	TmrB family transcriptional regulator		
1297	3717	2.09	Nmar_0063	hypothetical protein		
41	231	3.05	Nmar_0455	hypothetical protein, putatively involved in adhesion		
6	227	6.04	Nmar_0456	putative cell wall surface anchor family protein, large adhesion protein		Adhesion
2135	26172	4.11	Nmar_0459	putative serine rich protein involved in cell adhesion		
70	429	3.15	NMAR_RS05400	hypothetical protein		
578	6629	4.13	Nmar_1201	S-Layer		S-layer
924	8057	3.62	Nmar_1246	hypothetical protein		
184	445	1.83	Nmar_1340	TFB		
154	469	2.15	Nmar_1353	hemerythrin domain-containing protein		MCO
2980	7730	1.88	Nmar_1354*	MCO4a		

Adhesion
protein

(S-layer)

Sialidases
MCO3

(Missing
S-layer)

Adhesion
protein
(S-layer)

TPM		Log2 FC	Locus	Information	<i>N. viennensis</i>	Genomic region
Ctrl	BF					
47	2255	5.88	NVIE_000940	cell surface protein with DUF11 domain, putative aggregation protein	Adhesion	
1652	28590	4.41	NVIE_000970	putative serine rich protein involved in cell adhesion		
287	2405	3.36	NVIE_000990*	hypothetical protein, putative glycogen biosynthesis		
50	1271	4.98	NVIE_001000	putative surface-associated Ca2+-binding protein, Haemolysin-type		
27	806	5.22	NVIE_001020*	putative cell wall surface anchor family protein, large adhesion protein		
63	1318	4.69	NVIE_001850	exported protein of unknown function	copC/copD	
1174	9330	3.30	NVIE_014250	exported protein of unknown function		
538	2865	2.72	NVIE_014290*	hypothetical protein, putative cation channel protein		
107	2601	4.92	NVIE_014300	CopC/CopD		
248	6133	4.94	NVIE_1457	exported protein of unknown function, inbetween copC/copD		
355	1352	2.24	NVIE_014310*	CopC/CopD	MCO4a	
3552	9968	1.8	NVIE_017730	MCO4a		
430	1825	2.38	NVIE_017740*	antibiotic biosynthesis monooxygenase		
39	5453	7.45	NVIE_019250	MCO4b		

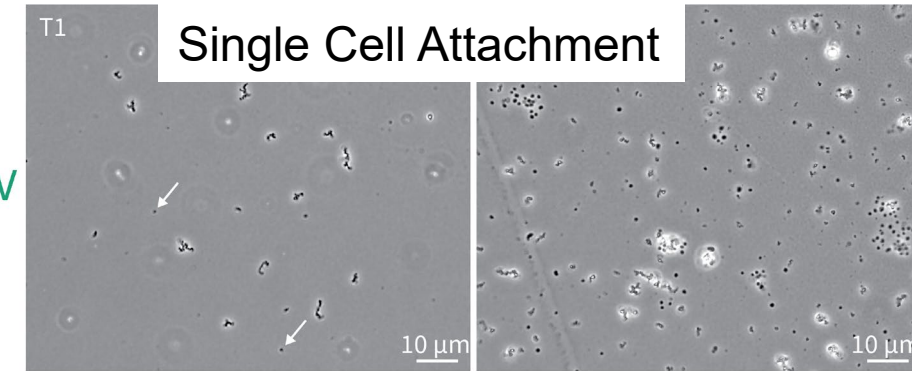
		Log2 FC	Locus	Information	<i>N. franklandianus</i>	
Ctrl	BF					
64	352	3.01	NFRAN_1082*	CopD	copC/copD	
601	4457	3.43	NFRAN_1083	exported protein of unknown function, inbetween copC/copD		
287	2444	3.64	NFRAN_1084	CopC		
2296	14073	3.16	NFRAN_2029	MCO3	MCO	
1514	9353	3.17	NFRAN_2030	MCO3		
1539	8886	3.08	NFRAN_2032	ferredoxin family protein		
1170	6995	3.13	NFRAN_2033	antibiotic biosynthesis monooxygenase	Sialidases	
837	2333	2.02	NFRAN_2077	hypothetical protein		
83	1356	4.58	NFRAN_2146	sialidase family protein		
165	3649	5.02	NFRAN_2154	sialidase family protein	MCO	
65	1448	5.03	NFRAN_2155	cytochrome c biogenesis protein CcdA		
3803	16583	2.66	NFRAN_2792	MCO4b		
658	809	0.30	NFRAN_2798*	MCO4a		
2849	12045	2.64	NFRAN_RS13445	hypothetical protein		
785	4757	3.19	NFRAN_RS13965	hypothetical protein		

