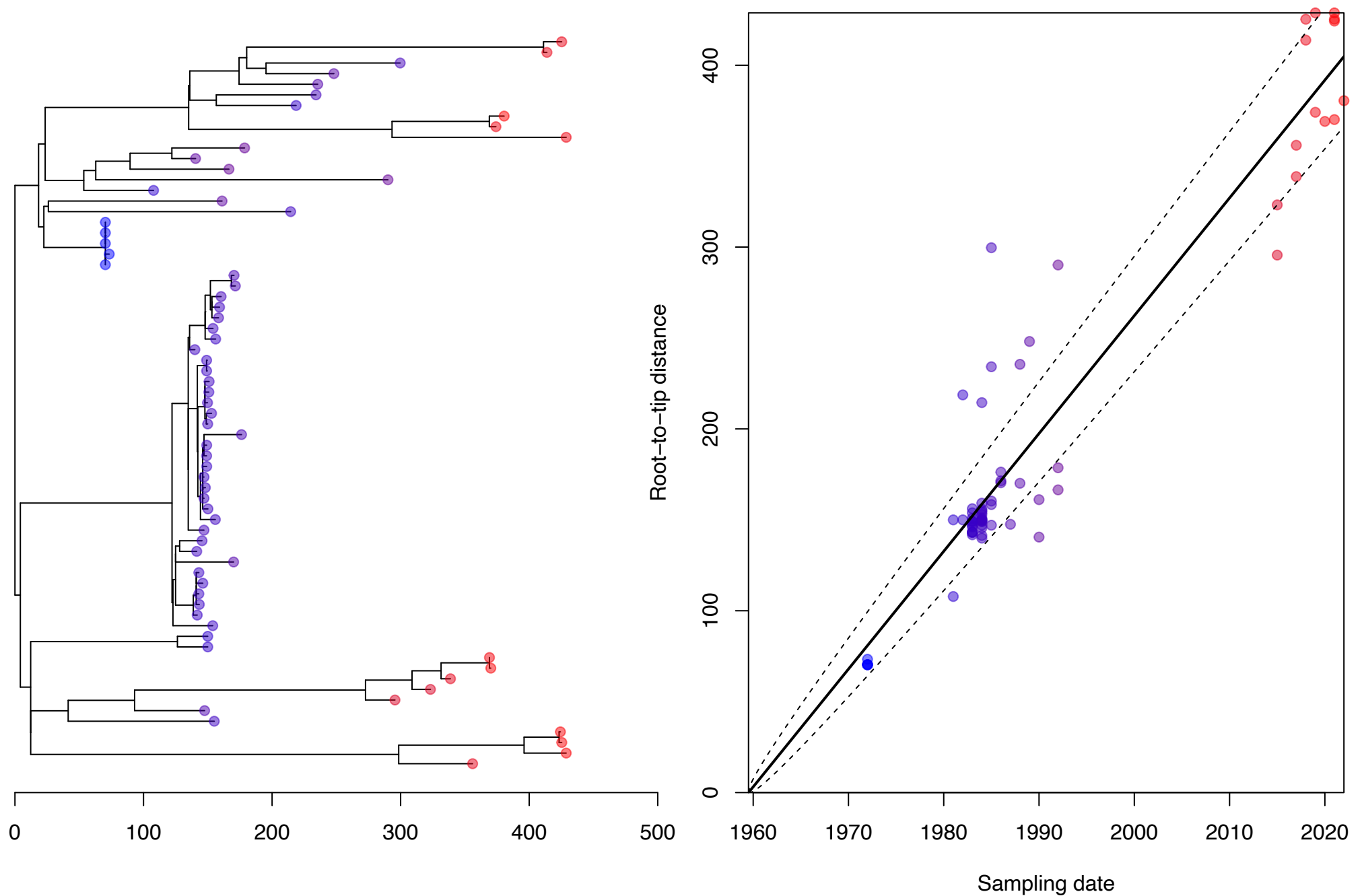


Rate=6.48e+00,MRCA=1959.52,R2=0.90,p<1.00e-04



Maximum likelihood whole genome SNP tree of ST239, ST7844, ST368 and ST241 MRSA (n = 69) adjusted with Bayesian dating of nodes on the left. Root-to-tip distances mapped to sampling date with linear regression shown on the right.