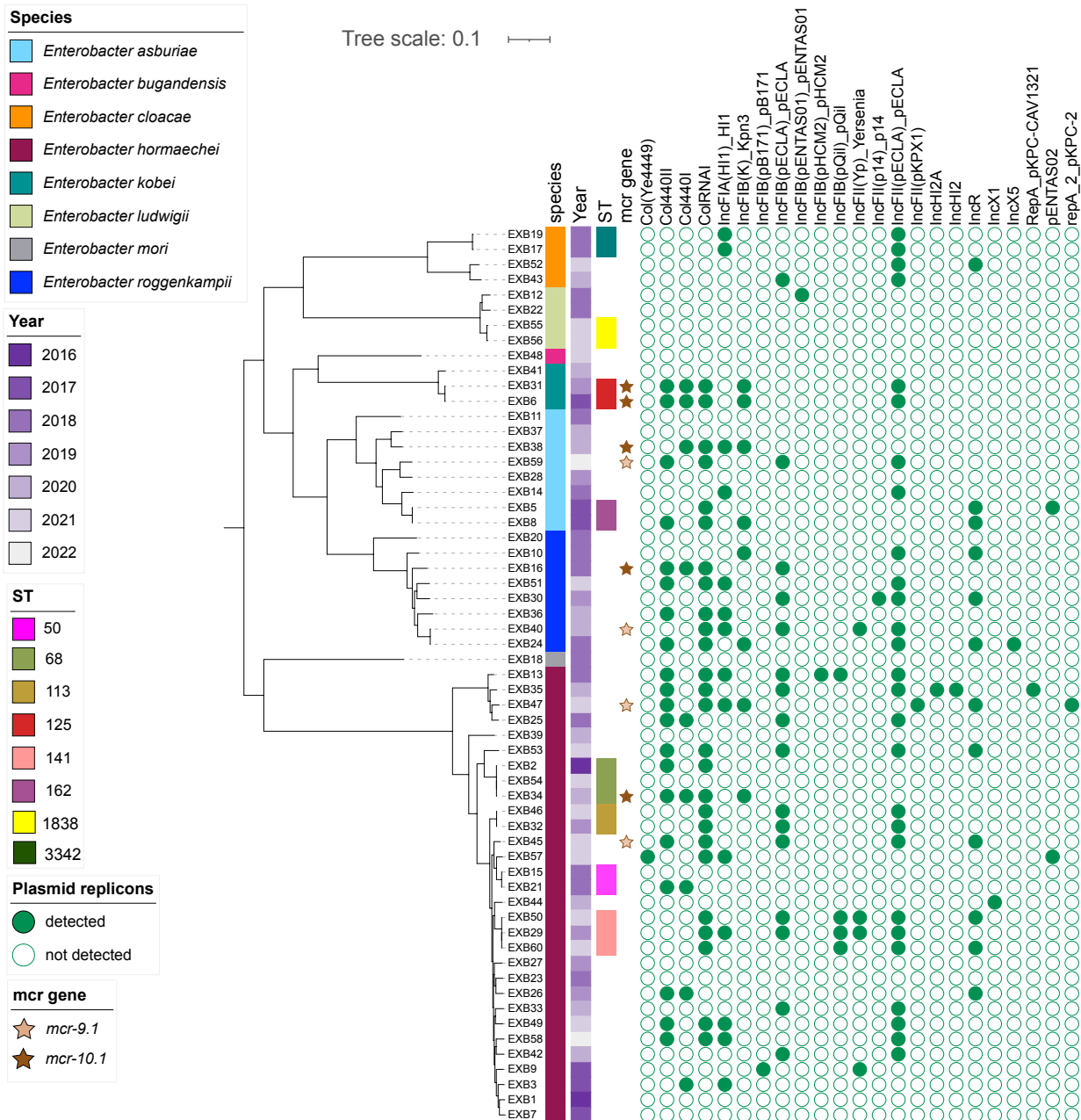


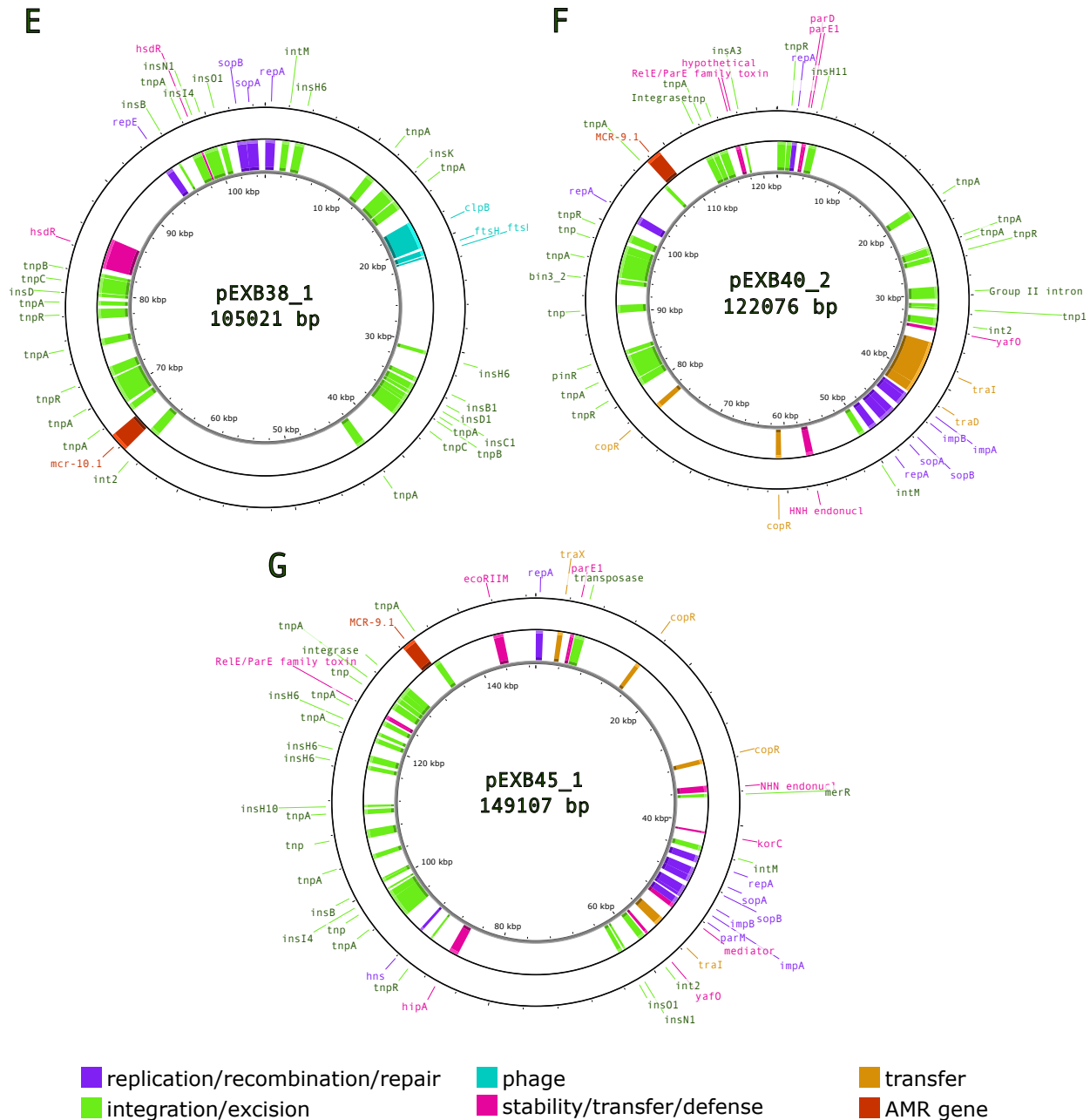
Dissemination dynamics of colistin resistance genes *mcr-9* and *mcr-10* across diverse Inc plasmid backbones

