



# Article

**Extended Data Fig. 10 | Comparison of *M. smithii* divergence dates from BEAST2 analysis compared with raw genetic distance calculations.** Related to Fig. 3, see Supplementary Information section 8. **a**, The different *M. smithii* groups and genetic distances calculated are shown. **b**, Pairwise sequence divergences between M1 and M2 strains ( $n = 96$ ), A and M1 strains ( $n = 48$ ) and A and M2 strains ( $n = 8$ ). Data are presented as box plots (middle line, median; lower hinge, first quartile; upper hinge, third quartile; upper whisker extends from the hinge to the largest value no further than  $1.5 \times$  the interquartile range from the hinge; lower whisker extends from the hinge to the smallest value at most  $1.5 \times$  the interquartile range from the hinge; data beyond the end of the whiskers are individually plotted outlying points). **c, d**, Comparison of the distribution of systematic differences between M1 and M2 and A and M2 divergences (**c**) and BEAST2 estimates (**d**). **c**, Systematic differences based on pairwise sequence divergences (measured by the single-nucleotide variant

rate) between M1 and M2 and A and M2 strains. **d**, Products of the clock rates (substitutions per site per year) inferred using BEAST2<sup>93</sup> (Supplementary Table 7) and the inferred age of the common ancestor of the ancient strains. **e, f**, Comparison of distribution of pairwise time-resolved systematic differences based on raw sequences divergence (**e**) and the distribution of existing inferred clock rates (**f**). **e**, Time-resolved systematic differences calculated by dividing systematic differences (**c**) with the average <sup>14</sup>C date of the palaeofaeces used in molecular clocking analysis. **f**, Clock rates inferred by BEAST2 analysis (Supplementary Table 7). **g**, Raw-sequence-based divergence dates between A and M1 strains, recalibrated using time-resolved systematic differences. **h**, Distribution of raw-sequence-based divergence dates when low-frequency outliers are excluded. **i**, Distribution of estimated divergence dates between A and M1 strains based on BEAST2 analysis.