		Log2 FC	Locus	Information	<i>N. maritimus</i>	
Ctrl	BF					
195	703	2.34	Nmar_0010	archaeal heat shock protein Hsp20	TFB	
355	1349	2.44	Nmar_0013	TFB		
1665	7969	2.72	Nmar_0033	winged HTH domain-containing protein		
741	2357	2.21	Nmar_0034	TmrB family transcriptional regulator	Adhesion	
1297	3717	2.09	Nmar_0063	hypothetical protein		
41	231	3.05	Nmar_0455	hypothetical protein, putatively involved in adhesion		
6	227	6.04	Nmar_0456	putative cell wall surface anchor family protein, large adhesion protein	S-layer	
2135	26172	4.11	Nmar_0459	putative serine rich protein involved in cell adhesion		
70	429	3.15	NMAR_RS05400	hypothetical protein		
578	6629	4.13	Nmar_1201	S-Layer	MCO	
924	8057	3.62	Nmar_1246	hypothetical protein		
184	445	1.83	Nmar_1340	TFB		
154	469	2.15	Nmar_1353	hemerythrin domain-containing protein		
2980	7730	1.88	Nmar_1354*	MCO4a		

Adhesion
protein

S-layer

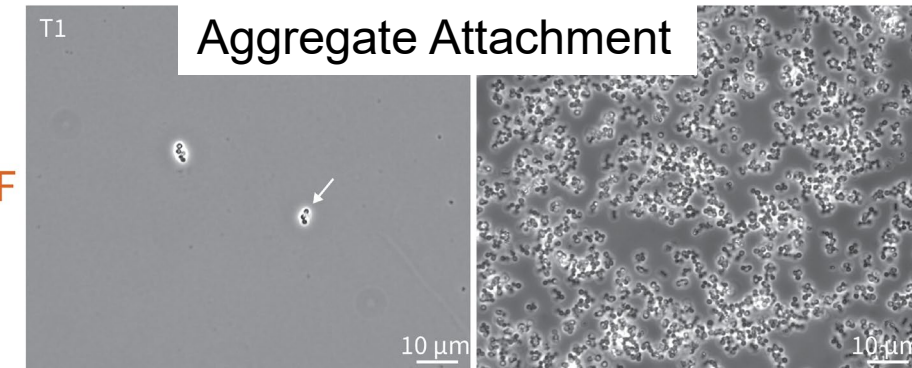
NV



Sialidases
MCO3

Missing
S-layer

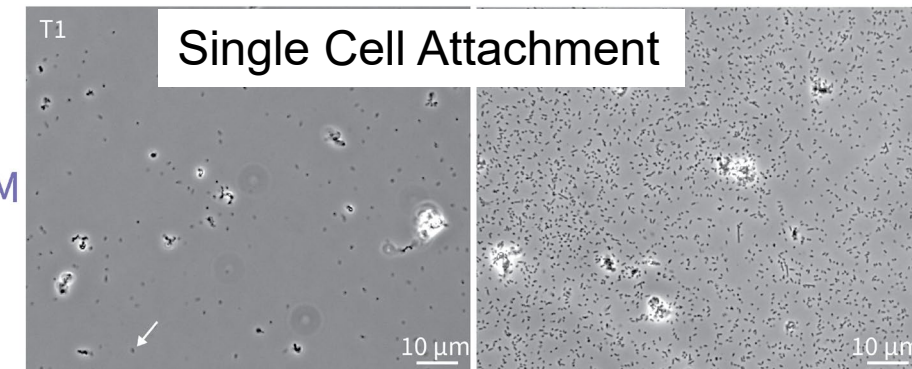
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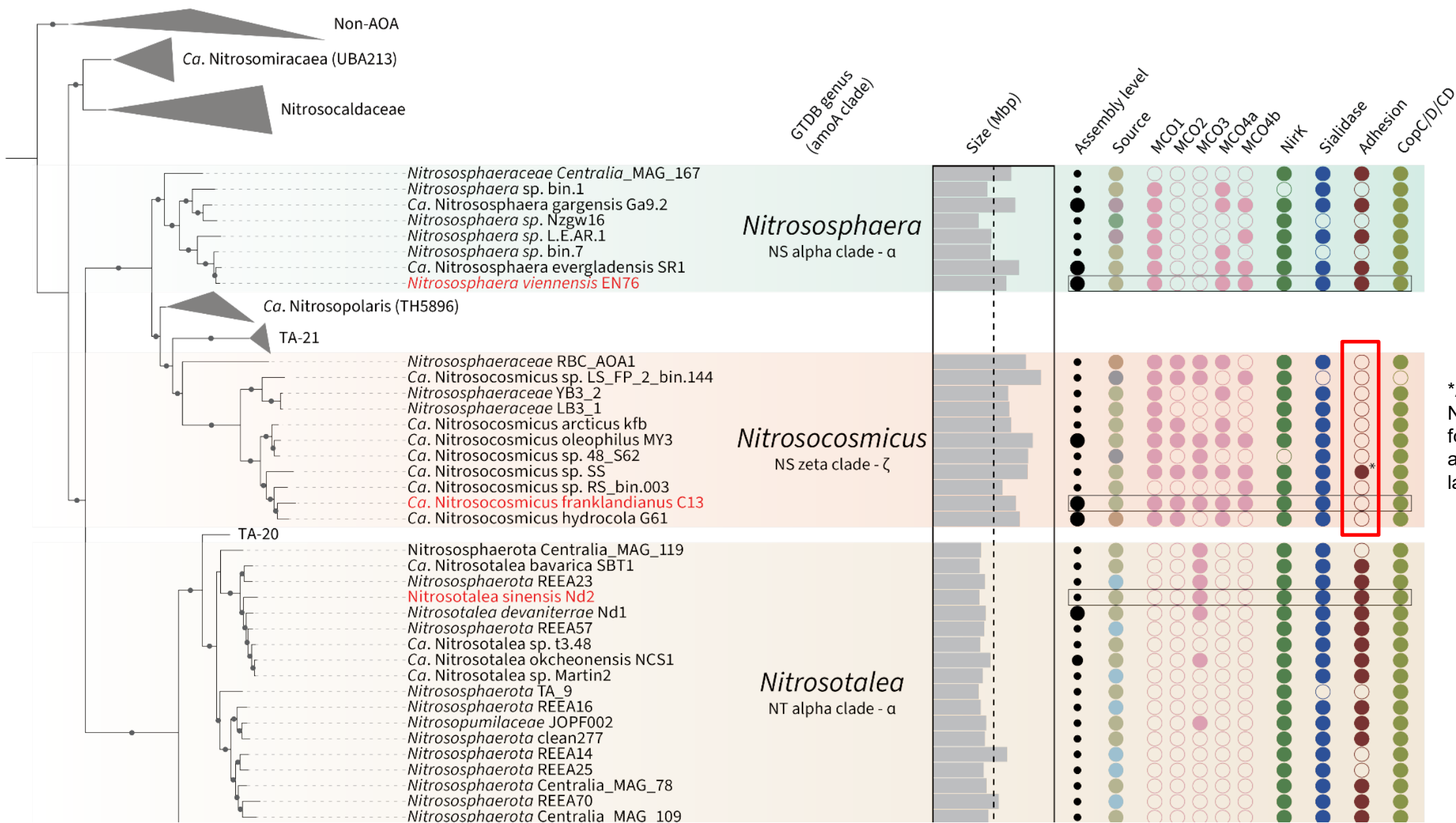


