

FIG. 1. Identified mMutations identified in *gyrA*, *gyrB*, *parC* and *parE* in 100 clinical isolates. (A) Frequency and nature of the mutations found in the QRDRs of *gyrA*, *gyrB*, *parC* and *parE* in 100 clinical *Pseudomonas aeruginosa* isolates. Labels indicate the mutations with wild type allele, amino acid position and mutant allele and the number of strains harboring this mutation. 'Δ' indicates a deletion at the specified position. 'wt' indicates wild type allele or a silent mutation. (B) Co-occurrence of mutations in the QRDRs of *gyrA*, *gyrB*, *parC*, *parE* in the individual clinical *P. aeruginosa* strains. The fraction of isolates with a single mutation is depicted in light gray, with a double mutation in dark gray and with a triple mutation in black. The fraction of isolates without any identified QRDR mutation is shown in white.

mutation in QRDR

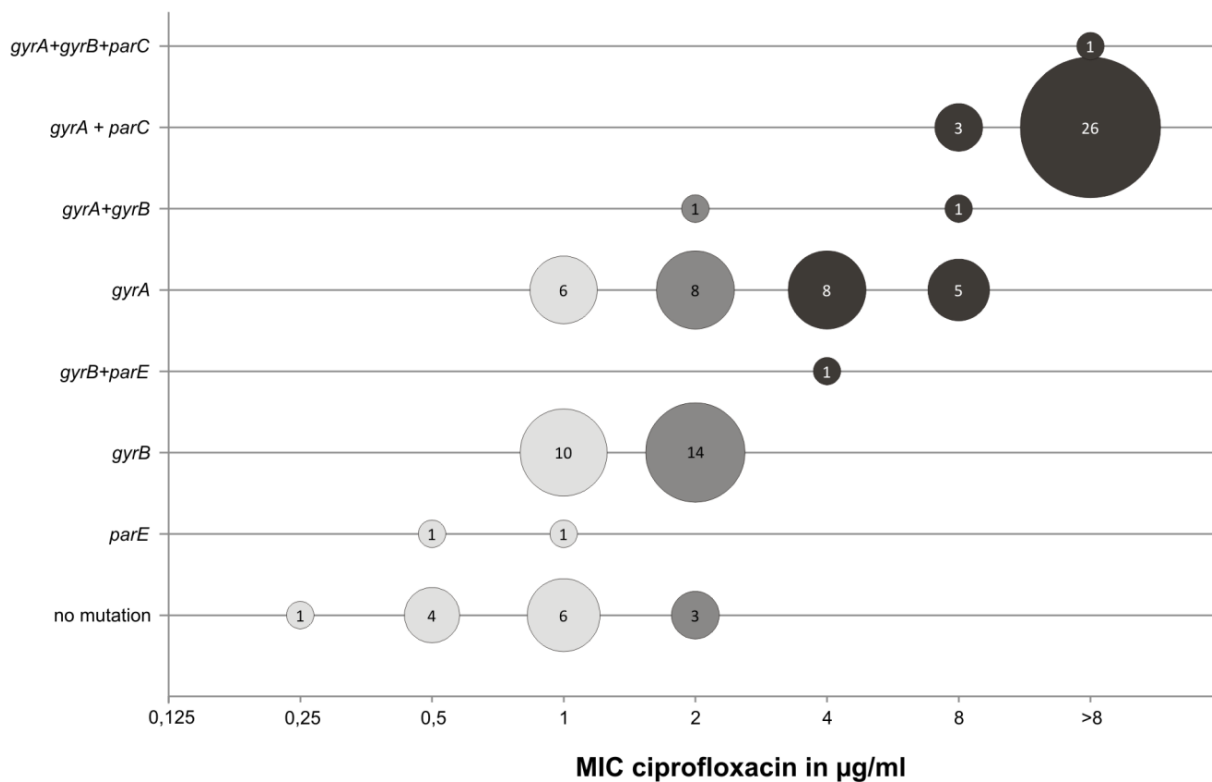


FIG. 2. Correlation of the minimal inhibitory concentration (MIC) values for ciprofloxacin and with the presence of mutations in the QRDRs of *gyrA*, *gyrB*, *parC* and *parE* (and combinations thereof) of 100 *P. aeruginosa* clinical isolates.

The number written inside a circle displays the amount of isolates with the same combination of MIC and genotype. The color of the circles represent the clinical breakpoints according to CLSI standards with light gray, gray and dark gray representing sensitive, intermediate and resistant, respectively.

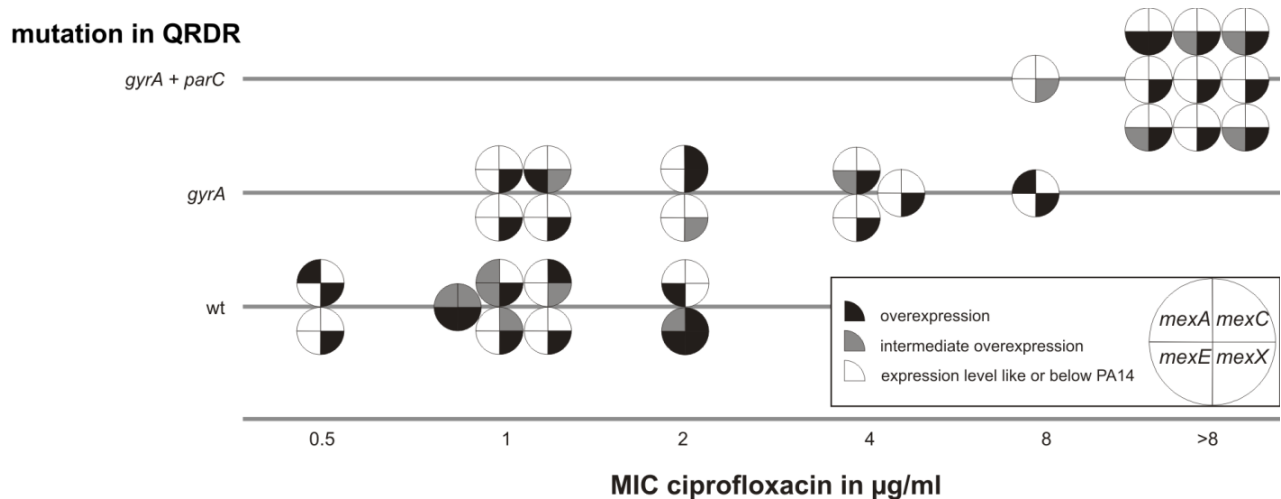


FIG. 3. Influence of multidrug efflux (MEX) pump overexpression and QRDR mutation on ciprofloxacin MIC. The variations of MIC values for a particular genotype cannot be explained by the additional expression of multidrug efflux (MEX) pumps. The figure shows the expression of four MEX pumps in 29 selected clinical *P. aeruginosa* isolates. Each circle represents one clinical isolate while each quarter represents one efflux pump (top left: MexAB-OprM, top right: MexCD-OprJ, bottom left: MexEF-OprN and bottom right: MexXY-OprM) with black quarters representing an overexpression of a pump, gray quarters representing borderline expression and white quarter representing wild -type expression levels (according to Carbot et al. 2011). The isolates were arranged according to their QRDR genotype (wild type, single mutation in *gyrA* or simultaneous mutation in *gyrA* and *parC*) and their ciprofloxacin MIC.