

Fig. S1. Pairwise core-genome SNP differences between South Tunisian *S. sonnei* sequences after removing recombination sites.

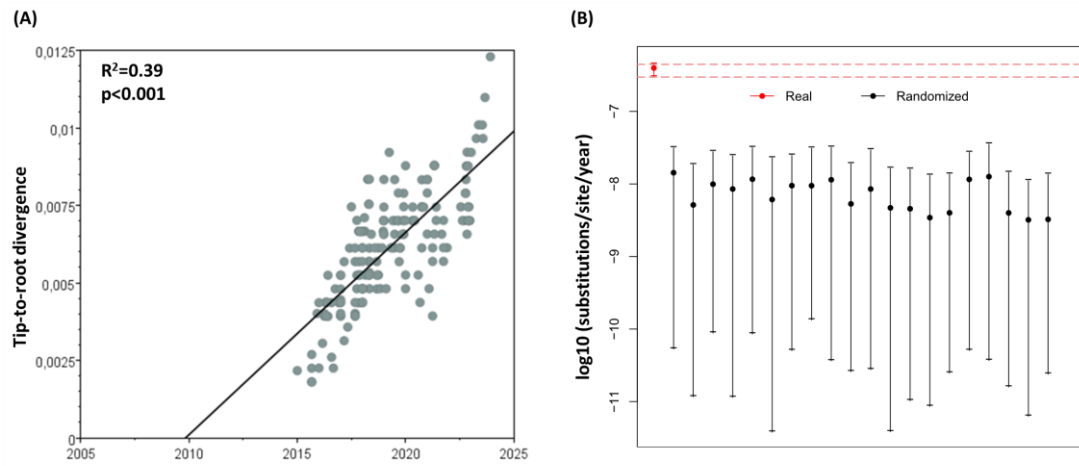


Fig. S2. Temporal signal assessment preceding phylodynamic analysis of South Tunisian *Shigella sonnei* belonging to the HC10-20663 genotype.

To strengthen the temporal signal, 147 additional international sequences from strains isolated before 2022 were incorporated.

A: Tip-to-root regression analysis generated using TempEst. Pearson correlation p -value and R^2 displayed in the plot.

B: Date-randomization test conducted with the PlotDRT function in the TipDatingBeast R package.

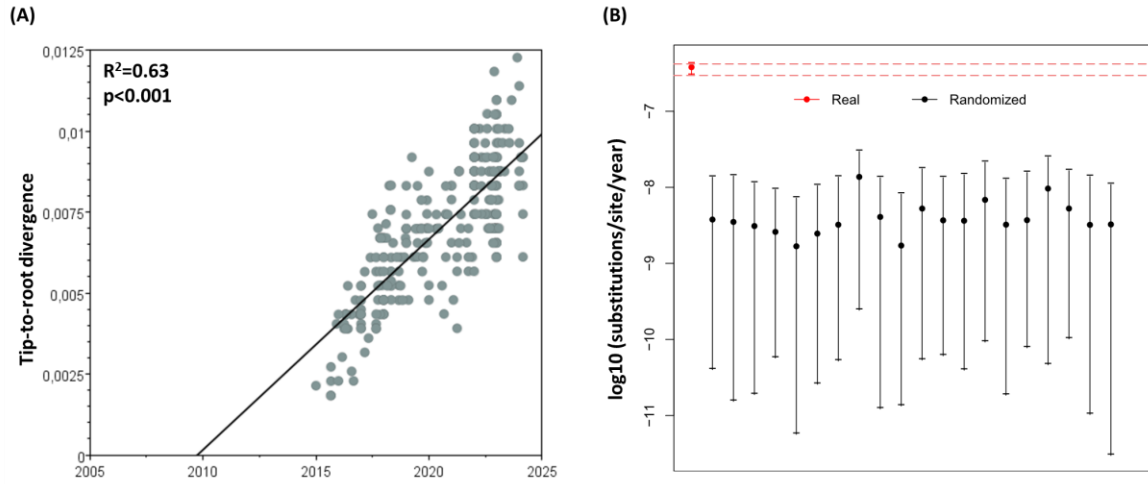


Fig. S3. Temporal signal assessment preceding phylodynamic and phylogeographic analyses of the HC10-20663 genotype internationally.