Adhesion
protein

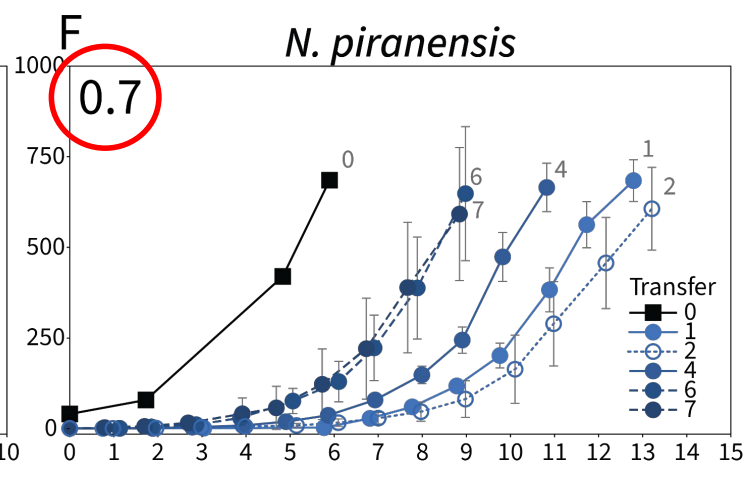
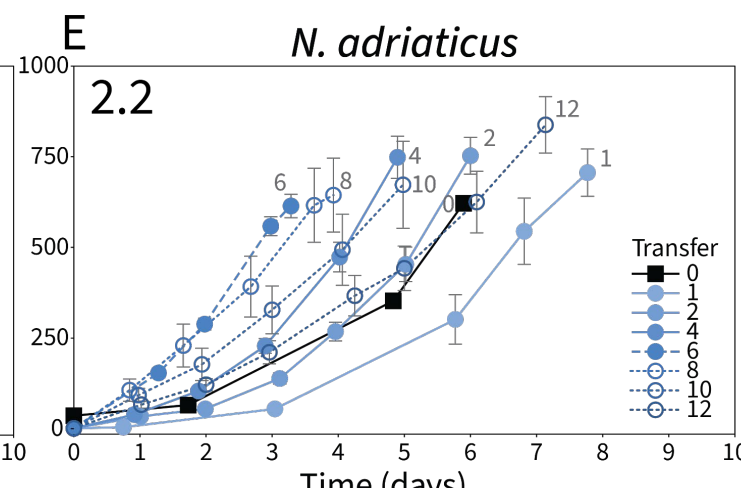
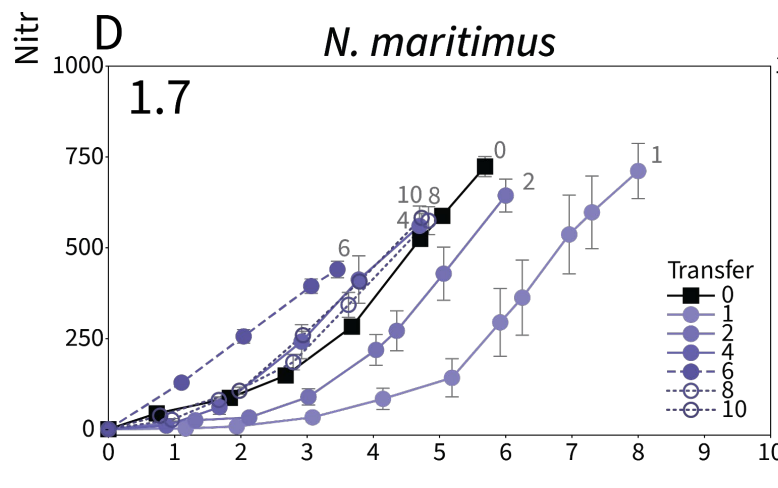
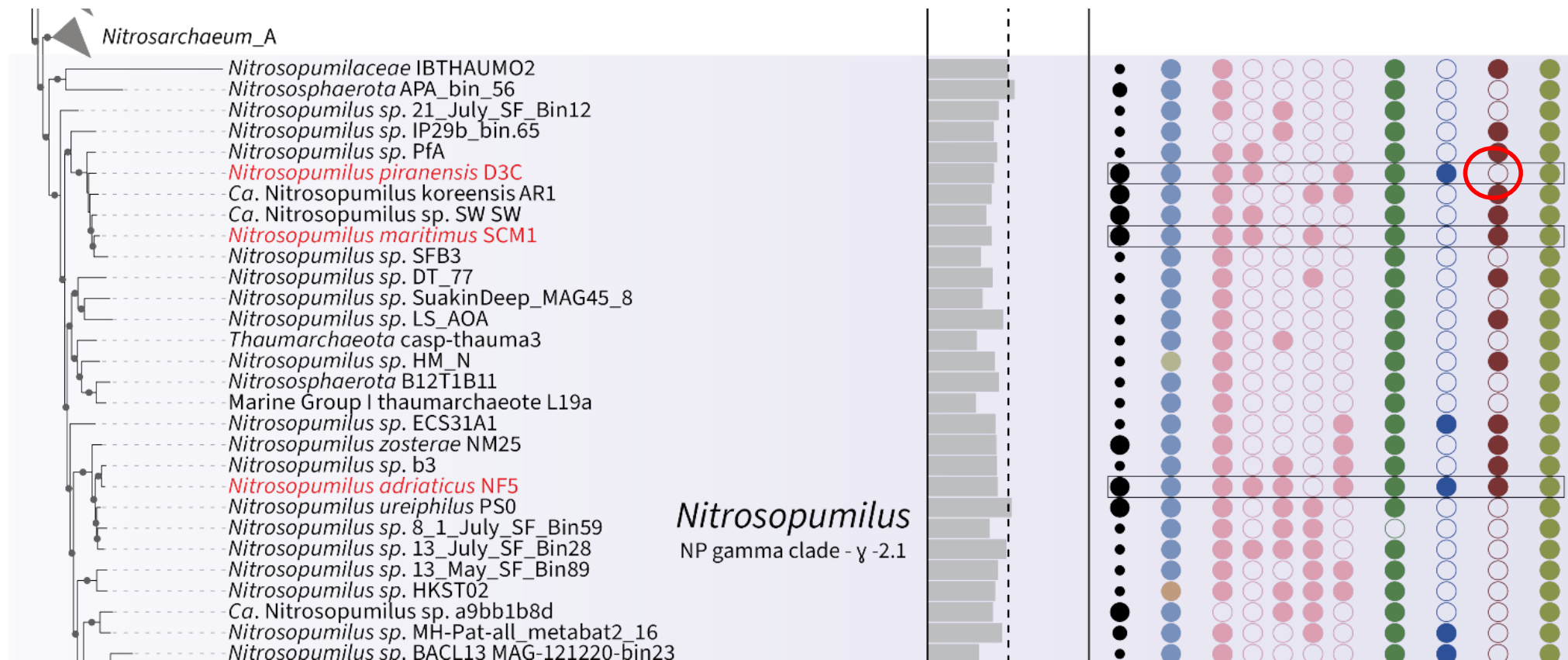
S-layer

NM





*All isolated *Nitrosocosmicus* form aggregates and lack an S-layer



TPM		Log2 FC	Locus	Information	<i>N. viennensis</i>	Genomic region
Ctrl	BF					
47	2255	5.88	NVIE_000940	cell surface protein with DUF11 domain, putative aggregation protein		
1652	28590	4.41	NVIE_000970	putative serine rich protein involved in cell adhesion		
287	2405	3.36	NVIE_000990*	hypothetical protein, putative glycogen biosynthesis		Adhesion
50	1271	4.98	NVIE_001000	putative surface-associated Ca2+-binding protein, Haemolysin-type		
27	806	5.22	NVIE_001020*	putative cell wall surface anchor family protein, large adhesion protein		
63	1318	4.69	NVIE_001850	exported protein of unknown function		
1174	9330	3.30	NVIE_014250	exported protein of unknown function		
538	2865	2.72	NVIE_014290*	hypothetical protein, putative cation channel protein		
107	2601	4.92	NVIE_014300	CopC/CopD		copC/copD
248	6133	4.94	NVIE_1457	exported protein of unknown function, inbetween copC/copD		
355	1352	2.24	NVIE_014310*	CopC/CopD		
3552	9968	1.8	NVIE_017730	MCO4a		MCO4a
430	1825	2.38	NVIE_017740*	antibiotic biosynthesis monooxygenase		
39	5453	7.45	NVIE_019250	MCO4b		MCO4b

