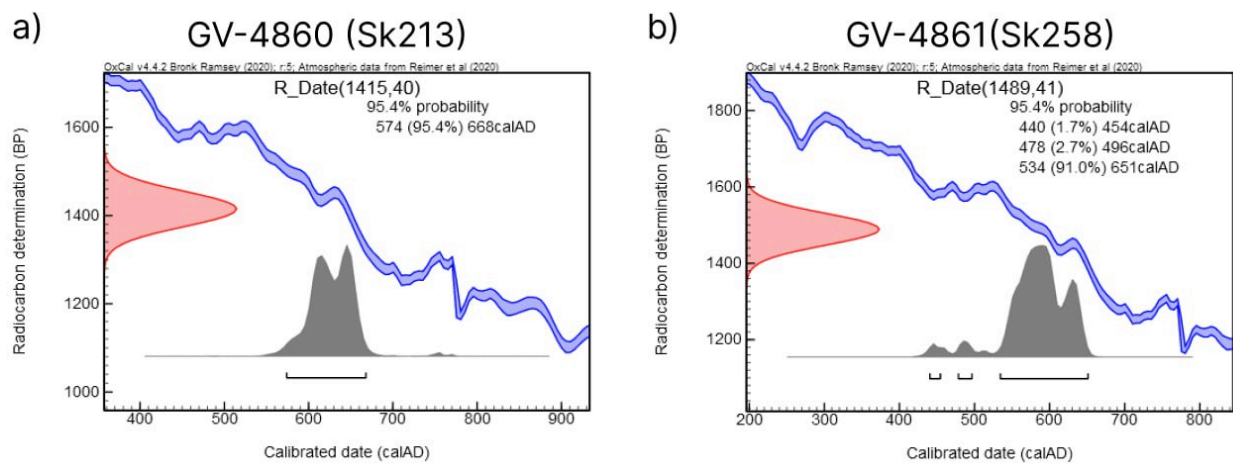


An ancient *Erysipelothrix rhusiopathiae* genome recovered from 1400-year-old human remains in the Northern Caucasus

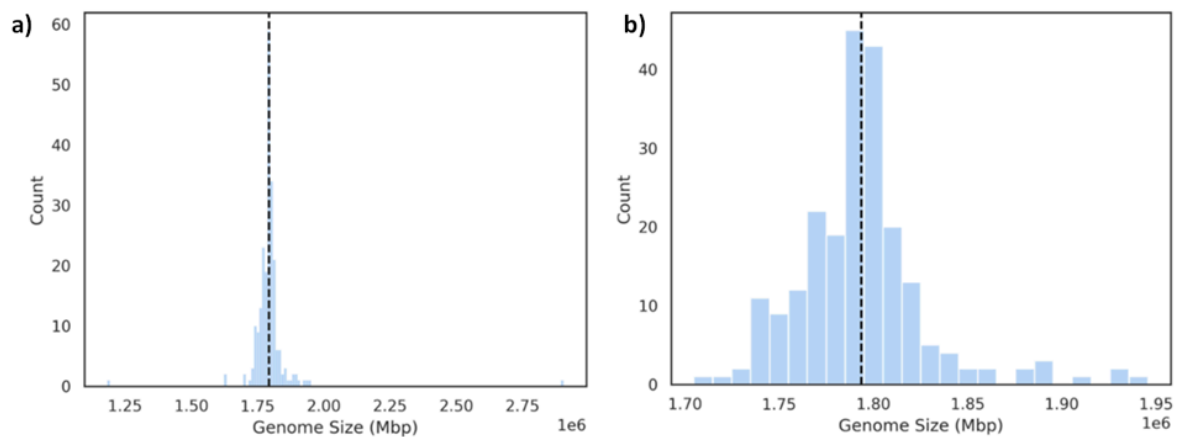
SUPPLEMENTARY FIGURES

Supplementary Figure 1. Calibration of the radiocarbon age to calendar years was based on the IntCal20 calibration curve using the OxCal 4.4 software for sample GV-4860 (a) and GV-4861 (b).



