The G132S Mutation Enhances the Resistance of *Mycobacterium tuberculosis* β-Lactamase against Sulbactam

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**ABSTRACT:** The current rise of antibiotic resistant forms of *Mycobacterium tuberculosis* is a global health threat that calls for new antibiotics. The β-lactamase BlaC of this pathogen prevents the use of β-lactam antibiotics, except in combination with a β-lactam inhibitor. To understand if exposure to such inhibitors can easily result in resistance, a BlaC evolution experiment was performed, studying the evolutionary adaptability against the inhibitor sulbactam. Several amino acid substitutions in BlaC were shown to confer reduced sensitivity to sulbactam. The G132S mutation causes a reduction in the rate of nitrocefin and ampicillin hydrolysis and simultaneously reduces the sensitivity for sulbactam inhibition. Introduction of the side chain moiety of Ser132 causes the 104–105 peptide bond to assume the cis conformation and the side chain of Ser104 to be rotated toward the sulbactam adduct with which it forms a hydrogen bond not present in the wild-type enzyme. The gatekeeper residue Ile105 also moves. These changes in the entrance of the active site can explain the decreased affinity of G132S BlaC for both substrates and sulbactam. Our results show that BlaC can easily acquire a reduced sensitivity for sulbactam, with a single-amino acid mutation, which could hinder the use of combination therapies.

*Mycobacterium tuberculosis* (Mtb) infection ranks among the top 10 causes of death worldwide, with 1.4 million deaths reported in 2019. 1 The treatment of this infection, which currently consists of the administration of four types of antibiotics for a period of six months to two years, is becoming increasingly difficult due to the rise in antibiotic resistant Mtb strains. 1, 2 The gene for BlaC, an Ambler class A β-lactamase, 3, 4 is chromosomally encoded in Mtb, rendering treatment of tuberculosis (TB) with β-lactam antibiotics ineffective. 5 However, in light of the current problems with combatting extensively drug resistant Mtb, this type of antibiotic might provide new opportunities. 6–10 There are several Food and Drug Administration-approved compounds available that have the ability to inhibit BlaC, which could constitute an alternative treatment in combination with β-lactam antibiotics. 11–12 Among clinically approved inhibitors for BlaC are clavulanic acid, sulbactam, tazobactam, and avibactam. 13–16

The inhibitor for class A β-lactamases that was first discovered and is the best-studied is clavulanic acid. Structurally, it is similar to penicillin and inhibits the enzyme by the formation of a covalent bond with Ser70. The adduct can be hydrolyzed slowly at a rate that strongly depends on the ions present in solution. 17 However, various chemical rearrangement reactions can occur in the adduct and multiple trans-enamine adducts have been found using mass spectrometry and X-ray diffraction of crystals. Some adducts are nonhydrolyzable and lead to an inactivated enzyme. 18–20

Sulbactam is a synthetic inhibitor that was developed in 1978 by Wayne E. Barth. 14 It is structurally similar to clavulanic acid and currently used in the clinic in combination with either ampicillin or cefoperazone. 15, 21 It has also shown potential to be used in combination with meropenem. 22 Little is known regarding the mechanism(s) by which sulbactam inhibits BlaC. The inhibitor acts as a substrate that is slowly converted. After inhibition, the enzyme returns to an active state within 30 min, 18 which is faster than other first-generation inhibitors do. 17–19–23 Using mass spectroscopy, Hugonnet and colleagues observed the enzyme–inhibitor complex, 18 which has since been crystallized. 20, 24 The crystal structure of the *trans*-enamine adduct formed by BlaC and sulbactam [Protein Data Bank (PDB) entry 6H2K] 20 shows differences in the loop region between residues Asp100 and Val108 (Ambler numbering), 25 when compared to the resting state enzyme (PDB entry SOYO), 17 but other parts of the enzyme are minimally affected.

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We wondered whether evolution against sulbactam inhibition through mutations in BlaC could easily occur, which could have a negative bearing on the effectiveness of combination therapy. Laboratory evolution yielded mutations A55E, G132S, D172N, and G269S, and their effects on enzyme structure and stability as well as activity and sulbactam inhibition are described. Of these mutants, only BlaC G132S exhibits reduced sensitivity for sulbactam inhibition for the purified enzyme. The crystal structure of the sulbactam adduct shows clear differences with that of wild-type BlaC. The possible mechanism of reduced sulbactam sensitivity is discussed.