		Log2 FC	Locus	Information	<i>N. franklandianus</i>	Genomic region
Ctrl	BF					
64	352	3.01	NFRAN_1082*	CopD		
601	4457	3.43	NFRAN_1083	exported protein of unknown function, inbetween copC/copD		copC/copD
287	2444	3.64	NFRAN_1084	CopC		
2296	14073	3.16	NFRAN_2029	MCO3		
1514	9353	3.17	NFRAN_2030	MCO3		MCO
1539	8886	3.08	NFRAN_2032	ferredoxin family protein		
1170	6995	3.13	NFRAN_2033	antibiotic biosynthesis monooxygenase		
837	2333	2.02	NFRAN_2077	hypothetical protein		
83	1356	4.58	NFRAN_2146	sialidase family protein		
165	3649	5.02	NFRAN_2154	sialidase family protein		Sialidases
65	1448	5.03	NFRAN_2155	cytochrome c biogenesis protein CcdA		
3803	16583	2.66	NFRAN_2792	MCO4b		MCO
658	809	0.30	NFRAN_2798*	MCO4a		
2849	12045	2.64	NFRAN_RS13445	hypothetical protein		
785	4757	3.19	NFRAN_RS13965	hypothetical protein		

		Log2 FC	Locus	Information	<i>N. maritimus</i>	Genomic region
Ctrl	BF					
195	703	2.34	Nmar_0010	archaeal heat shock protein Hsp20		
355	1349	2.44	Nmar_0013	TFB		TFB
1665	7969	2.72	Nmar_0033	winged HTH domain-containing protein		
741	2357	2.21	Nmar_0034	TmrB family transcriptional regulator		
1297	3717	2.09	Nmar_0063	hypothetical protein		
41	231	3.05	Nmar_0455	hypothetical protein, putatively involved in adhesion		
6	227	6.04	Nmar_0456	putative cell wall surface anchor family protein, large adhesion protein		Adhesion
2135	26172	4.11	Nmar_0459	putative serine rich protein involved in cell adhesion		
70	429	3.15	NMAR_RS05400	hypothetical protein		
578	6629	4.13	Nmar_1201	S-Layer		S-layer
924	8057	3.62	Nmar_1246	hypothetical protein		
184	445	1.83	Nmar_1340	TFB		
154	469	2.15	Nmar_1353	hemerythrin domain-containing protein		MCO
2980	7730	1.88	Nmar_1354*	MCO4a		

CopC/D

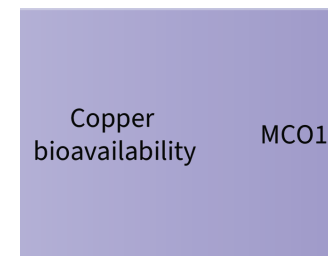
Several Transcription Factor Changes
*a switch of the dominant transcription factor

TPM		Log2 FC	Locus	Information	<i>N. viennensis</i>	Genomic region
Ctrl	BF					
47	2255	5.88	NVIE_000940	cell surface protein with DUF11 domain, putative aggregation protein		
1652	28590	4.41	NVIE_000970	putative serine rich protein involved in cell adhesion		
287	2405	3.36	NVIE_000990*	hypothetical protein, putative glycogen biosynthesis		Adhesion
50	1271	4.98	NVIE_001000	putative surface-associated Ca2+-binding protein, Haemolysin-type		
27	806	5.22	NVIE_001020*	putative cell wall surface anchor family protein, large adhesion protein		
63	1318	4.69	NVIE_001850	exported protein of unknown function		
1174	9330	3.30	NVIE_014250	exported protein of unknown function		
538	2865	2.72	NVIE_014290*	hypothetical protein, putative cation channel protein		
107	2601	4.92	NVIE_014300	CopC/CopD		copC/copD
248	6133	4.94	NVIE_1457	exported protein of unknown function, inbetween copC/copD		
355	1352	2.24	NVIE_014310*	CopC/CopD		
3552	9968	1.8	NVIE_017730	MCO4a		MCO4a
430	1825	2.38	NVIE_017740*	antibiotic biosynthesis monooxygenase		
39	5453	7.45	NVIE_019250	MCO4b		MCO4b

		Log2 FC	Locus	Information	<i>N. franklandianus</i>	
64	352	3.01	NFRAN_1082*	CopD		
601	4457	3.43	NFRAN_1083	exported protein of unknown function, inbetween copC/copD		copC/copD
287	2444	3.64	NFRAN_1084	CopC		
2296	14073	3.16	NFRAN_2029	MCO3		
1514	9353	3.17	NFRAN_2030	MCO3		MCO
1539	8886	3.08	NFRAN_2032	ferredoxin family protein		
1170	6995	3.13	NFRAN_2033	antibiotic biosynthesis monooxygenase		
837	2333	2.02	NFRAN_2077	hypothetical protein		
83	1356	4.58	NFRAN_2146	sialidase family protein		
165	3649	5.02	NFRAN_2154	sialidase family protein		Sialidases
65	1448	5.03	NFRAN_2155	cytochrome c biogenesis protein CcdA		
3803	16583	2.66	NFRAN_2792	MCO4b		MCO
658	809	0.30	NFRAN_2798*	MCO4a		
2849	12045	2.64	NFRAN_RS13445	hypothetical protein		
785	4757	3.19	NFRAN_RS13965	hypothetical protein		

