

Supplementary Figures

Recent independent emergence of multiple multi-drug resistant *Serratia marcescens* clones within the United Kingdom and Ireland

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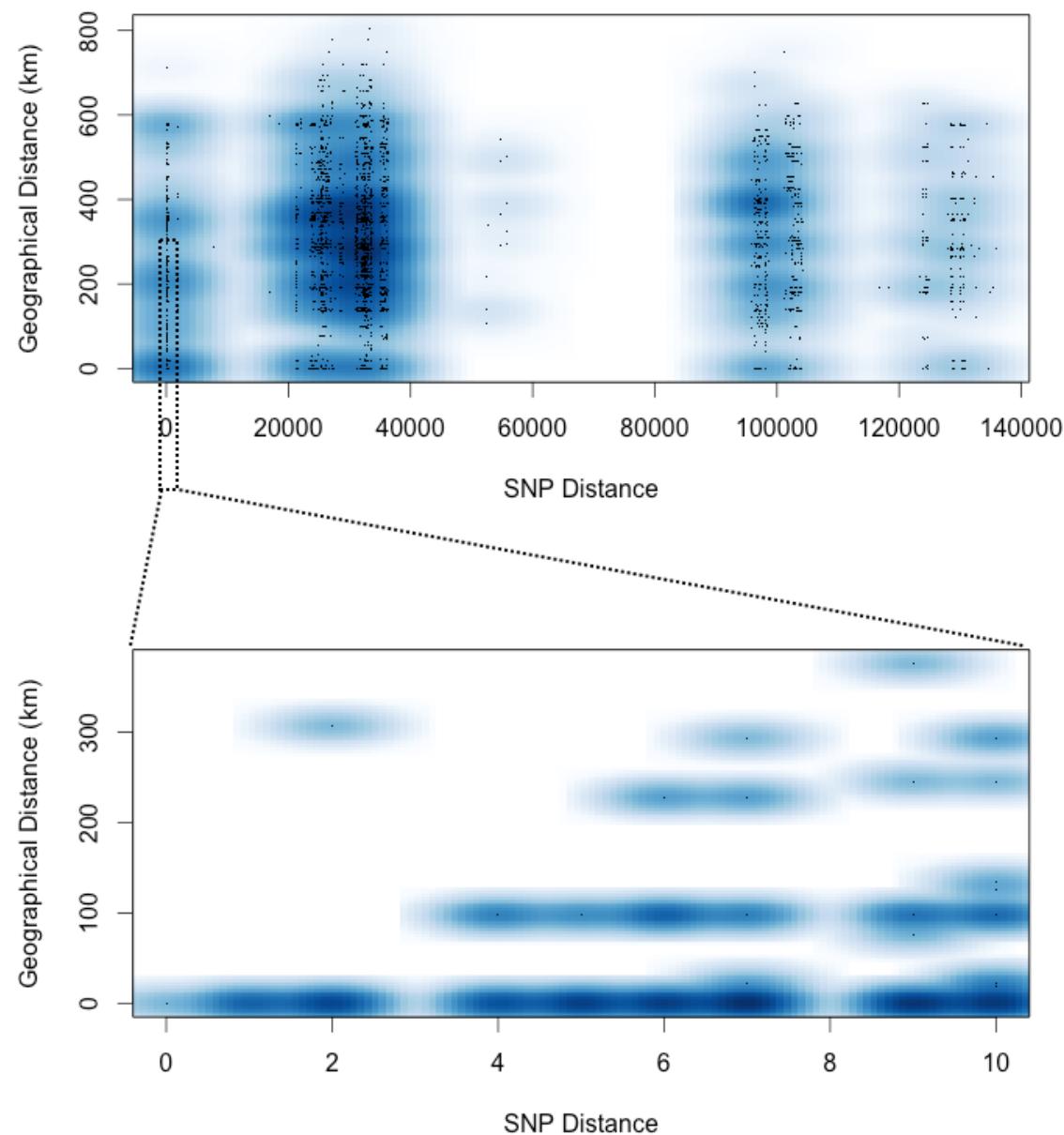


Figure S1. Plot of pairwise SNP distance versus the pairwise geographical distance for each isolate in the collection. The colour strength corresponds to data point densities.