## MATERIALS AND METHODS

The inhibitors sulbactam, avibactam, and clavulanic acid were purchased from Sigma-Aldrich, MedChemExpress, and Matrix Scientific, respectively. It was found that quality can vary between suppliers.

**Screening Assays.** Laboratory evolution was performed using polymerase chain reaction (PCR) with DreamTaq DNA Polymerase (Thermo Scientific) under non-optimal conditions (2 mM MgCl₂ and 0.2 mM MnCl₂) and an unbalanced ratio of nucleotides (0.2 mM dATP, 0.2 mM dGTP, 0.52 mM dCTP, and 0.52 mM dTTP) to increase the error rate during DNA synthesis. The amplified region comprised the blaC gene with a twin-arginine translocation signal peptide sequence (Figure S1). Mutations were introduced only in the region of the mature enzyme, not the signal peptide. The product was used for a subsequent standard PCR to increase the quantity of DNA and create a construct with restriction sites. The mutated blaC genes were cloned behind the lac promoter in pUK21 through restriction and ligation. *Escherichia coli* KA797 cells²⁶ were transformed with the plasmid library and plated on selective lysogeny broth (LB) agar plates containing 50 μg/mL kanamycin, 10 μg/mL ampicillin, 1 mM isopropyl β-D-1-thiogalactopyranoside, and 4 μg/mL sulbactam, which is the minimum inhibitory concentration (MIC) for wild-type blaC in this expression system. Plates were incubated for 16 h at 37 °C. Colonies were used to inoculate LB containing kanamycin and incubated for 16 h at 37 °C and 250 rpm before plasmid isolation. To confirm that resistance was the consequence of mutations in the blaC gene, plasmids were used to re-transform fresh KA797 cells, which were plated on selective medium. Subsequently, the individual mutations were introduced into the wild-type gene using the QuikChange method (Agilent) and confirmed by DNA sequencing (Table S1).

**Inhibitor Susceptibility Assay.** Inhibitor resistance was tested in *E. coli* cells by adding 10 μL of KA797 pUK21-blaC liquid cultures with optical densities of 0.3, 0.03, 0.003, and 0.0003 on LB agar plates with various concentrations of the inhibitor and antibiotics. Plates were incubated for 16 h at 37 °C and imaged using Gel Doc XR+ (Bio-Rad) and ImageLab version 6.0.1 (Bio-Rad).

**Protein Production.** Protein was produced using *E. coli* BL21 (DE3) pLysS cells transformed with pET28a plasmids containing the blaC gene with an N-terminal His tag and TEV cleavage site (Figure S2). Protein was produced and purified as described previously.¹⁷ The size exclusion chromatography step was omitted. Samples for *in vitro* assays contained 100 mM sodium phosphate (pH 6.4).

**Circular Dichroism Spectroscopy.** Protein folding was analyzed using a J-815 circular dichroism (CD) spectrometer (Jasco) with a PTC-423S/15 temperature controller (Jasco). Protein samples were diluted to 10 μM and measured in a 1 mm QS High Precision Cell (Hellma Analytics). Spectra were recorded from 260 to 190 nm at 20 °C, and data were collected every 1 nm. Results from five data sets were added to enhance the signal-to-noise ratio.

**Thermal Shift Assay.** Thermal shift assays (TSAs) were performed using a CFX96 Touch Real-Time PCR detection system (Bio-Rad). Protein samples were diluted to a final concentration of 15 μM and mixed with 4× SYPRO Orange Protein Gel Stain (diluted from a 5000X stock as supplied by Sigma-Aldrich) to detect protein unfolding. The temperature (T) was increased from 20 to 80 °C in steps of 1 °C, and samples were incubated for 1 min at each temperature before detection of the fluorescence signal. Six-fold measurements were performed. Data were analyzed using OriginPro version 9.1 (OriginLab) and fit using eq 1.

\[
y(T) = A_2 + \frac{A_1 - A_2}{1 + e^{T - T_m}/dT}
\]  

where \(T_m\) is the melting temperature in degrees Celsius, \(A_1\) and \(A_2\) are the initial and final values of fluorescence, respectively, and dT describes the steepness of the change in fluorescence upon unfolding and is thus a measure of the degree of cooperativity.

