Correction: Exploring the contribution of efflux on the resistance to fluoroquinolones in clinical isolates of *Staphylococcus aureus*

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After the publication of our study [1], we became aware that the mutations in the quinolone resistance-determining region (QRDR) of the gene *grlA* were incorrectly described for some of the *Staphylococcus aureus* clinical isolates studied in this work. In particular, isolates SM1, SM10, SM14, SM17, SM25, SM27, SM43, SM46, SM47 and SM48 carry the GrlA double mutation S80Y/E84G; isolate SM52 carries the GrlA mutation S80Y; isolates SM3 and SM5 carry the GrlA double mutation S80F/E84G. The correct data can be found in Table 1.

All clinical isolates included in this study were selected upon a ciprofloxacin resistance phenotype and all the 25 representative isolates screened for mutations conferring resistance to fluoroquinolones.

### Table 1 Genotypic and phenotypic characterization of *S. aureus* clinical isolates

| Isolate | PFE pattern | QRDR mutations | MIC (mg/L) |
|---------|-------------|----------------|------------|
|         |             | GrlA GyrA       | EtBr CIP NOR NAL |
|         |             |                | EI TZ CPZ EI TZ CPZ EI TZ CPZ EI TZ CPZ |
| ATCC25923 | - | WT WT | 6.25 0.75 0.75 | 0.25 0.25 0.25 | 0.5 0.125 0.125 | 0.125 0.125 64 n.d. n.d. |
| ATCC25923* | - | WT WT | 200 25 12.5 | 1 0.25 0.25 | 2 0.25 0.25 | 64 n.d. n.d. |
| SM1 | A2 | S80Y/E84G S84L | 16 4 4 | 128 32 64 | 512 128 256 | 256 64 64 |
| SM10 | A4 | S80Y/E84G S84L | 16 2 4 | 128 64 64 | 512 128 128 | 128 64 64 |
| SM14 | A3 | S80Y/E84G S84L | 16 4 4 | 256 32 128 | 1024 128 256 | 256 64 64 |
| SM17 | A4 | S80Y/E84G S84L | 16 4 4 | 256 64 64 | 1024 256 512 | 256 64 64 |
| SM25 | A1 | S80Y/E84G S84L | 8 2 4 | 128 32 64 | 512 64 128 | 256 64 64 |
| SM27 | A4 | S80Y/E84G S84L | 16 4 4 | 256 32 64 | 512 128 256 | 256 64 64 |
| SM43 | A1 | S80Y/E84G S84L | 16 2 4 | 128 64 64 | 512 128 128 | 128 256 64 |
| SM46 | A1 | S80Y/E84G S84L | 16 4 4 | 128 64 64 | 512 128 256 | 256 64 64 |
| SM47 | A1 | S80Y/E84G S84L | 8 2 4 | 256 32 64 | 512 128 256 | 256 64 64 |
| SM48 | A1 | S80Y/E84G S84L | 8 4 4 | 256 32 64 | 512 128 256 | 256 64 64 |
| SM50 | B1 | S80F/E84K S84L | 8 1 2 | 64 16 16 | 256 32 64 | 128 64 64 |
| SM52 | C1 | S80Y S84L | 16 1 2 | 16 8 8 | 64 32 32 | 128 32 64 |

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fluoroquinolone resistance carried QRDR mutations in both grlA and gyrA genes. All the mutations found have been described in literature as associated with fluoroquinolone resistance in S. aureus clinical isolates [2].

As stated previously in our study, the majority of the isolates presented a double mutation in GrlA together with a single mutation in GyrA. Eleven isolates carried the GrlA and GyrA mutations S80Y/E84G and S84L, respectively; three isolates carried mutations GrlA S80F/E84K and GyrA S84L and two isolates carried mutations GrlA S80F/E84G and GyrA S84L. The remaining nine isolates carried a single mutation in both genes, in three distinct arrangements (Table 1).

Despite this correction in the QRDR mutations carried by some of the isolates studied, the main findings of our study are not altered. In particular, our data show the potential role played by efflux systems in the development of resistance to fluoroquinolones in clinical isolates of S. aureus, independently of the mutations occurring in the target genes.

We apologize for any inconvenience that this may have caused to the readers.

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Table 1 Genotypic and phenotypic characterization of S. aureus clinical isolates (Continued)

| Isolate | GrlA Mutations | GyrA Mutations | MIC CIP | MIC NOR | MIC NAL | MIC TZ | MIC CPZ | MIC n.d. |
|---------|----------------|----------------|--------|--------|--------|-------|--------|--------|
| SM2     | S80F/E84K      | S84L           | 2      | 2      | 16     | 128   | 32     | 16     |
| SM3     | S80F/E84G      | S84L           | 1      | 1      | 16     | 8     | 8      | 64     |
| SM4     | S80F           | S84L           | 4      | 2      | 1      | 8     | 8      | 64     |
| SM5     | S80F/E84G      | S84L           | 4      | 2      | 32     | 16    | 16     | 128    |
| SM6     | S80F           | E88K           | 4      | 2      | 1      | 16    | 16     | 16     |
| SM7     | S80F           | S84L           | 2      | 2      | 1      | 8     | 8      | 64     |
| SM8     | S80F           | E88K           | 4      | 2      | 1      | 16    | 8      | 128    |
| SM12    | S80F           | S84L           | 2      | 2      | 1      | 16    | 8      | 64     |
| SM16    | S80F           | E88K           | 4      | 2      | 1      | 16    | 16     | 128    |
| SM22    | S80F/E84G      | S84L           | 8      | 4      | 128    | 16    | 32     | 128    |
| SM34    | S80F/E84K      | S84L           | 4      | 2      | 64     | 16    | 32     | 16     |
| SM40    | S80F           | S84L           | 8      | 4      | 128    | 16    | 32     | 128    |

aIsolates in bold correspond to the EtBrCW-positive isolates. bWT: wild-type; S: serine; F: phenylalanine; E: glutamate; K: lysine; Y: tyrosine; L: leucine; G: glycine.

Values in bold-type correspond to a MIC decrease of ≥ four-fold in the presence of the efflux inhibitor (EI) in comparison to the values with no EI [10]. The concentration of each EI used is defined in the Methods section. EtBr: ethidium bromide; CIP: ciprofloxacin; NOR: norfloxacin; NAL: nalidixic acid; TZ: thioridazine; CPZ: chlorpromazine; n.d.: not determined.