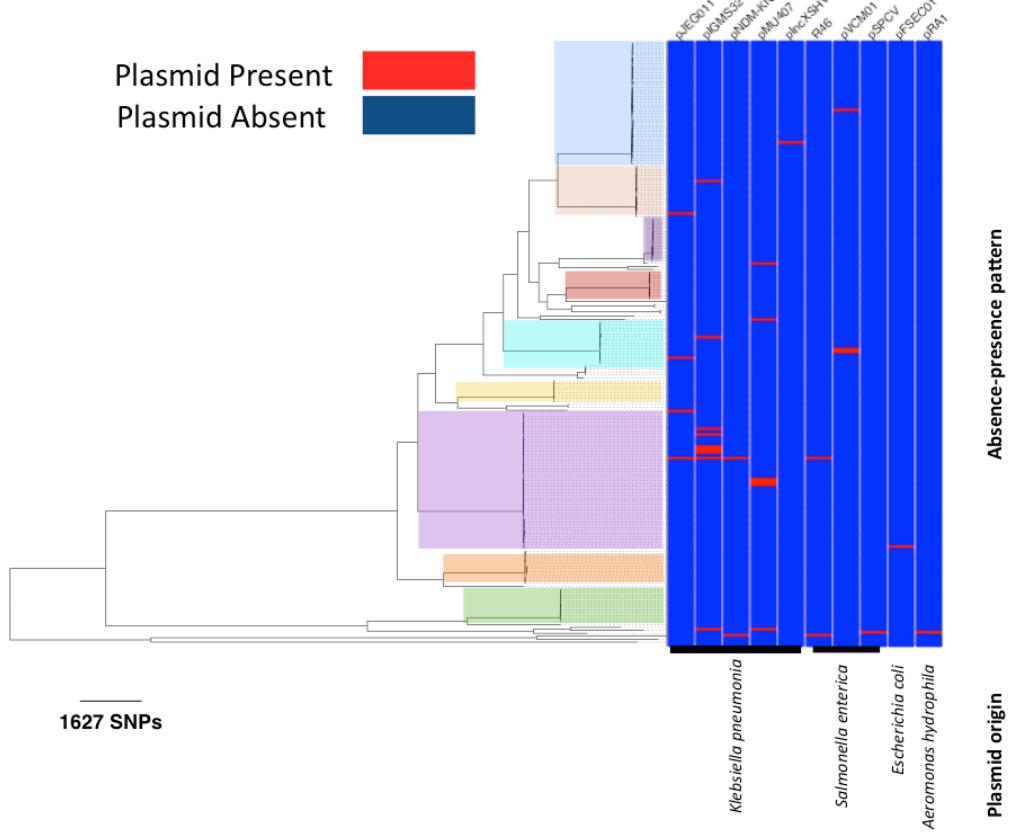


Figure S2. Distribution of different plasmids identified by PlasmidFinder across the maximum likelihood phylogenetic tree. The colours on the phylogenetic tree correspond to the major clades in Figure 3A.