**Kinetic Analysis and In Vitro Inhibition Experiments.** Kinetic parameters were determined for nitrocefin (BioVision) and ampicillin (Serva) as substrates. Measurements were performed in triplicate in a 10 mm QS High Precision Cell (Hellma Analytics), using a PerkinElmer Lambda 800 UV−vis spectrometer thermostated at 25 °C. Nitrocefin hydrolysis by 2 nM BlaC was measured in the presence of 7.6 μM bovine serum albumin (BSA) (Sigma-Aldrich) and various concentrations of substrate, followed for 3 min at 486 nm (\(ε_{486} = 11300 \text{ M}^{-1} \text{ cm}^{-1}\)).²⁷ Ampicillin conversion by 10 nM BlaC was followed for 4 min at 235 nm (\(ε_{235} = 861 \text{ M}^{-1} \text{ cm}^{-1}\)). The kinetic curves were fit, and kinetic parameters were obtained using Origin version 9.1 and eq 2:

\[
v_I = \frac{k_{cat}[E][S]_0}{K_M + [S]_0}
\]  

doing the steepness of the change in

\[
E + S \rightleftharpoons ES \rightarrow ES^* \rightarrow E + P_i
\]

where E, S, and I represent BlaC, nitrocefin, and sulbactam, respectively, \(P_s\) and \(P_i\) are the hydrolyzed forms of S and I, respectively, and \(ES, EI, ES^*,\) and \(EI^*\) represent the noncovalent and covalent intermediates, respectively. The
values for $k_1 - k_4$ were obtained by simulation of the reaction curve in the absence of sulbactam and later fixed in the fitting of $k_1 - k_4$ to 0.51 $\mu$M$^{-1}$ s$^{-1}$, 76.5 s$^{-1}$, 380 s$^{-1}$, and 120 s$^{-1}$ for wild-type BlaC and 0.071 $\mu$M$^{-1}$ s$^{-1}$, 10.8 s$^{-1}$, 380 s$^{-1}$, and 120 s$^{-1}$ for BlaC G132S, respectively.

**Nuclear Magnetic Resonance (NMR) Experiments.**

HNCA spectra for BlaC G132S and BlaC D172N and TROSY-HSQC$^{30,31}$ spectra for all mutants were recorded at 25 °C using a Bruker AVIII HD 850 MHz spectrometer equipped with a TCI cryoprobe. Samples contained ~0.15 mM $[^{15}$N]$[^{13}$C$]BlaC or $[^{15}$C$][^{15}$N]$[^{13}$C$]BlaC$ samples in 100 mM sodium phosphate (pH 6.4) and 6% D$_2$O. Data were processed with Toppin 4.0.6 (Bruker Biospin) and analyzed using CCPNmr Analysis.31 Spectra were compared to the TROSY-HSQC and HNCA spectra of wild-type BlaC.17 and average chemical shift perturbations (CSPs) of backbone amides were calculated using eq 4.

$$\Delta \delta = \sqrt{\frac{1}{2} \left( \Delta \delta_1^2 + \left( \frac{\Delta \delta_2}{5} \right)^2 \right)}$$

where $\Delta \delta_1$ and $\Delta \delta_2$ are the differences in chemical shifts in ppm in spectra of the mutant and wild-type enzymes for $^{1}$H and $^{15}$N, respectively. The assignments of the backbone amide resonances have been deposited in the BMRB as entries 50565, 7A5T, 7A71, 7A72, and 7A5W for BlaC A55E, G132S, and D172N and PDB entry 6H2K20 for G132S with sulbactam. Model building and refinement were performed using Coot and REFMAC.35 The model was further optimized using the PDB-REDO Web server.6 A number of residues were modeled in two conformations: Arg128 and Ile186 for A55E, Ser130, Ile186, Asn197, Arg204, Lys219, Met264, and Glu283 for G132S; Arg39, Lys93, Met264, and Tyr272 for G132S with sulbactam; and Arg128, Ser130, and Met264 for D172N. For G132S and G132S with sulbactam, Ser104 was found in the trans conformation.

**Mass Spectrometry.**

Samples of 20 μM BlaC or BlaC G132S in 100 mM sodium phosphate (pH 6.4) were incubated for 5 min at 25 °C in the absence or presence of 100 μM sulbactam. The buffer was exchanged with 10 mM ammonium acetate (pH 7) using Micro Bio-Spin 6 columns (Bio-Rad), and a 1 μL sample was loaded onto a nanoEase M/Z protein BEH C4 column (Waters) and analyzed using a MALDI Synapt G2-Si mass spectrometer (Waters). Data were analyzed using MassLynx MS (Waters).

