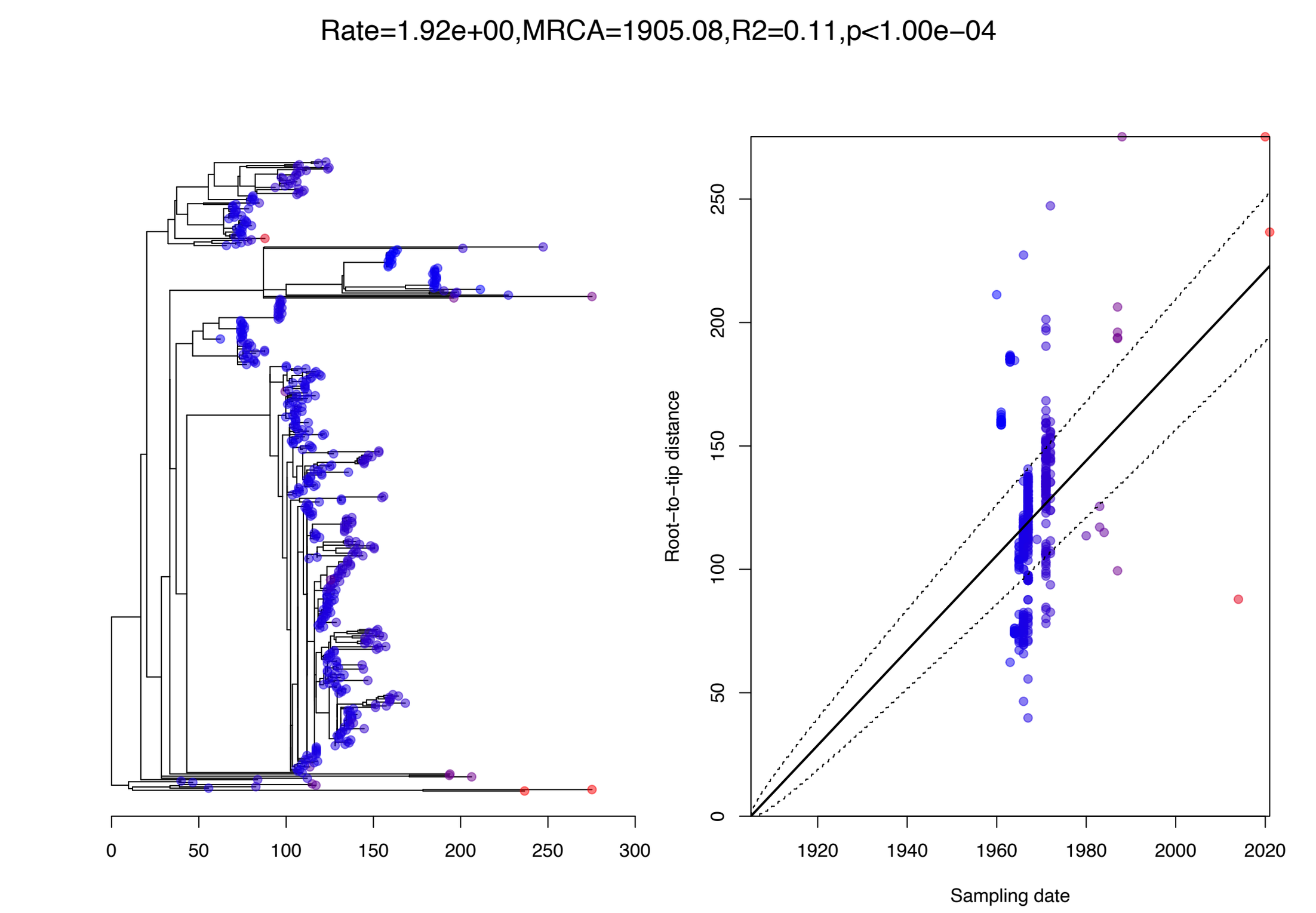

Maximum likelihood whole genome SNP tree of ST247 and ST250 MRSA (n = 445) adjusted with Bayesian dating of nodes on the left. Root-to-tip distances mapped to sampling date with linear regression shown on the right.