

Supporting Information

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Table S1. Geographic origin of *Euplotes nobilii* strains

Strains	Collection sites	Latitude/longitude	Isolator, year
<i>Antarctic</i>			
AC-1	Icaro Faraglione Campus (Antarctica)	S 74°41'/E 163°59'	Valbonesi A., 1988
Far	"	"	"
Sop	"	"	"
AC-3	Observatory Forecast Campus (Antarctica)	S 74°44'/E 164°00'	"
AC-4	Edmonson Point (Antarctica)	S 74°19'/E 165°07'	"
AC-5	"	"	"
Ed.Po-6	"	"	Luporini P., 2003
<i>Fuegian</i>			
IsH3-1	Hoste Island, Tierra del Fuego (Chile)	S 55°15'/W 69°00'	Luporini P., 2008
PA1-1	Punta Arenas, Tierra del Fuego (Chile)	S 53°08'/W 70°54'	"
PNA-1h	Puerto Natales, Tierra del Fuego (Chile)	S 51°43'/W 72°31'	"
PUN1	Pinguinera Seno Otway, Tierra del Fuego (Chile)	S 52°59'/W 71°14'	"
<i>Arctic</i>			
1QAA	Qaanaaq, Greenland (Denmark)	N 77°28'/W 69°20'	Dini F., 2006
5QAA15	"	"	"
2QAN1	Thule, Greenland (Denmark)	N 76°32'/W 68°50'	"
3QAN7	"	"	"
4QN9	Siorapaluk, Greenland (Denmark)	N 77°46'/W 70°48'	"
4ILa4	Ilulissat, Greenland (Denmark)	N 69°13'/W 51°06'	"
4Pym4	Pyramiden, Svalbard (Norge)	N 78°39'/E 16°22'	Dini F., 2004

Table S2. Analytic dataset of the measurements and counts carried out on *E. nobilii* strains

Strains	Morphological traits measured (µm) or counted										
	1	2	3	4	5	6	7	8	9	10	11
<i>Antarctic</i>											
AC-1	40.70 ± 1.83	27.50 ± 2.32	23.10 ± 1.29	46.20 ± 4.49	8.10 ± 0.32	10	3.60 ± 0.52	5	8.20 ± 0.42	21.20 ± 1.32	38.60 ± 0.97
AC-3	40.67 ± 1.84	26.95 ± 2.13	23.14 ± 1.23	45.53 ± 5.49	8.10 ± 0.32	10	3.50 ± 0.53	5	7.90 ± 0.32	21.20 ± 1.62	38.20 ± 1.33
AC-4	40.54 ± 2.06	27.55 ± 2.13	23.60 ± 1.15	48.58 ± 4.59	8.30 ± 0.48	10	3.20 ± 0.42	5	8.40 ± 0.70	21.30 ± 0.95	38.89 ± 0.86
AC-5	39.85 ± 2.56	27.81 ± 1.62	23.57 ± 1.77	48.40 ± 3.69	8.00 ± 0.00	10	3.70 ± 0.48	5	8.30 ± 0.67	21.30 ± 1.64	37.93 ± 1.22
Far	41.00 ± 2.11	27.20 ± 2.86	22.90 ± 0.88	47.40 ± 3.27	8.00 ± 0.00	10	3.40 ± 0.52	5	8.40 ± 0.70	21.80 ± 1.48	38.70 ± 1.16
Sop	40.50 ± 2.42	29.50 ± 2.42	22.90 ± 1.29	49.30 ± 6.17	8.20 ± 0.42	10	3.40 ± 0.52	5	8.60 ± 0.70	21.30 ± 1.16	37.90 ± 1.10
Ed.Po-6	42.40 ± 1.65	29.70 ± 1.89	25.60 ± 1.17	43.80 ± 3.33	7.80 ± 0.63	10	3.00 ± 0.00	5	8.70 ± 0.67	21.20 ± 1.03	35.30 ± 0.82
<i>Fuegian</i>											
IsH3-1	40.75 ± 1.92	27.94 ± 2.35	22.52 ± 0.77	47.69 ± 2.26	8.10 ± 0.57	10	3.40 ± 0.52	5	8.70 ± 0.67	21.60 ± 1.71	38.29 ± 1.54
PA1-1	40.47 ± 2.67	25.26 ± 2.95	22.77 ± 0.72	46.48 ± 2.35	8.00 ± 1.05	10	3.30 ± 0.67	5	7.90 ± 0.57	21.40 ± 1.17	38.74 ± 0.96
PNA1-h	40.54 ± 2.75	26.47 ± 3.57	23.62 ± 0.86	48.14 ± 3.66	7.80 ± 1.03	10	3.40 ± 0.52	5	8.50 ± 0.53	21.50 ± 2.32	38.36 ± 1.00
PUN1	41.03 ± 2.53	27.10 ± 2.60	23.31 ± 0.82	47.32 ± 3.88	8.20 ± 0.42	10	3.30 ± 0.48	5	8.50 ± 0.71	21.80 ± 1.69	38.53 ± 1.24
<i>Arctic</i>											
1QAA	40.60 ± 1.90	26.20 ± 1.23	24.70 ± 1.16	47.80 ± 3.22	8.00 ± 0.47	10	3.00 ± 0.00	5	9.70 ± 0.48	22.50 ± 1.27	37.50 ± 1.18
2QAN1	41.94 ± 1.59	26.42 ± 0.92	25.32 ± 1.13	48.75 ± 2.59	8.10 ± 0.57	10	3.00 ± 0.00	5	9.60 ± 0.52	22.30 ± 1.34	37.09 ± 1.14
3QAN7	40.84 ± 2.04	26.35 ± 0.93	25.57 ± 0.94	49.53 ± 5.57	8.40 ± 0.52	10	3.00 ± 0.00	5	9.30 ± 0.48	22.20 ± 1.99	37.44 ± 1.21
4QN9	39.90 ± 1.52	26.80 ± 1.14	24.70 ± 0.95	46.10 ± 1.79	7.60 ± 0.52	10	3.10 ± 0.32	5	10.10 ± 0.74	23.00 ± 1.33	38.30 ± 1.16
5QAA15	40.30 ± 1.42	27.10 ± 0.99	25.50 ± 0.71	45.60 ± 4.17	7.90 ± 0.57	10	3.00 ± 0.00	5	8.40 ± 0.52	21.90 ± 1.37	36.30 ± 1.49
4ILa4	40.80 ± 2.20	26.70 ± 1.34	25.60 ± 0.97	48.50 ± 5.10	8.00 ± 0.67	10	3.00 ± 0.00	5	9.40 ± 0.70	22.20 ± 1.69	37.50 ± 1.35
4Pym4	39.40 ± 1.35	26.10 ± 1.91	23.70 ± 0.67	44.40 ± 3.72	8.10 ± 0.32	10	3.40 ± 0.52	5	8.60 ± 0.70	22.40 ± 0.70	39.00 ± 1.05