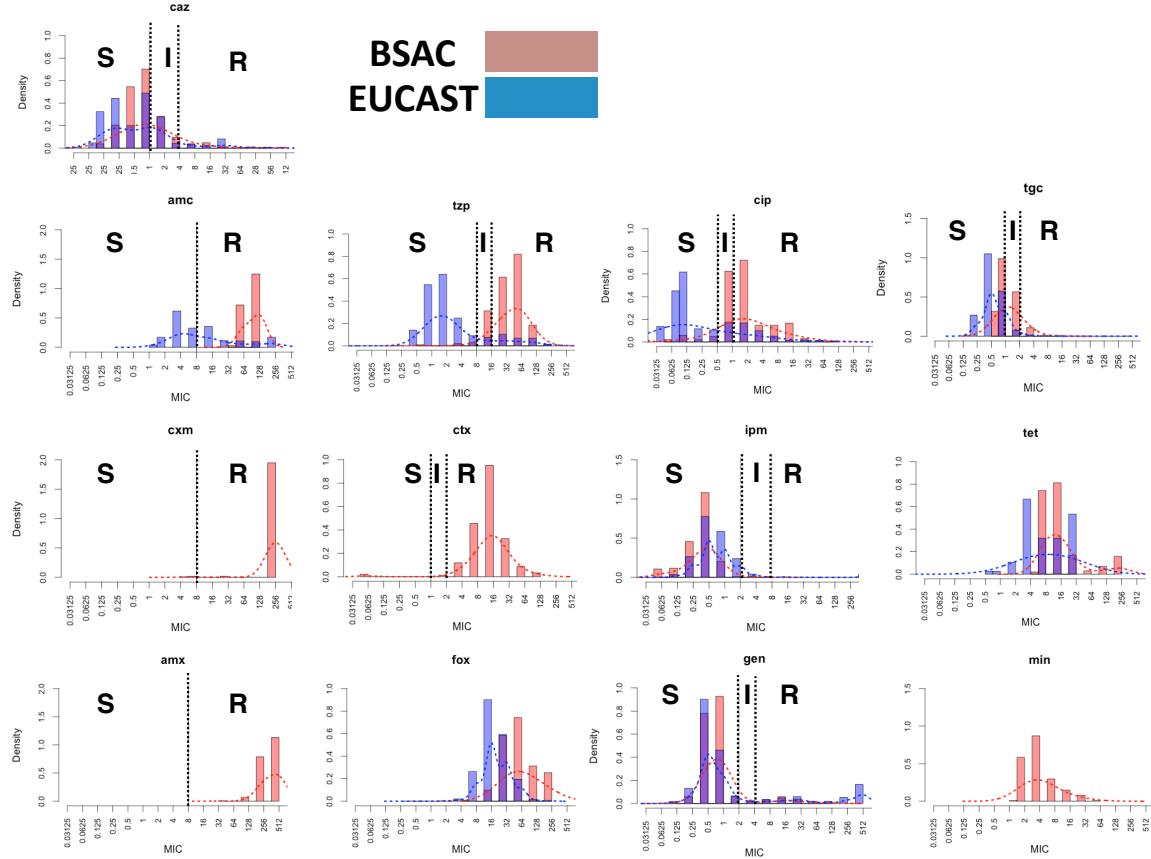


Figure S3. The distributions of MIC values for 13 antimicrobials for the BSAC collection (shown in red). If available, the distributions from the European Committee on Antimicrobial Susceptibility Testing website (EUCAST) are also depicted (in blue). The vertical dashed lines show the clinical cut-offs for resistance and intermediate sensitivity, respectively. The letters S, R and I stand for susceptible, resistant and intermediate, respectively. The dashed blue and red curves are density curves that show the continuous MIC distributions for the EUCAST and BSAC collections, respectively.

