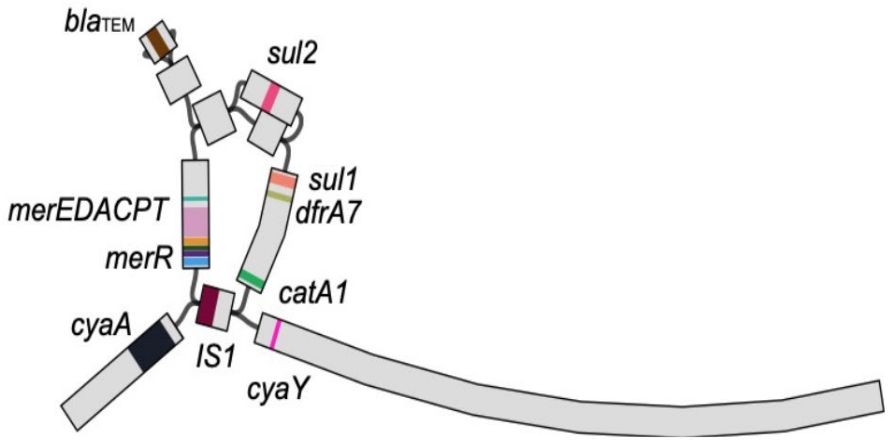
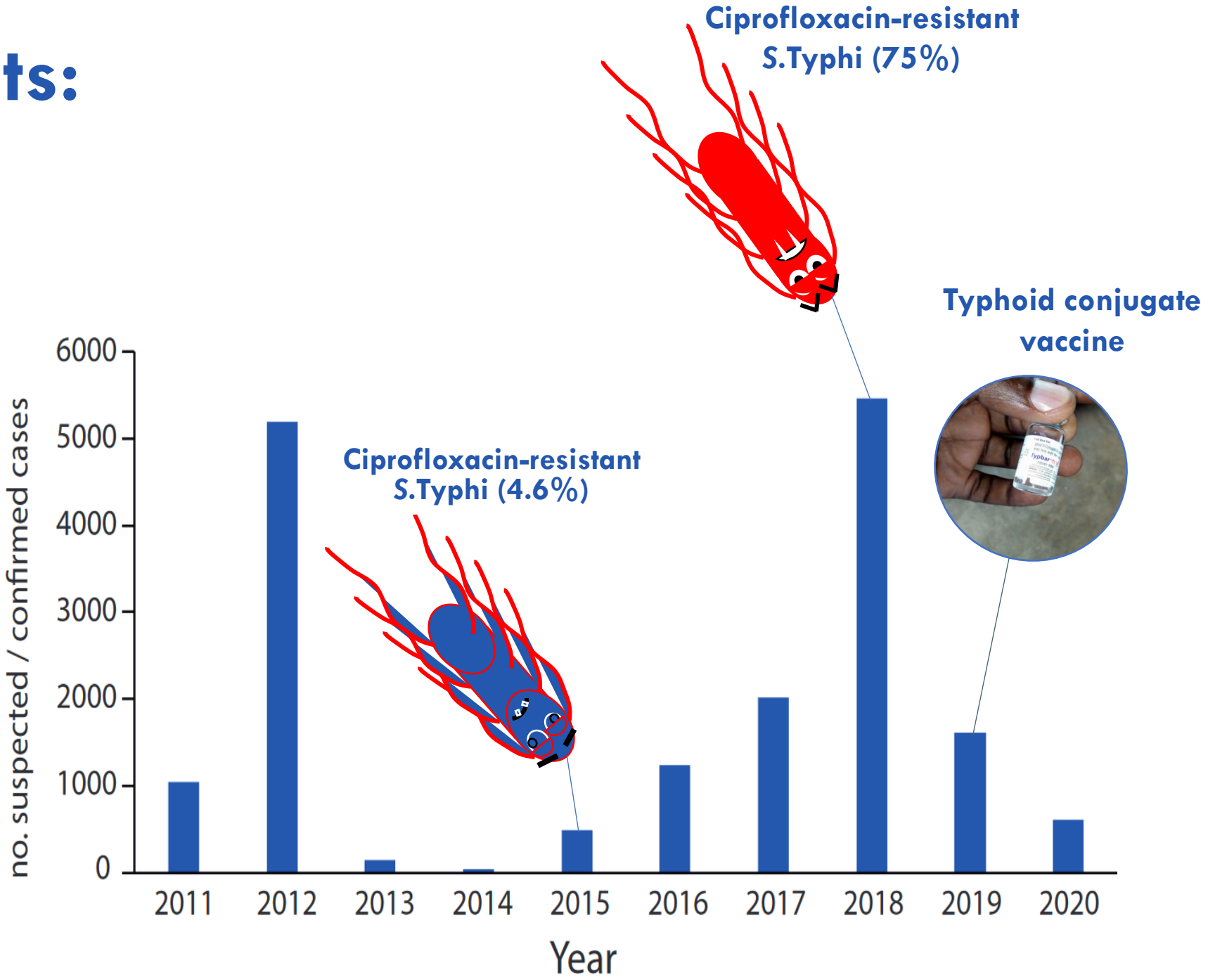