1, body length; 2, body width; 3, length of buccal field; 4, macronucleus length; 5, kinety number; 6, number of fronto-ventral cirri; 7, number of caudal cirri; 8, number of transverse cirri; 9, kinetosome number of the median kinety; 10, number of oral membranelles; and 11, number of polygons (alveoli) adjacent to the median kinety.

Table S3. GenBank accession numbers of the *E. nobilii* strain SSU-rRNA gene sequences

Strains	Accession numbers
1QAA	GU479378
2QAN1	GU479379
3QAN7	GU479380
4QN9	GU479383
5QAA15	GU479384
4ILa4	GU479381
4Pyrm4	GU479382
AC-1	GU479385
AC-3	GU479386
AC-4	EF094969
AC-5	GU479387
Far	GU479389
Sop	EF094970
Ed.Po-6	GU479388
IsH3-1	GU479390
PA1-1	GU479391
PNA-1h	GU479392
PUN1	GU479393

Table S4. Input for the structure calculation and characterization of the bundle of 20 energy-minimized DYANA conformers representing the *En-A1* pheromone NMR structure

Quantity	Value*
NOE upper distance constraints [†]	877
Intraresidual	209
Short-range	235
Medium-range	204
Long-range	229
Disulfide bond distance constraints [‡]	24
Dihedral angle constraints	207
Residual target function value [Å ²]	0.71 ± 0.08 (0.56–0.83)
Residual NOE violations	
Number ≥ 0.1 Å	6 ± 3 (2–12)
Maximum [Å]	0.13 ± 0.01 (0.11–0.16)
Residual dihedral angle violations	
Number ≥ 2.5°	1 ± 1 (0–2)
Maximum [°]	2.61 ± 1.24 (0.13–6.43)
AMBER energies [kcal/mol]	
Total	–1814 ± 29
van der Waals	–184 ± 9
Electrostatic	–2064 ± 26
Rmsd from ideal coordinates	
Bond length [Å]	0.0077 ± 0.0005 (0.0071–0.0089)
Bond angles [°]	1.90 ± 0.10 (1.70–2.07)
Rmsd from mean coordinates [Å] [§]	
Backbone (2–53)	0.34 ± 0.05 (0.26–0.48)
All heavy atoms (2–53)	0.65 ± 0.07 (0.53–0.77)
Ramachandran plot statistics [¶]	
Most favored regions [%]	74.2
Additional allowed regions [%]	21.2
Generously allowed regions [%]	3.5
Disallowed regions [%]	1.1

*Except for the top two entries, average values and corresponding standard deviations in the 20 energy-minimized conformers are given. Minimal and maximal values are given in parentheses.

[†]The NOE upper distance limits reported here are those that were determined in the seventh cycle by the CANDID program.

[‡]Standard distance restraints for disulfide bridges were imposed for the cysteine pairs 12–38, 23–34, 30–58, and 35–47.

[§]The numbers in parentheses indicate the residues for which the rmsd was calculated.

[¶]As determined by PROCHECK.