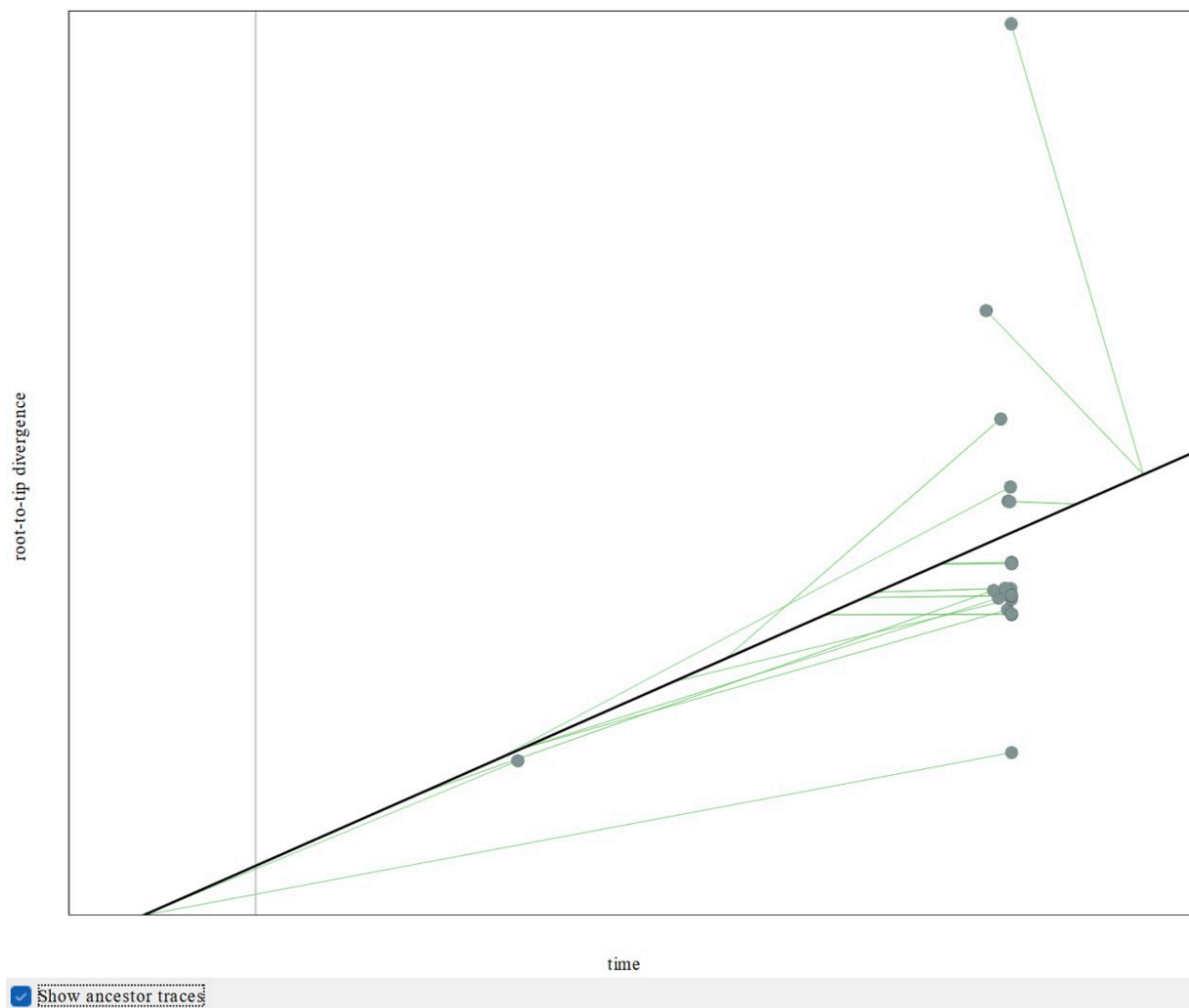
a) Calibration of the radiocarbon age for sample GV-4860 (Sk213). **b)** Calibration of the radiocarbon age for sample GV-4861 (Sk258).

Supplementary Figure 2. The distribution of the lengths of *E. rhusiopathiae* genomes presented in the NCBI assembly database (as of 05/24/2024).



a) All 225 genomes. **b)** After removing the drop-down points (ASM990626v1, ASM990626v1, ASM2907209v1, ASM2907209v1, ASM2907304v1, ASM2907304v1, Rumen uncultured genome RUG11795, Rumen uncultured genome RUG14284, Rumen uncultured genome RUG14284). The X-axis indicates the number of nucleotides in the genome. The Y-axis indicates the number of genomes. The median value of the genome lengths is 1,793,558 bps. The average value of the genome lengths is 1,791,746.6bp.

Supplementary Figure 3. Plot of the root-to-tip linear regression for ancient ERA_01 and 18 modern genomes phylogenetically closest to him.



The X-axis indicates the collection date. The Y-axis - distance (“Root-to Tip” divergence) between heterochronous genomes. Regression lines are shown gray. Ancestor traces in part B are shown green. Gray dots represent each genome. The regression line has a positive slope,

but some genomes lie to the significantly distant part from the regression line. Thus, we don't observe temporal signal here either.

Supplementary Figure 4. Amino acid and nucleotide substitutions in the ancient *spaA* gene compared to genes from strains Fujisawa (SpaA groupe 2), GCF_900637845.1 (SpaA groupe 1) and closest moderne ERR3933026. Discriminative positions according to the Forde scheme are shown on the left and additional SNPs observed are shown on the right.

AA pos	55	70	178	195	303	238	287	AA pos
Fujisawa	V	K	G	D	G	L	N	Fujisawa
GCF_900637845.1	I	N	D	N	E	L	N	GCF_900637845.1
ERR3933026	I	N	D	N	E	L	N	ERR3933026
ERA01	I	N	D	N	E	L	N	ERA01

N pos	163	164	165	208	209	210	532	533	534	583	584	585	907	908	909	712	713	714	859	860	861	N pos
Fujisawa	G	T	A	A	A	T	G	G	T	G	A	T	G	G	G	C	T	A	A	A	C	Fujisawa
GCF_900637845.1	A	T	A	A	A	A	G	A	T	A	A	T	G	A	G	C	T	A	A	A	T	GCF_900637845.1
ERR3933026	A	T	A	A	A	A	G	A	T	A	A	T	G	A	G	C	T	A	A	A	C	ERR3933026
ERA01	A	T	A	A	A	A	G	A	T	A	A	T	G	A	G	T	T	A	A	A	C	ERA01

The ancient genome ERA_01 has 5 discriminative SNP's typical for the SpaA group 1. Additionally, we observe in the ancient genome two unique synonymical SNP's (relative to typical *spaA* groupe 1 sequence from genome GCF_900637845.1) in position 712 and 861.