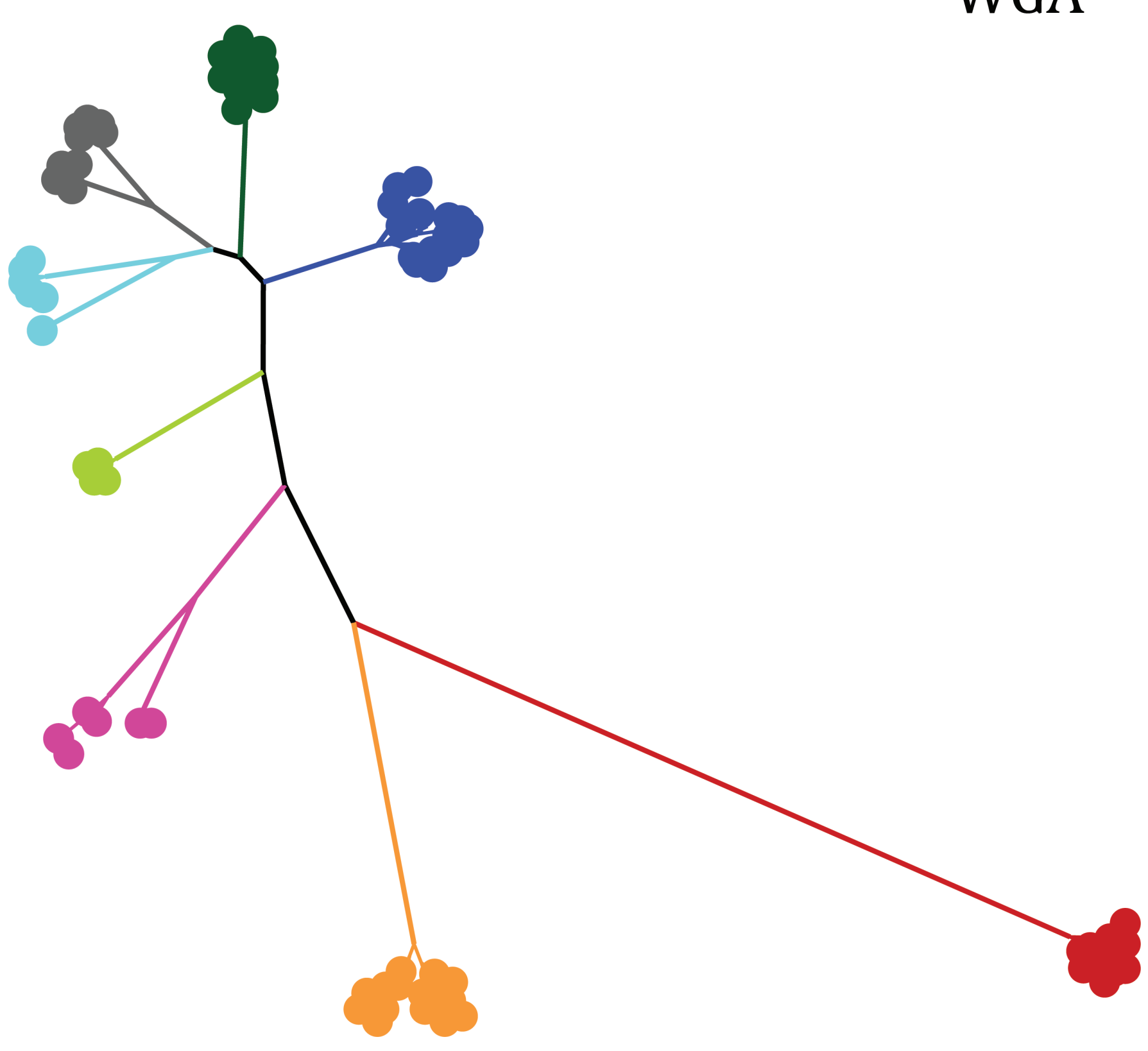
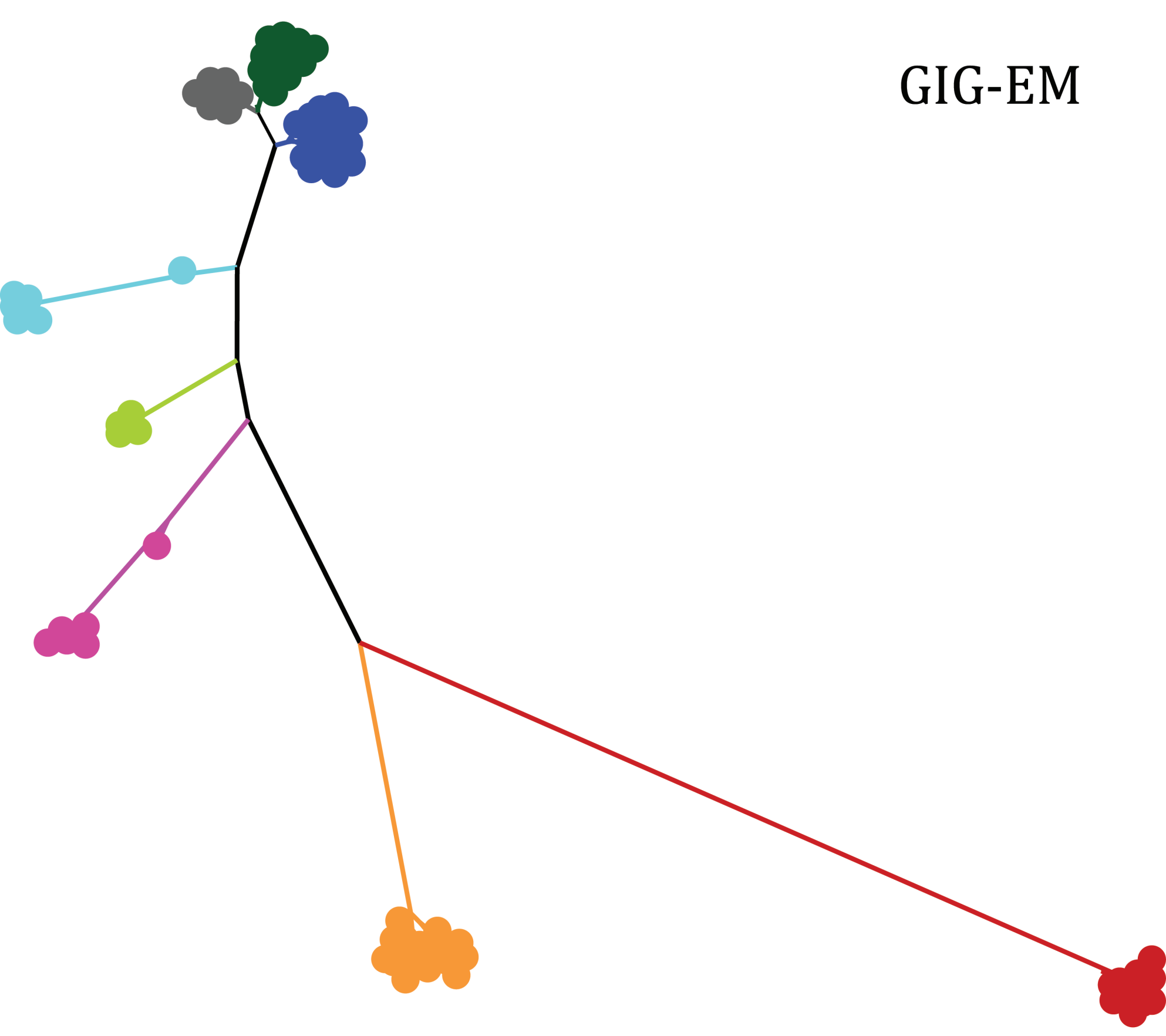


Comparison of WGA, pubMLST and GIG-EM phylogenies using the DECA genomes as a test genome collection. Phylogenetic trees inferred from 78 genomes in the DECA collection. Trees were inferred from concatenated alignments from a whole genome alignment (WGA), the GIG-EM 3-gene system, or the pubMLST 7-gene system. Branches are colored to show clade membership, but are not associated with an established phylotype. Each genome was assigned to a branch based on its location in the WGA phylogeny. Each tree was inferred with a maximum likelihood algorithm in RAxML.

WGA



GIG-EM



pubMLST

