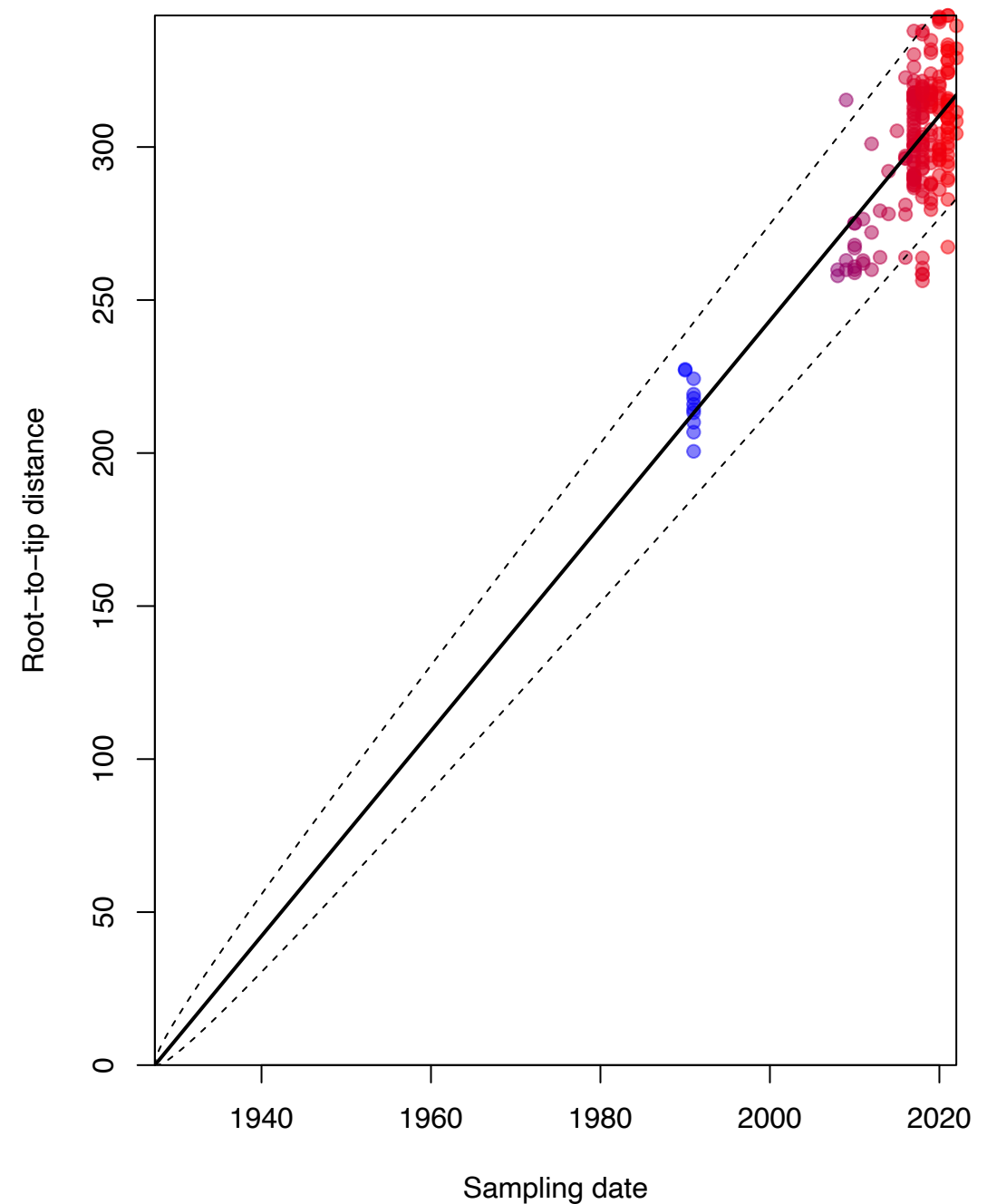
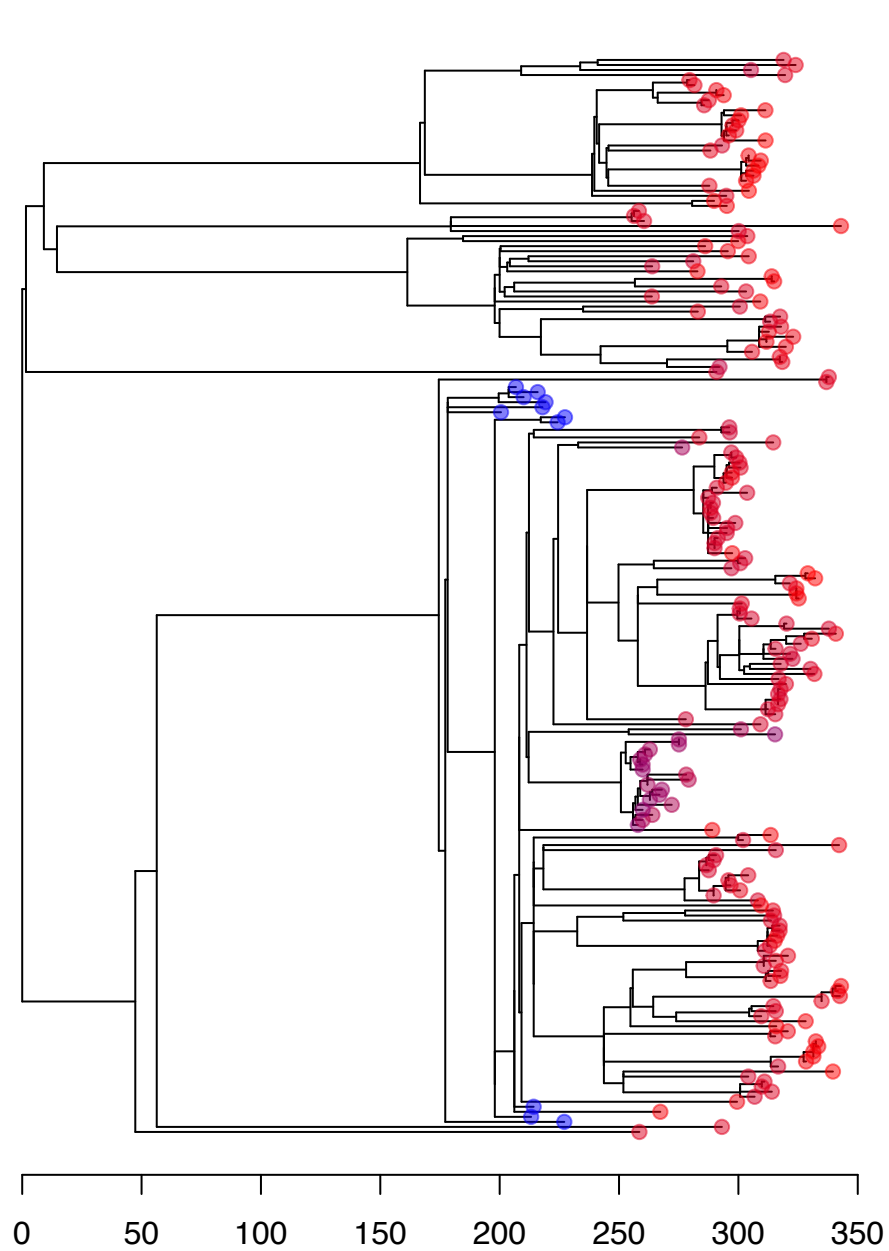


Rate=3.35e+00,MRCA=1927.41,R2=0.64,p<1.00e-02



Maximum likelihood whole genome SNP tree of ST247 and ST22 MRSA (n = 214) adjusted with Bayesian dating of nodes on the left. Root-to-tip distances mapped to sampling date with linear regression shown on the right.