The genetic landscape of *Salmonella enterica* serovar Typhi in Zimbabwe before the introduction of TCV

Tapfumanei Mashe,
Zimbabwe

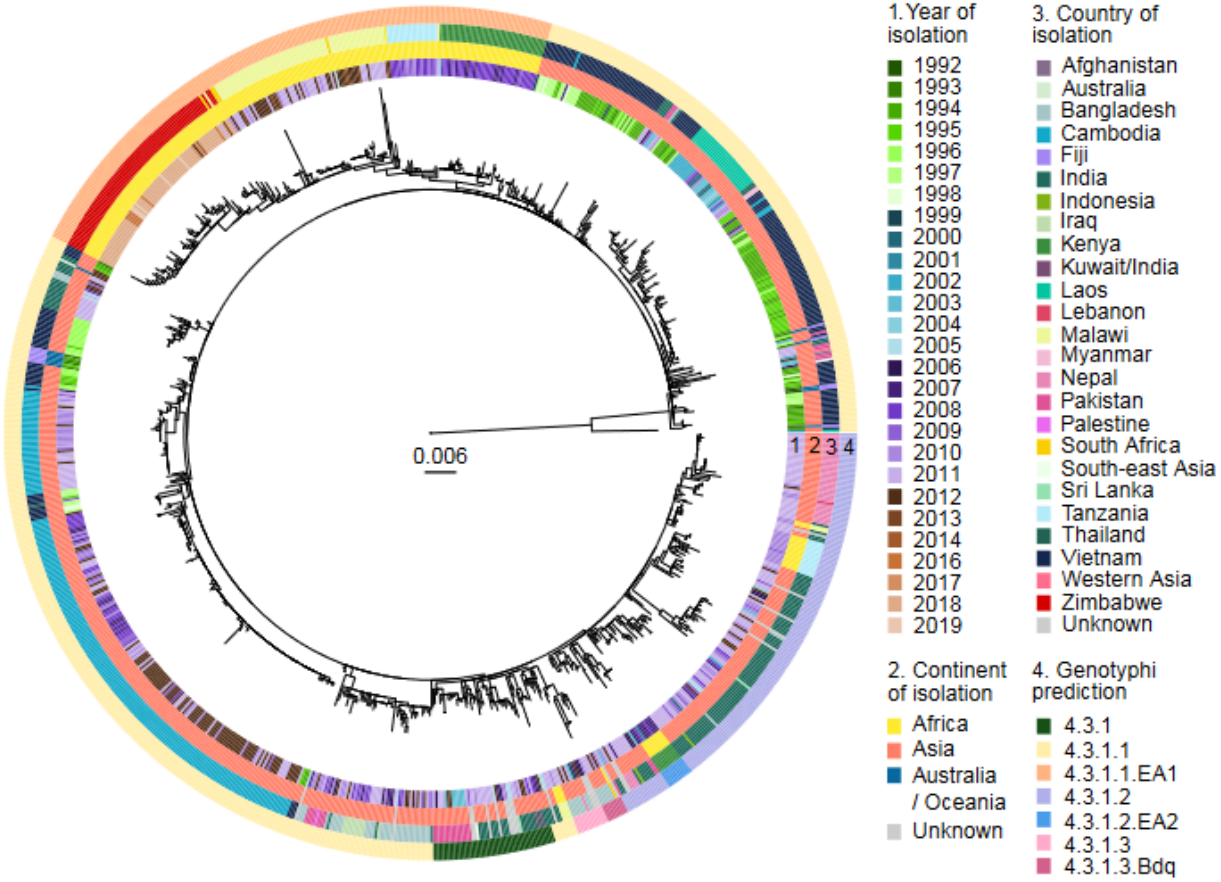
Major Highlights:

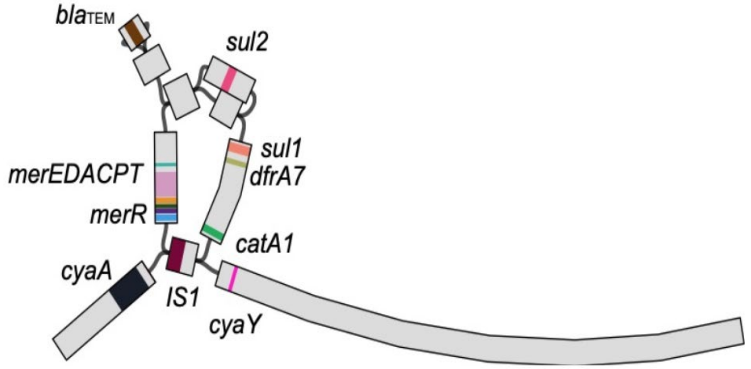


Methods:

We analyzed the population structure, gene flux and sequence polymorphisms in the context of the genome sequence of 1 904 *S.* Typhi strains isolated from 65 countries to reconstruct the evolution of antimicrobial resistance (AMR) and the spread of endemic strains in Zimbabwe

Major Findings:





Multidrug-resistant genotype 4.3.1.1 (H58):

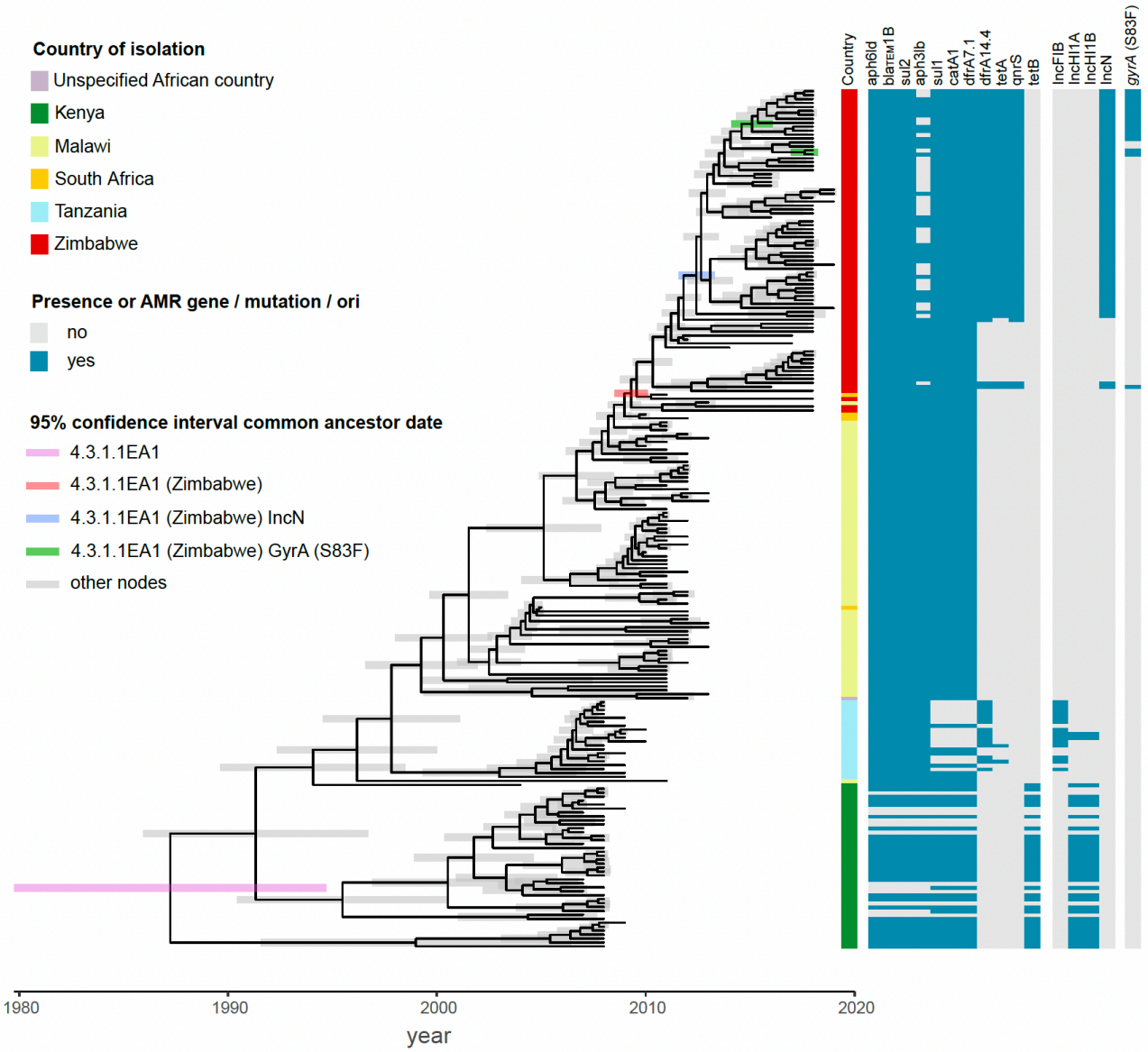
- H58 strains spread to Zimbabwe from neighboring countries around 2009
- IncN plasmid carrying a *qnrS* gene
- Mutation in the quinolone resistance-determining region of the *gyrA* gene

Susceptible *S.* Typhi genotype 3.3.1

Conclusions:

- The most common strain of *S.* Typhi circulating in Zimbabwe is genotype 4.3.1.1EA1
- Fluoroquinolone resistance emerged around 2015 (*qnrS* + *gyrA* S83F)
- This study provides baseline information regarding circulating strains for future evaluation to determine the impact of the introduction of the typhoid conjugate vaccine program in Harare

Emergence of fluoroquinolone resistance in 4.3.1.1EA1 in Zimbabwe



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