A: Tip-to-root regression analysis generated using TempEst. Pearson correlation p -value and R^2 displayed in the plot.

B: Date-randomization test conducted with the PlotDRT function in the TipDatingBeast R package.

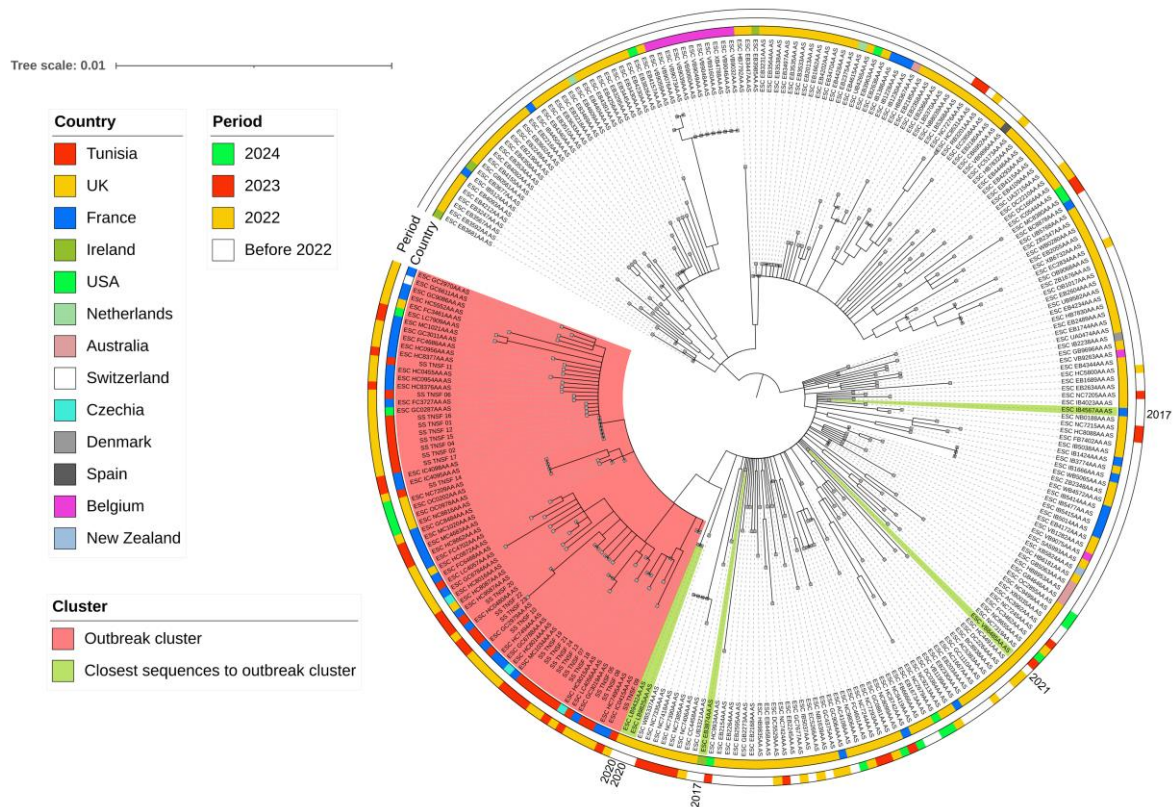


Fig. S4. Maximum likelihood phylogenetic tree of international HC10-20662 sequences

The outbreak cluster is highlighted in red. The sequences with the highest genetic relatedness to the outbreak cluster are highlighted in green.