Supporting Information

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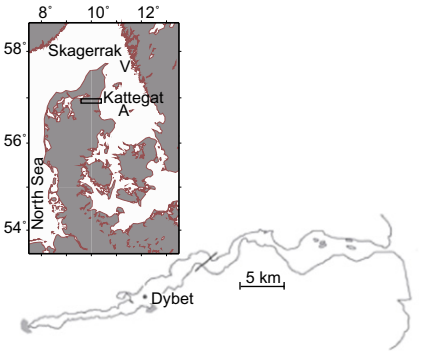

Fig. S1. Map of Denmark showing the location of the Mariager Fjord and the sampling station (Dybet) with a maximum depth of 30 m. The line indicates the distinction between the outer and inner parts of the Mariager Fjord. Populations from the open sea (Kattegat) were established from sediment samples collected at Anholt (A) and Vinga (V).

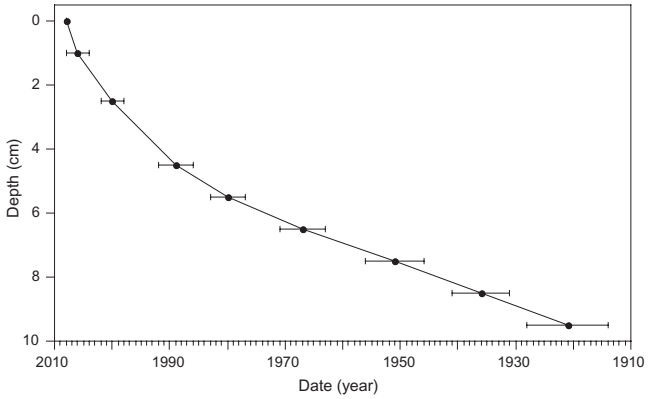

Fig. S2. Results of the regression line plot, showing depth of analyzed sediment layers from the sediment core MF08/II and the corresponding age of these layers. Bars indicate error age.

Table S1. Summary of observed heterozygotes (H_O) and expected heterozygotes (H_E) for each group of strains established from resting stages germinated from discrete sediment layers of the sediment core collected from the Mariager Fjord (samples 1–7) and the two open-sea stations (Anholt and Vinga) at each locus

Sample (N)	S.mar1	S.mar2	S.mar3	S.mar4	S.mar5	S.mar6	S.mar7	S.mar8
Sample 1 (11*)								
N_A	5	8	2	4	10	8	5	8
H_E	0.67	0.87	0.10	0.40	0.90	0.85	0.76	0.90
H_O	0.27†	1.00	0.10	0.36	0.56†	0.50†	0.30†	0.25†
a	0.22	0	0	0.01	0.16	0.16	0.24	0.32
Sample 2 (10*)								
N_A	4	7	1	3	8	8	4	7
H_E	0.66	0.79	0.00	0.42	0.90	0.88	0.68	0.84
H_O	0.30†	0.89	0.00	0.30	0.50†	0.63	0.33†	0.22†
a	0.20	0	0	0.06	0.18	0.09	0.17	0.31
Sample 3 (34)								
N_A	7	10	3	8	18	17	8	15
H_E	0.61	0.89	0.09	0.59	0.94	0.91	0.48	0.87
H_O	0.28†	0.81	0.03†	0.61	0.28†	0.70†	0.29†	0.48†
a	0.20	0.02	0.05	0	0.33	0.09	0.12	0.20
Sample 4 (29)								
N_A	7	9	2	5	17	11	6	11
H_E	0.66	0.87	0.18	0.35	0.87	0.80	0.42	0.90
H_O	0.35†	0.84	0.12	0.28	0.24†	0.76	0.19†	0.15†
a	0.18	0	0.05	0.05	0.32	0.01	0.15	0.38
Sample 5 (23)								
N_A	4	11	3	6	12	14	10	11
H_E	0.55	0.83	0.24	0.55	0.91	0.90	0.78	0.89
H_O	0.17†	0.83	0.17	0.39	0.25†	0.54†	0.33†	0.50†
a	0.23	0	0.04	0.09	0.33	0.17	0.24	0.19
Sample 6 (26)								
N_A	7	10	4	6	12	14	8	11
H_E	0.67	0.87	0.15	0.51	0.89	0.84	0.78	0.89
H_O	0.24†	0.75	0.08	0.44	0.33†	0.64†	0.40†	0.50†
a	0.25	0.05	0.06	0.04	0.28	0.10	0.20	0.19
Sample 7 (25)								
N_A	5	12	2	6	17	13	7	9
H_E	0.66	0.92	0.22	0.54	0.89	0.88	0.69	0.82
H_O	0.25†	0.88	0.17	0.52	0.38†	1.00	0.10†	0.39†
a	0.21	0	0.04	0	0.26	0	0.34	0.22
Anholt (42)								
N_A	16	9	2	5	19	18	4	11
H_E	0.91	0.81	0.27	0.62	0.94	0.92	0.70	0.78
H_O	0.38†	0.78	0.05†	0.51	0.50†	0.63†	0.35†	0.26†
a	0.27	0	0.16	0.06	0.22	0.14	0.20	0.28
Vinga (45)								
N_A	15	9	3	7	21	19	4	12
H_E	0.89	0.87	0.29	0.59	0.95	0.92	0.61	0.86
H_O	0.2†	0.85	0.07†	0.57	0.31†	0.90	0.28†	0.24†
a	0.36	0	0.17	0	0.32	0	0.19	0.32

a, null allele frequency calculated using the method from Brookfield (1); H_E, expected heterozygotes; H_O, observed heterozygosity; N_A, number of alleles per locus.

*Low sample size.

†Significant homozygote excess ($P < 0.05$) after Bonferroni corrections.

1. Brookfield JFY (1996) A simple new method for estimating null allele frequency from heterozygote deficiency. *Mol Ecol* 5:453–455.