		Log2 FC	Locus	Information	<i>N. maritimus</i>	
195	703	2.34	Nmar_0010	archaeal heat shock protein Hsp20		
355	1349	2.44	Nmar_0013	TFB		TFB
1665	7969	2.72	Nmar_0033	winged HTH domain-containing protein		
741	2357	2.21	Nmar_0034	TmrB family transcriptional regulator		
1297	3717	2.09	Nmar_0063	hypothetical protein		
41	231	3.05	Nmar_0455	hypothetical protein, putatively involved in adhesion		
6	227	6.04	Nmar_0456	putative cell wall surface anchor family protein, large adhesion protein		Adhesion
2135	26172	4.11	Nmar_0459	putative serine rich protein involved in cell adhesion		
70	429	3.15	NMAR_RS05400	hypothetical protein		
578	6629	4.13	Nmar_1201	S-Layer		S-layer
924	8057	3.62	Nmar_1246	hypothetical protein		
184	445	1.83	Nmar_1340	TFB		
154	469	2.15	Nmar_1353	hemerythrin domain-containing protein		MCO
2980	7730	1.88	Nmar_1354*	MCO4a		

CopC/D



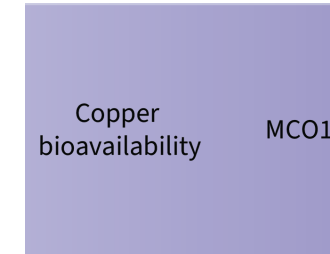
57	113	1.28	NVIE_000600
122	39	-1.34	NVIE_026950
113	155	1.01	NFRAN_0604
4	6	0.90	Nmar_1663
2	2	0.53	Nmar_1131

TPM		Log2 FC	Locus	Information	<i>N. viennensis</i>	Genomic region
Ctrl	BF					
47	2255	5.88	NVIE_000940	cell surface protein with DUF11 domain, putative aggregation protein		
1652	28590	4.41	NVIE_000970	putative serine rich protein involved in cell adhesion		
287	2405	3.36	NVIE_000990*	hypothetical protein, putative glycogen biosynthesis		Adhesion
50	1271	4.98	NVIE_001000	putative surface-associated Ca2+-binding protein, Haemolysin-type		
27	806	5.22	NVIE_001020*	putative cell wall surface anchor family protein, large adhesion protein		
63	1318	4.69	NVIE_001850	exported protein of unknown function		
1174	9330	3.30	NVIE_014250	exported protein of unknown function		
538	2865	2.72	NVIE_014290*	hypothetical protein, putative cation channel protein		
107	2601	4.92	NVIE_014300	CopC/CopD		copC/copD
248	6133	4.94	NVIE_1457	exported protein of unknown function, inbetween copC/copD		
355	1352	2.24	NVIE_014310*	CopC/CopD		
3552	9968	1.8	NVIE_017730	MCO4a		MCO4a
430	1825	2.38	NVIE_017740*	antibiotic biosynthesis monooxygenase		
39	5453	7.45	NVIE_019250	MCO4b		MCO4b

		Log2 FC	Locus	Information	<i>N. franklandianus</i>	
Ctrl	BF					
64	352	3.01	NFRAN_1082*	CopD		
601	4457	3.43	NFRAN_1083	exported protein of unknown function, inbetween copC/copD		copC/copD
287	2444	3.64	NFRAN_1084	CopC		
2296	14073	3.16	NFRAN_2029	MCO3		
1514	9353	3.17	NFRAN_2030	MCO3		MCO
1539	8886	3.08	NFRAN_2032	ferredoxin family protein		
1170	6995	3.13	NFRAN_2033	antibiotic biosynthesis monooxygenase		
837	2333	2.02	NFRAN_2077	hypothetical protein		
83	1356	4.58	NFRAN_2146	sialidase family protein		
165	3649	5.02	NFRAN_2154	sialidase family protein		Sialidases
65	1448	5.03	NFRAN_2155	cytochrome c biogenesis protein CcdA		
3803	16583	2.66	NFRAN_2792	MCO4b		MCO
658	809	0.30	NFRAN_2798*	MCO4a		
2849	12045	2.64	NFRAN_RS13445	hypothetical protein		
785	4757	3.19	NFRAN_RS13965	hypothetical protein		

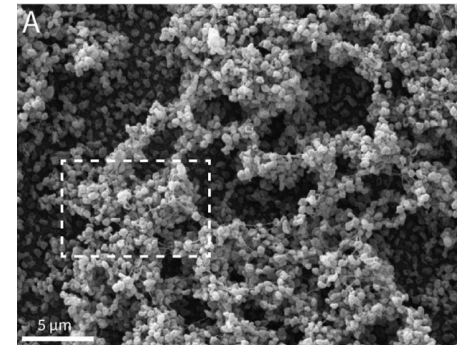
		Log2 FC	Locus	Information	<i>N. maritimus</i>	
Ctrl	BF					
195	703	2.34	Nmar_0010	archaeal heat shock protein Hsp20		
355	1349	2.44	Nmar_0013	TFB		TFB
1665	7969	2.72	Nmar_0033	winged HTH domain-containing protein		
741	2357	2.21	Nmar_0034	TmrB family transcriptional regulator		
1297	3717	2.09	Nmar_0063	hypothetical protein		
41	231	3.05	Nmar_0455	hypothetical protein, putatively involved in adhesion		
6	227	6.04	Nmar_0456	putative cell wall surface anchor family protein, large adhesion protein		Adhesion
2135	26172	4.11	Nmar_0459	putative serine rich protein involved in cell adhesion		
70	429	3.15	NMAR_RS05400	hypothetical protein		
578	6629	4.13	Nmar_1201	S-Layer		S-layer
924	8057	3.62	Nmar_1246	hypothetical protein		
184	445	1.83	Nmar_1340	TFB		
154	469	2.15	Nmar_1353	hemerythrin domain-containing protein		MCO
2980	7730	1.88	Nmar_1354*	MCO4a		

