

# [Qac resistant genes](https://assignbuster.com/qac-resistant-genes/)

Biocides based on QACs are widely used for disinfection and preventing the infection and the transmission of bacteria in a hospital, veterinary or industrial environment. Extensive and inadequate use of these disinfectants for disinfection could lead to a selective pressure for survival of bacterial strains with qac resistance genes, thus creating a potentially serious problem of infection control in hospitals and clinical settings.

Consequently, the emergence of qac resistance genes that code for resistance to disinfectants among various subtypes of staphylococci, including S. aureus and coagulase-negative staphylococci (CNS), have been reported in human clinical isolates and general environment and several qac genes have been identified52, 66, 68, 93, 96.. (1) In general, QAC resistant genes are plasmid-born and code for the expression of multidrug efflux pumps, which are membrane-bound transport proteins. These proteins are PMF-dependent cation export proteins for expelling toxic substrates including QACs, some other cationic biocides, and intercalating dyes, such as ethidium bromide (EBR) (21). Presence of these genes may allow microorganisms to survive in a hostile environment containing disinfectants and antimicrobial agents. According to their different structures, the gene determinants belong to one of two membrane transportation families, the major facilitator family (MFS) and the small multidrug resistant family (SMR)52. Information about location and resistance patterns to biocides of these qac genes can be seen in Table 2.

QacA/B and smr, ranked the first two, are the most frequently reported qac genes. The increased resistance to biocides is closely associated with the presence of both qacA and smr. (23).

In 1999, Noguchi performed a study to investigate the distribution of the S. aureus isolates carrying qacA/B or qacC gene in clinical isolates in Japan. According to his results, the prevalence of qacA/B was 10/71 (14%) and qacC was 20/71 (28%) MRSA isolates. Later studies also performed by Noguchi revealed that the prevalence of MRSA with qacA/B had reached 41. 6% (372/894) across the Asian area, and MRSA with qacC gene in India was up to 31. 6%. Similar studies conducted in Hong Kong reported different results95, with 41. 2% (21/51) S. aureus isolated from nurses found to carry the qacA/B gene, and frequency of qacC gene was only 11. 8% (6/51), which was quite low compared to Noguchi’s study82.[1]

In addition, MRSA isolates resistant to disinfectants and antiseptics have been reported (7). In the isolates of MRSA, the carriage of qacA was more common than smr (9).

Recently, several novel plasmid-borne genes, qacG, qacH, qacJ , qacE and qacE Δ 1, were detected in staphylococci and some gram negative bacteria associated with infection diseases(1). However, the prevalence of these genes are commonly quite lower than that of qacA/B.

qac A/B gene

QacA and qacB resistance genes are harboured on plasmids which belong to the MFS family. Lyon et al. demonstrated that the qacA gene was present on plasmid pSK57 together with resistance genes for β-lactamase and heavy metals (21, 23). It is suggested that qacA is homological with another antibiotic resistant gene tet , and encodes the QacA protein which has 514 amino acids and belongs to the major facilitator superfamily (MFS) 92.

Sequence analysis suggests that the qacA pump, which has a 14 TMS configuration, confers resistance via the export of the compound by the proton motive force (PMF) to a wide range of structurally diverse hydrophobic drugs including QACs (such as cetrimide), ethidium bromide, and other organic cations.

The qacB gene is located on plasmid pSK23 again together with β-lactam and heavy metal resistance genes which shows high similarity with qacA 73 (23-24). QacA and qacB are considered to be virtually the same as it is not possible to distinguish between them by simple PCR, there being differences in only seven nucleotide substitutions. The molecular structure difference between qacA and qacB is just 7 nucleotide substitutions, these two transporters have similar binding affinities and identical binding sites for monovalent cations. However, qacA mediates resistance to both monovalent and divalent cations while qacB confers less or no resistance to divalent cations and can only expel QACs and intercalating dyes from the cell.

Smr gene

QacC , which has also been known as qacD or ebr , has been renamed smr. It is plasmid borne, often on small plasmids of less than 3kb and belongs to the SMR family.

Smr is the smallest of the multidrug resistance transporters. Its small size makes it unique as a secondary transporter. The product encoded by qacC gene contains 107 amino acids and has four large hydrophobic segments, all which have the potential to traverse the cell membrane. Studies101 have shown that QacC protein not only mediates multidrug export but functions as a multidrug exporter.

Smr can transport several different compounds such as QACs, ethidium bromide and other compounds, but it is more limited than qacA (9, 26).[2] The schematic representation of the QacC polypeptide can be seen in Fig. 3.

This gene was mostly detected in clinical isolates of S. aureus and other staphylococci species(15). The smr gene has been shown to be located on a large (> 20kb) conjugative plasmid with multiple resistance determinants such as pSK41 and on small (<3kb) nonconjugative plasmids such as pSK89 (17, 20, 23). A recent study83 has revealed that the qacC gene in S. epidermidis confers resistance to a number of beta -lactam antibiotics and to ethidium bromide, and this is the first report of a small multidrug resistance pump involved in resistance to beta -lactam antibiotics.

qacG gene

qacG gene was first isolated from staphylococcal plasmid pST94 with 2. 3kb in 199952. The 107 amino acid protein QacG encoded by qacG gene, belonging to the SMR family, shows 69. 2% and 45% similarity with small multidrug resistant protein Smr and QacE, respectively. The qacG – and smr -harbouring isolates showed small differences in MIC values to BC (8–10 mg/l) and Eb (20–40 mg/l).

QacG protein confers resistance to Eb and QACs via proton dependent efflux. There is little differences between qacG isolates and smr isolates in MIC values of BC and Eb, and it is suggested that the QacG protein uses the same resistance mechanism as the Smr protein52. The location of the hydrophobic amino acid in QacG and Smr is similar, however, QacG differed from Smr in 33 of 107 amino acid proteins dispersed throughout the protein52.

qacH gene

In 1998, Heir93 isolated a new staphylococcal gene, qacH, from a strain of Staphylococcus saprophyticus . The qacH gene is harbored on the 2. 4kb plasmid (p2H6), and mediates resistance to QACs. QacH protein encoded by the qacH gene contains 107 amino acids and shows strong homology with the small multidrug resistance protein family. Further study suggests that similarity of QacH with Smr and QacG is 78% and 70%, respectively93. However, QacH conferred high-level resistance to ethidium bromide and low-level resistance to proflavine, which differs from Smr and QacG . 93

qacJ gene

QacJ gene locates on a 2650bp plasmid pNVH01 in equine S. aureus , S. intermedius and S. simulans , and was first identified in Norway, 200367. The plasmid pNVH01 belongs to the plasmid pC194 family of rolling circle replication and contains two open reading frame, designated repNVH01 and qacJ 67 . qacJ encodes a putative protein QacJ with 107 amino acid. Homology analysis shows that QacJ is a new group of the Smr protein family, and the similarity with other smr protein members is shown to be: Smr (72. 5%), QacG (82. 6%), and QacH (73. 4%). Compared with Smr, QacG and QacH, QacJ confers an increased resistance level to BC, but mediates the same resistant level against CTAB with Smr67.