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	f from resting stages germinated from discrete sediment layers of the sediment core collected from
the Mariac	ger Fjord (samples 1–7) and the two open-sea stations (Anholt and Vinga) at each locus

$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Sample (N)	S.mar1	S.mar2	S.mar3	S.mar4	S.mar5	S.mar6	S.mar7	S.mar8
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	Sample 1 (11*))							
$\begin{array}{c c c c c c c c c c c c c c c c c c c $	N _A	5	8	2	4	10	8	5	8
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	HE	0.67	0.87	0.10	0.40	0.90	0.85	0.76	0.90
a 0.22 0 0 0.01 0.16 0.16 0.24 0.32 Sample 2 (10*) NA 4 7 1 3 8 8 4 7 He 0.66 0.79 0.00 0.42 0.90 0.88 0.68 0.84 0.42 a 0.20 0 0 0.66 0.18 0.09 0.31 0.31 Sample 3 (34) 8 18 17 8 15 MA 7 10 3 8 18 17 8 0.87 a 0.20 0.02 0.05 0 0.33 0.09 0.12 0.20 Sample 4 (29) 5 17 1 6 11 MA 7 9 2 5 17 10 0.15 0.38 Sample 5 (23) 0.84 0.12 0.28 0.24' 0.76 0.19'	Ho	0.27 [†]	1.00	0.10	0.36	0.56 [†]	0.50 ⁺	0.30 [†]	0.25 ⁺
$\begin{array}{l c c c c c c c c c c c c c c c c c c c$	a	0.22	0	0	0.01	0.16	0.16	0.24	0.32
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Sample 2 (10*))							
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	NA	4	7	1	3	8	8	4	7
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	HE	0.66	0.79	0.00	0.42	0.90	0.88	0.68	0.84
a 0.20 0 0 0.06 0.18 0.09 0.17 0.31 Sample 3 (34) <t< td=""><td>Ho</td><td>0.30[†]</td><td>0.89</td><td>0.00</td><td>0.30</td><td>0.50[†]</td><td>0.63</td><td>0.33[†]</td><td>0.22⁺</td></t<>	Ho	0.30 [†]	0.89	0.00	0.30	0.50 [†]	0.63	0.33 [†]	0.22 ⁺
$\begin{array}{l c c c c c c c c c c c c c c c c c c c$	a	0.20	0	0	0.06	0.18	0.09	0.17	0.31
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Sample 3 (34)								
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	N _A	7	10	3	8	18	17	8	15
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	H _E	0.61	0.89	0.09	0.59	0.94	0.91	0.48	0.87
a 0.20 0.02 0.05 0 0.33 0.09 0.12 0.20 Sample 4 (29)	Ho	0.28 [†]	0.81	0.03 [†]	0.61	0.28 [†]	0.70 ⁺	0.29 [†]	0.48 [†]
$\begin{array}{l c c c c c c c c c c c c c c c c c c c$	a	0.20	0.02	0.05	0	0.33	0.09	0.12	0.20
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Sample 4 (29)								
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	NA	7	9	2	5	17	11	6	11
$H_0^ 0.35^+$ 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) V V V V V V V M_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^+ Sample 6 (26) V V V V V 0.64^+ 0.40^+ 0.50^+ A 0.24^+ $0.75^ 0.08$ 0.44 0.33^+ 0.64^+ 0.40^+ 0.50^+ A $0.5^ 0.87^ 0.50^+$ $0.88^ 0.68^ 0.88^ 0.68^$	H⊧	0.66	0.87	0.18	0.35	0.87	0.80	0.42	0.90
a 0.18 0 0.05 0.05 0.32 0.01 0.15 0.38 Sample 5 (23) NA 4 11 3 6 12 14 10 11 He 0.55 0.83 0.24 0.55 0.91 0.90 0.78 0.89 Ho 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) NA 6 12 14 8 11 He 0.67 0.87 0.15 0.51 0.89 0.84 0.78 0.89 Ho 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) NA 12 2 6	Ho	0.35 ⁺	0.84	0.12	0.28	0.24 [†]	0.76	0.19 [†]	0.15 ⁺
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	a	0.18	0	0.05	0.05	0.32	0.01	0.15	0.38
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Sample 5 (23)								
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	NA	4	11	3	6	12	14	10	11