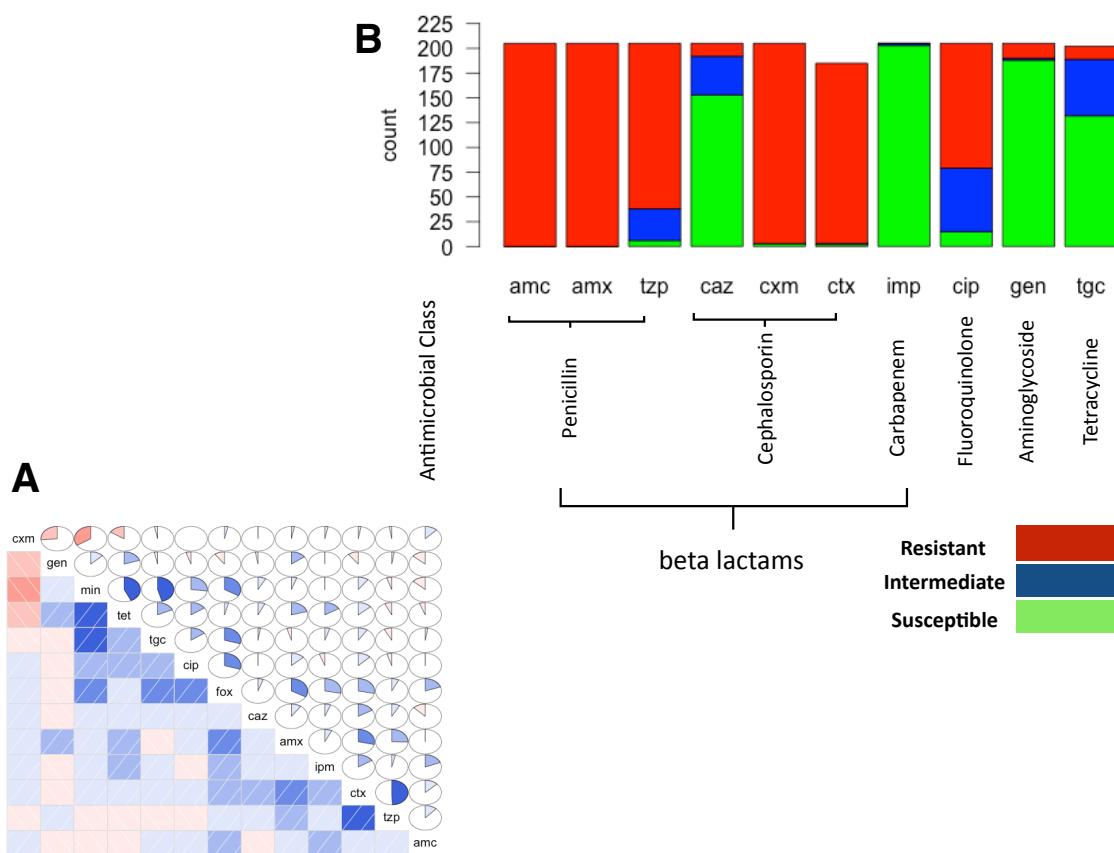


Figure S4. A) Correlogram of MIC values. Blue and red colours show positive and negative correlations between MIC values for pairs of antimicrobials. B) Charts of antimicrobial resistance determined by phenotypic testing for the antibiotics for which clinical breakpoints are defined. The abbreviations of antimicrobials are: amoxicillin (amx), cefuroxime (cxm), amoxicillin-clavulanate (amc), cefotaxime (ctx), cefoxitin (fox), imipenem (imp), piperacillin-tazobactam (tzp), ciprofloxacin (cip), ceftazidime (caz), gentamicin (gen), tigecycline (tgc), minocycline (min) and tetracycline (tet).

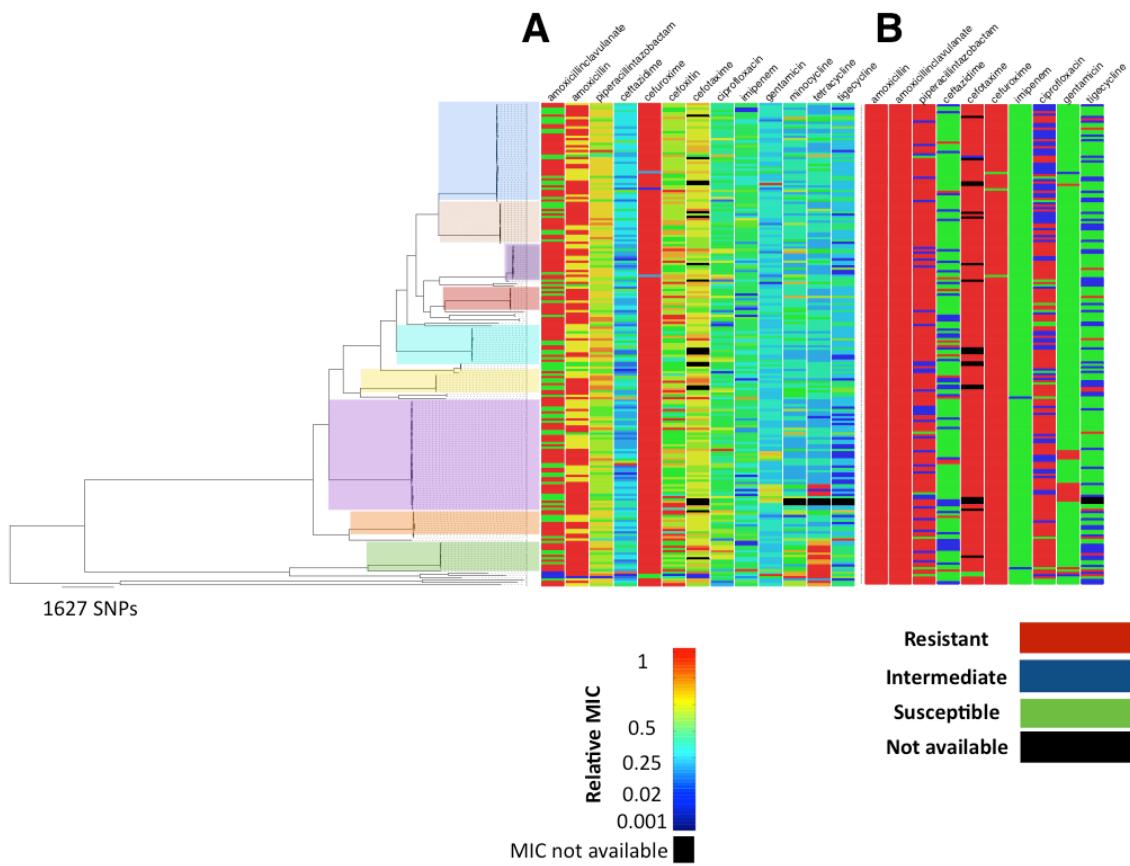


Figure S5. A) Distribution of MIC values across the phylogenetic tree for various antimicrobials. B) Distribution of antimicrobial resistance across the phylogenetic tree determined by phenotypic testing for the antimicrobials for which clinical breakpoints are defined. The colours on the phylogenetic tree correspond to major clades in Figure 3A.