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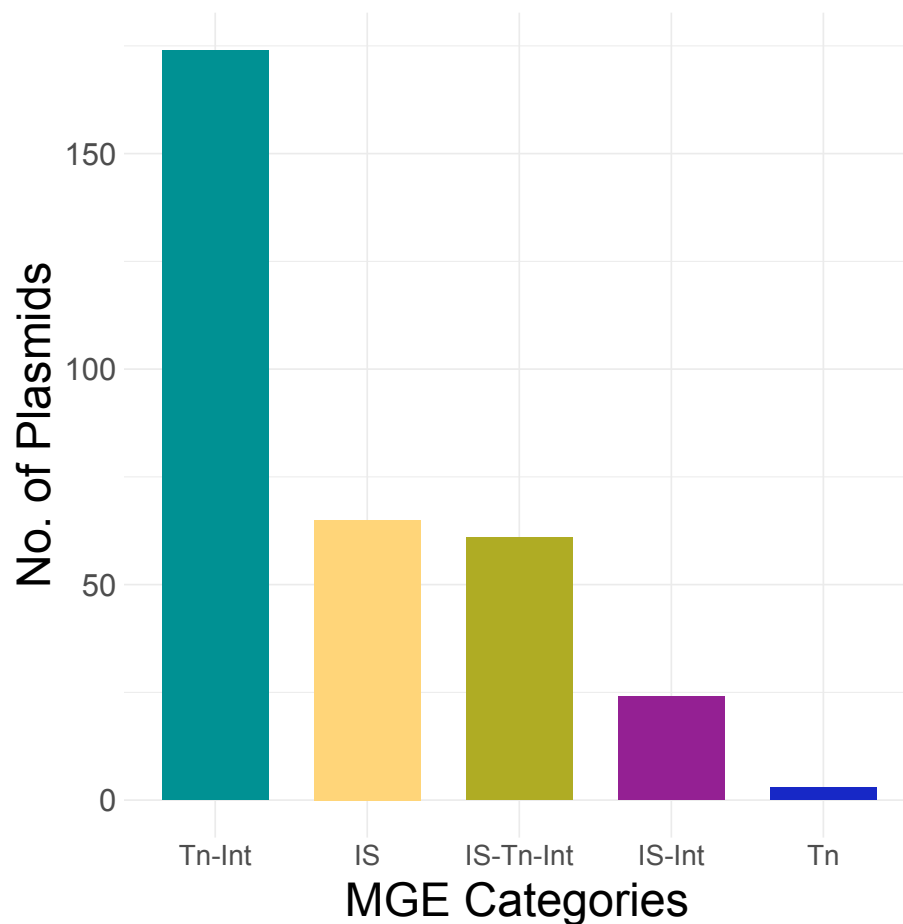
Supplementary figures



Supplementary Figure S1. *Enterobacter* spp. from bloodstream infections in Dartmouth-Hitchcock Medical Center, New Hampshire, USA. (A) A maximum likelihood phylogenetic tree based on 957,227 single nucleotide polymorphisms (SNP) extracted from the 3.18 Mb sequence alignment of 712 core genes. The tree is rooted at the midpoint. Tree scale indicates the number of nucleotide substitutions per site. Colored strips next to the tree show the *Enterobacter* species, year of isolation, sequence type (ST) of two or more representative genomes, and *mcr* gene variants. The distribution of different plasmid replicon types is indicated by the green (present) or white (absent) circles. Details of the genomic features of the 59 *Enterobacter* isolates are presented in Supplementary Data 2.



Supplementary Figure S2. Circular topology of the plasmid genome assemblies bearing *mcr-9.1* or *mcr-10.1* derived from *Enterobacter* genomes from DHMC sequenced in this study. The plasmid maps show the *mcr* gene (labeled in red) and other genes involved in replication/recombination/repair, integration/excision, stability/defense, and phage elements in plasmids (detected in each plasmid). (A) p_EXB6_1 (B) p_EXB16_1 (C) p_EXB31_1 (D) p_EXB34_1, (E) p_EXB38_1 (F) p_EXB40_2 (G) p_EXB45_1. Details of their genomic features are presented in Supplementary Data 4.



Supplementary Figure S3. Presence and types of mobile genetic elements (MGE) in the global plasmid genome assemblies (n = 326). Acronyms: Tn: transposons, Int: integrons, IS: insertion sequences. Some MGE categories are a fusion of different kinds of MGEs, as in the case of Tn-Int, IS-Tn-Int, and IS-Int. Details of the MGE features of the genomes are presented in Supplementary Data 7.