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	H₌	0.55	0.83	0.24	0.55	0.91	0.90	0.78	0.89
a0.2300.040.090.330.170.240.19Sample 6 (26) N_A 710461214811HE0.670.870.150.510.890.840.780.89HO0.24 ⁺ 0.750.080.440.33 ⁺ 0.64 ⁺ 0.40 ⁺ 0.50 ⁺ a0.250.050.060.040.280.100.200.19Sample 7 (25)NA51226171379ME0.6660.920.220.540.890.880.690.82HO0.25 ⁺ 0.880.170.520.38 ⁺ 1.000.10 ⁺ 0.39 ⁺ a0.2100.0400.2600.340.22Aholt (42)NA169251918411HE0.910.810.270.620.940.920.700.78HO0.38 ⁺ 0.780.05 ⁺ 0.510.50 ⁺ 0.63 ⁺ 0.35 ⁺ 0.26 ⁺ NA159372119412HE0.890.870.290.590.920.610.88HO0.2700.160.060.220.140.200.28Vinga (45) N_A 159372119412HE0.890.870.29 </td <td>Ho</td> <td>0.17[†]</td> <td>0.83</td> <td>0.17</td> <td>0.39</td> <td>0.25[†]</td> <td>0.54[†]</td> <td>0.33[†]</td> <td>0.50^{+}</td>	Ho	0.17 [†]	0.83	0.17	0.39	0.25 [†]	0.54 [†]	0.33 [†]	0.50^{+}
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	a	0.23	0	0.04	0.09	0.33	0.17	0.24	0.19
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	Sample 6 (26)								
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	N _A	7	10	4	6	12	14	8	11
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	H_	0.67	0.87	0.15	0.51	0.89	0.84	0.78	0.89
a0.250.050.060.040.280.100.200.19Sample 7 (25) N_A 51226171379H_E0.660.920.220.540.890.880.690.82H_O0.25 ⁺ 0.880.170.520.38 ⁺ 1.000.10 ⁺ 0.39 ⁺ a0.2100.0400.2600.340.22Anholt (42)NA169251918411H_E0.910.810.270.620.940.920.700.78H_O0.38 [±] 0.780.05 [±] 0.510.50 [±] 0.63 [±] 0.35 [±] 0.26 [±] Vinga (45)N_A159372119412M_E0.890.870.290.590.950.920.610.86H_O0.2 [±] 0.850.07 ⁺ 0.570.31 ⁺ 0.900.28 [±] 0.24 [±] A0.3600.1700.3200.190.32	Ho	0.24 [†]	0.75	0.08	0.44	0.33 ⁺	0.64 [†]	0.40 [†]	0.50 [†]
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	a	0.25	0.05	0.06	0.04	0.28	0.10	0.20	0.19
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Sample 7 (25)								
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	N _A	5	12	2	6	17	13	7	9
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	H _F	0.66	0.92	0.22	0.54	0.89	0.88	0.69	0.82
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	Ho	0.25 [†]	0.88	0.17	0.52	0.38 [†]	1.00	0.10 [†]	0.39 [†]
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	a	0.21	0	0.04	0	0.26	0	0.34	0.22
$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	Anholt (42)								
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	N₄	16	9	2	5	19	18	4	11
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	H _F	0.91	0.81	0.27	0.62	0.94	0.92	0.70	0.78
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	Ho	0.38 [†]	0.78	0.05 ⁺	0.51	0.50 ⁺	0.63 [†]	0.35 [†]	0.26 ⁺
Vinga (45) N_A 159372119412 H_E 0.890.870.290.590.950.920.610.86 H_O 0.2 [†] 0.850.07 [†] 0.570.31 [†] 0.900.28 [†] 0.24 [†] a0.3600.1700.3200.190.32	a	0.27	0	0.16	0.06	0.22	0.14	0.20	0.28
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	Vinga (45)								
$ \begin{array}{cccccccccccccccccccccccccccccccccccc$	N _A	15	9	3	7	21	19	4	12
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	H₌	0.89	0.87	0.29	0.59	0.95	0.92	0.61	0.86
a 0.36 0 0.17 0 0.32 0 0.19 0.32	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.

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⁺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.