Global phylogenomics of multidrug resistant *Salmonella enterica* serotype Kentucky ST198

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Background

Salmonella enterica serovar Kentucky is a common cause of human salmonellosis

Antimicrobial resistance to multiple drugs, including ciprofloxacin, is emerging worldwide

Objective

Investigate phylogenetic structure and antimicrobial resistance

121 S. Kentucky isolates

Five continents

Humans, animals, food, environment 1937-2013

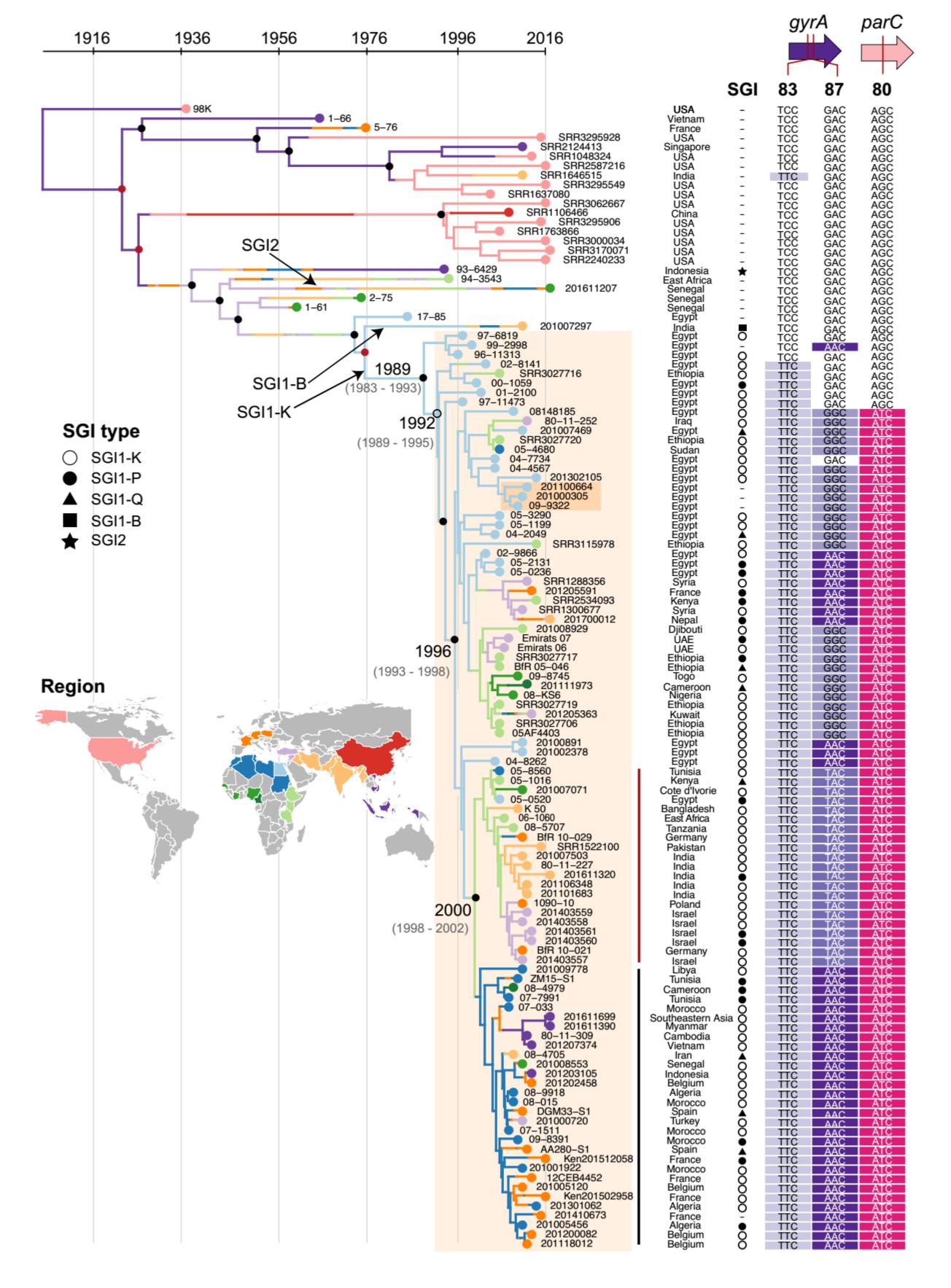


Figure 1. Phylogeographic analysis of *S.* Kentucky ST198 based on whole genome SNV data

Bayesian maximum clade credibility tree inferred using BEAST, with MDR lineage shaded orange. Dark orange box indicates three isolates from the same patient. Major internal nodes are labeled with circles indicating branch support (black, ≥95% posterior support; red, >70% posterior support); divergence date estimates (95% higher posterior density values) are provided for key points in the evolution of the MDR lineage. Leaf nodes are coloured by region of origin (see inset map). Coloured branches indicate inferred geographical distribution of internal branches, inferred using maximum likelihood ancestral trait reconstruction. Data columns indicate country of origin; SGI type (see inset legend); quinolone resistance-related codons, with resistance-associated alleles highlighted. Reference genome 201001922 is marked with red arrow.



Figure 2. Horizontally acquired resistance genes in the *S.* Kentucky ST198 MDR lineage

a, Dated Bayesian (BEAST) phylogeny for the MDR lineage, extracted from the tree shown in **Figure 1**. Leaf nodes are coloured by region of origin (see legend); orange box highlights three isolates recovered from the same patient over three years. **b-e** shows antimicrobial resistance features of each isolate in the tree. **b,** SGI type (see legend, dash indicates no SGI detected). **c,** Antimicrobial resistance phenotypes, indicated as boxes coloured by antimicrobial class (see legend, I in box denotes intermediate resistance). **d,** AMR genes located within the SGI are indicated with boxes coloured by antimicrobial class (* in box indicates gene is interrupted). **e,** plasmid incompatibility group(s) identified in each genome; antimicrobial resistance genes located within these plasmids are printed, coloured by antimicrobial class; genes in brackets are genes whose location was unable to be determined.

Main Findings

Most MDR Salmonella Kentucky circulating globally result from clonal expansion of a single lineage

Emergence of this lineage has been dated around 1989 in Egypt through acquisition of an AMR-associated *Salmonella* genomic island (SGI-1K)

Resistance to fluoroquinolones was acquired early in the clone's evolution through point mutations in *gyrA* and *parC*

AMR genes were acquired 30 years ago and continues to be accumulated through acquisition of various MDR plasmids able to confer resistance to last-line treatments



