CopC/D

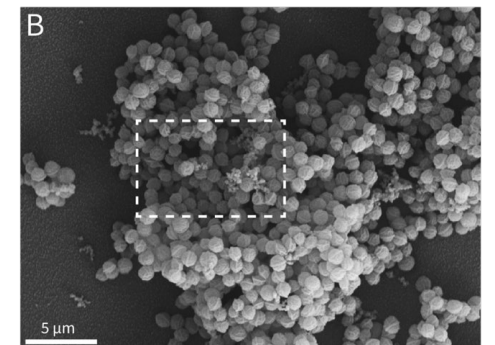


57	113	1.28	NVIE_000600
122	39	-1.34	NVIE_026950
113	155	1.01	NFRAN_0604
4	6	0.90	Nmar_1663
2	2	0.53	Nmar_1131

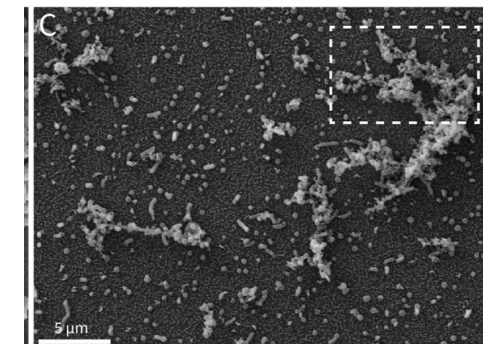
N. viennensis



N. franklandianus

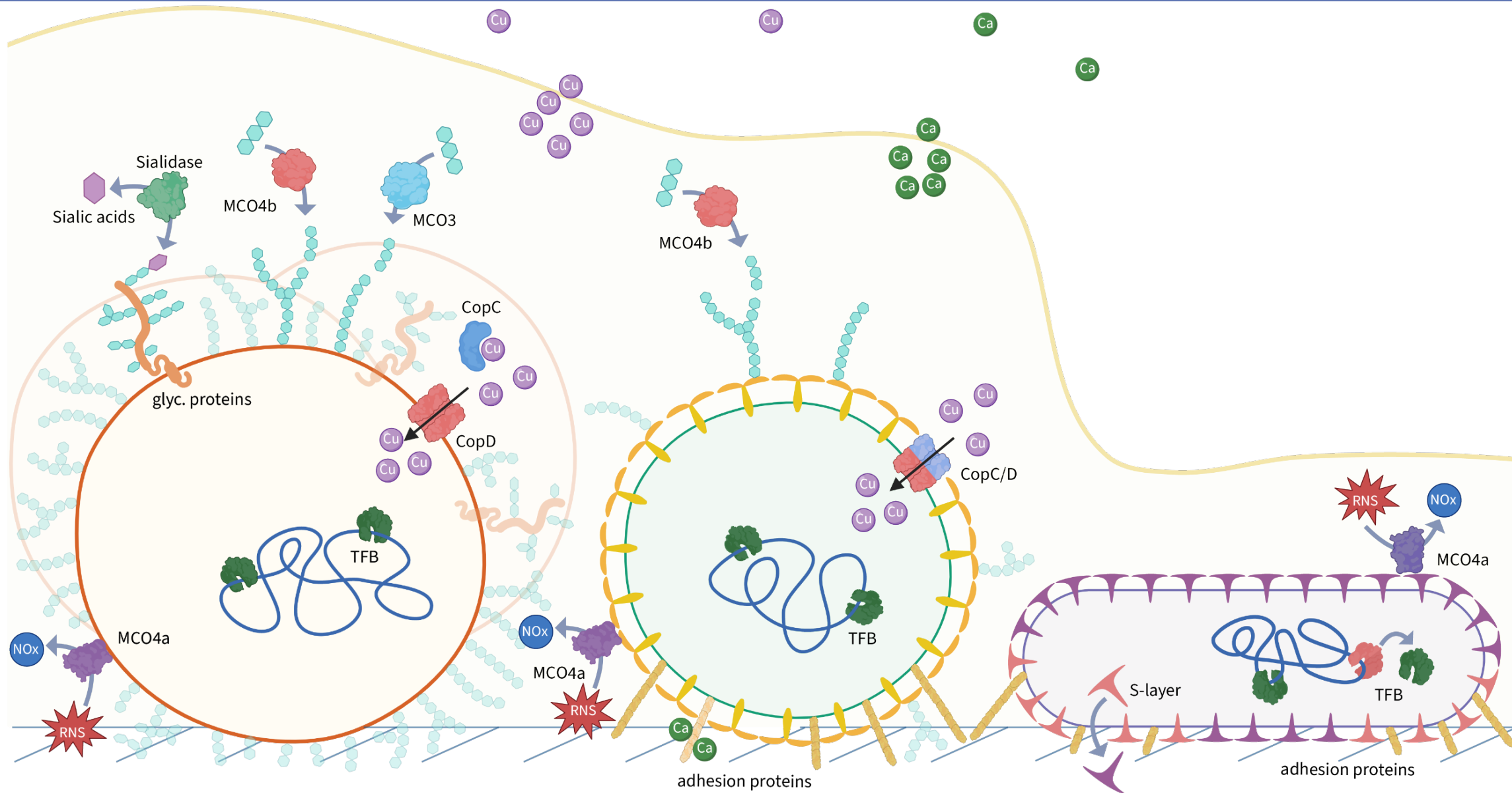


N. maritimus



Physiological Observations

1. Highly up-regulated genes are species specific
2. Multicopper oxidases are potentially involved in cell surface modification
3. Adhesion proteins support biofilm formation in species with an S-layer
4. Multi-dimensional biofilms may be copper limited
5. Marine strains may undergo a more drastic transcriptional adjustment



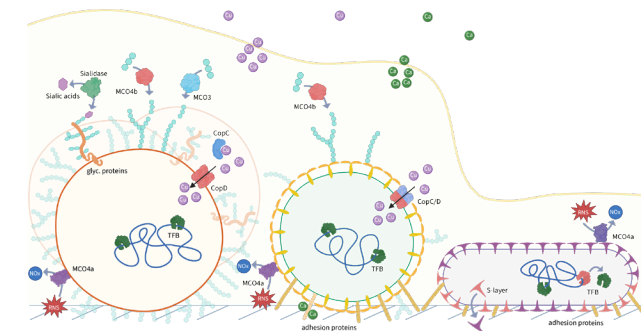
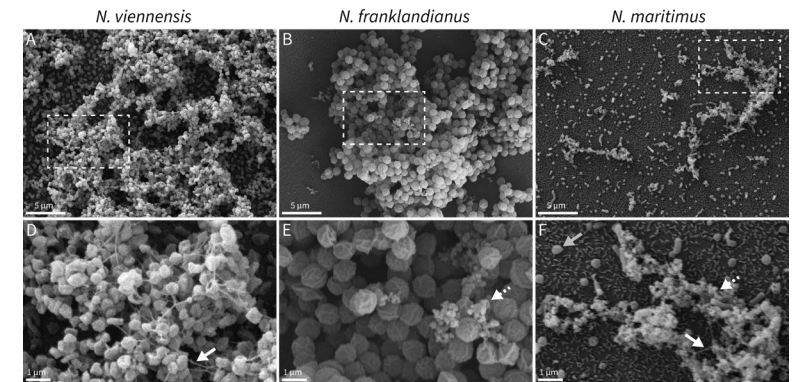
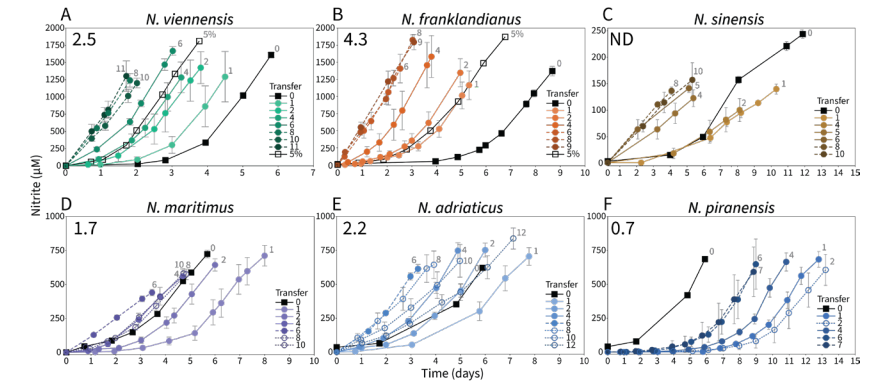
N. franklandianus

N. viennensis

N. maritimus

Conclusions

- All tested AOA have the capacity to form biofilms
- Soil strains exhibited the greatest capacity to form biofilms
- Growth as a biofilm is associated with distinct, species specific, physiological changes



Biofilm lifestyle as a common trait of ammonia-oxidizing archaea

 Maximilian Dreer,  Thomas Pribasnig,  Logan H. Hodgskiss,  Zhen-Hao Luo, Fran Pozaric,
 Christa Schleper

doi: <https://doi.org/10.1101/2024.11.18.624116>



Max Dreer



Thomas Pribasnig

Questions

- Is biofilm formation a common trait of AOA? **YES**
- Are there physiological responses associated with biofilms? **YES**
- Does biofilm growth affect nitrification? **YES**



Prof. Dr. Christa Schleper

Biofilm



Max Dreer



Thomas Pribasnig



Fran Pozaric



Dr. Zhen-Hao Luo



Dimitris Dalkidis



Dr. Logan Hodgskiss



Ülkü Perier



Dr. Andrea Malits



Dr. Melina Kerou



Thank You!



Marlene Urban



Hadis Sajedi



Marina Monserrat-Diez