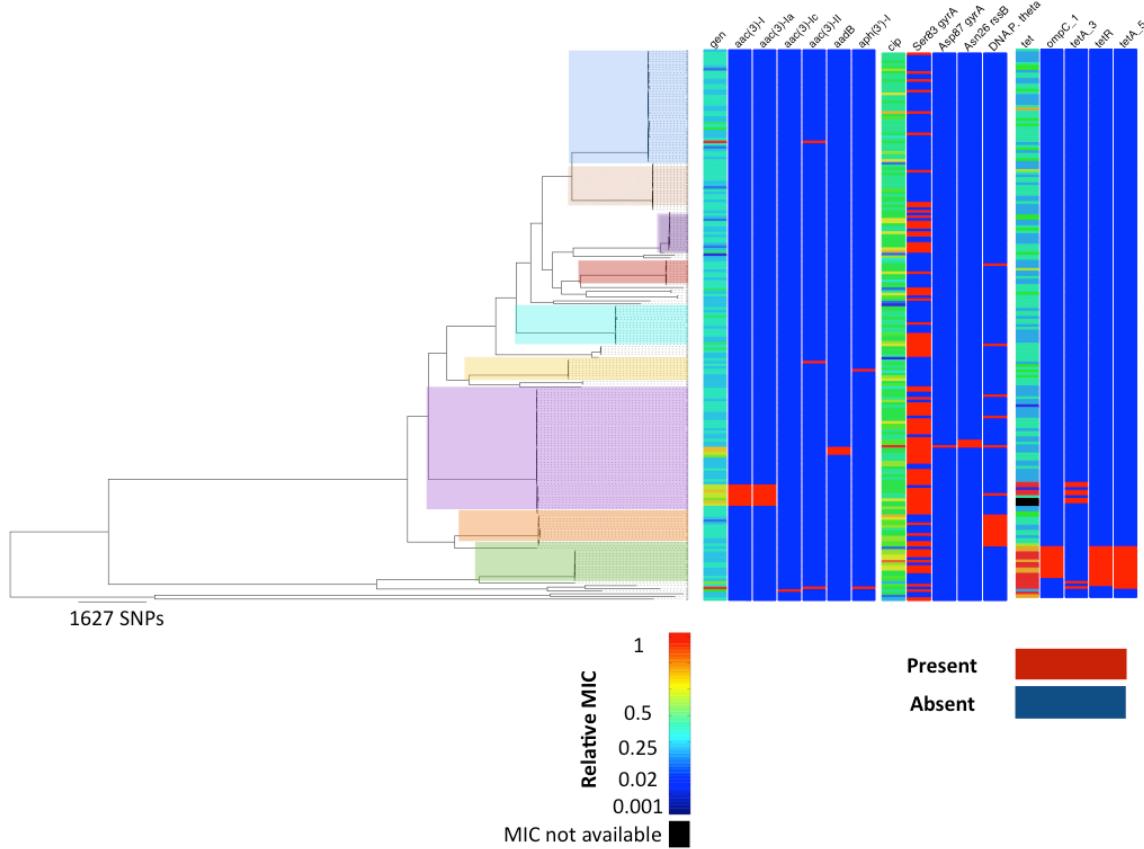


Figure S6. Phylogenetic distribution of antimicrobial resistance genes and mutations that are strongly correlated with MICs for gentamicin (gen), ciprofloxacin (cip) and tetracycline (tet). The first column in each block corresponds to MIC values for gentamicin, ciprofloxacin or tetracycline. The colours on the phylogenetic tree correspond to major clades in Figure 3A. The *rssB* gene is the regulator of the RNA polymerase, sigma S, involved in the general stress response (Hengge 2008). The *OmpC_1* protein is an outer-membrane porin protein, the expression of which is previously known to increase in response to tetracycline treatment (Zhang et al. 2008).

References

Hengge R. 2008. The two-component network and the general stress sigma factor RpoS (sigma S) in *Escherichia coli*. *Adv Exp Med Biol* **631**: 40-53.

Zhang DF, Jiang B, Xiang ZM, Wang SY. 2008. Functional characterisation of altered outer membrane proteins for tetracycline resistance in *Escherichia coli*. *Int J Antimicrob Agents* **32**: 315-319.