**RESULTS**

**Laboratory Evolution of the Mtb blaC Gene.** A blaC gene mutant library was generated using error-prone PCR and cloned into the pUK21 vector. A 42-amino acid E. coli twin-arginine transporter (Tat) signal was added at the N-terminus, causing BlaC to be transported to the periplasm of the E. coli cells to mimic closely the situation in Mtb.39–41 The resulting strains were screened for resistance against sulbactam in the presence of ampicillin. Plasmids from colonies that showed inhibitor resistance were isolated and sequenced. After 2 × 10$^6$ clones had been screened, a total of six amino acid substitutions were found in three different blaC clones (Table S3). The G132S mutation was found as a single mutation in one clone, but also in combination with A55E, D100E, and D179N in another clone. A third clone contained the D172N and G269S mutations. Four of these mutations, A55E, G132S, D17N, and G269S, caused resistance when present in the gene as single-amino acid substitutions, albeit to different degrees (Figure 1 and Figure S3). E. coli cells producing wild-type BlaC were able to grow on plates containing <8 μg/mL sulbactam in the presence of 10 μg/mL ampicillin, whereas the cells producing BlaC mutants were able to grow on plates containing at least 10 μg/mL sulbactam. Additive effects with regard to sulbactam resistance were not observed when combining the mutations that originated from the same clone (Figure 1).

**Protein Folding and Thermal Stability.** Overexpression of the BlaC variants, without the signal peptide and with a
ampicillin. There appears to be a decrease in substrate affinity yet shows distinct differences in the activity of BlaC G132S. BlaC D172N can convert BSA17 and is 10-fold higher than those in the absence of substrate. The conversion is similar to that of wild-type BlaC in the presence of nitrocefin. The parameters for the conversion of ampicillin as the temperature was increased resulted in a 5-fold higher $K_{cat}$ value for BlaC G132S, indicating a lower affinity for this mutant for sulbactam (Figure 4 and Table S5). The rates of acylation ($k_{cat}$) and hydrolysis ($k_{a}$) are similar to those of wild-type BlaC.

Curiously, the degree of inhibition of BlaC A55E, BlaC D172N, and BlaC G269S was similar to that of the wild type, even though these variants displayed increased resistance against inhibition in vitro. To test whether a difference in temperature was the cause of this result, the experiment was repeated at 37 °C, to match the temperature of the in vivo inhibition tests. However, the same results were obtained, indicating that the temperature is not a factor contributing to differences observed between in vivo and in vitro results (Figure S5). We also tested whether the growth of these mutants at higher sulbactam concentrations could be caused by an improved ability to convert ampicillin. No evidence was found for this in either in vivo or in vitro experiments using single-amino acid mutants (Figure S6). Interestingly, the combination of mutations D172N and G269S increased the MIC from 60 to >100 μg/mL, which is higher than for either of the individual mutations.

**Structural Analysis.** To probe the effects of the mutations on the structure of the enzymes, 1H−15N HSQC spectra were recorded (Figures S7−S10) and averaged chemical shift perturbations (CSP) compared to the spectrum of wild-type BlaC. The combination of mutations D172N and G269S increased the percentage of the converted substrate after reaction for 15 min was compared for several concentrations of the inhibitor to the amount of product in the reaction without an inhibitor. Wild-type BlaC could convert 5% of the nitrocefin in the presence of the highest concentration of sulbactam tested, while BlaC G132S converts 25% (Figure 3). Fitting the product formation curves for wild-type BlaC and BlaC G132S according to model 3 resulted in a 5-fold higher $K_i$ value for BlaC G132S, indicating a lower affinity of this mutant for sulbactam (Figure 4 and Table S5). The rates of acylation ($k_{cat}$) and hydrolysis ($k_{a}$) are similar to those of wild-type BlaC.

![Figure 1](https://doi.org/10.1021/acs.biochem.1c00168)

**Figure 1.** In vivo activity of BlaC mutants in E. coli. Cultures of E. coli expressing the genes for wild-type BlaC or variants A55E, G132S, D172N, G269S, A55E/G132S, and D172N/G269S were spotted on a plate containing 10 μg/mL ampicillin and 8 μg/mL sulbactam. BlaC S70A cannot hydrolyze ampicillin and is used as a negative control. The two panels are pictures of details of a single LB-agar plate placed adjacently for easy comparability of the mutants.

![Figure 2](https://doi.org/10.1021/acs.biochem.1c00168)

**Figure 2.** BlaC mutants are well-folded and stable. (A) Circular dichroism spectra measured for BlaC mutants. (B) Thermal unfolding of BlaC mutants in the presence of SYPRO Orange. Each graph shows the normalized average of six measurements.
D172N mutation causes more prominent changes in the protein (Figure 5), both around the site of mutation and in the active site. Average CSPs of >0.5 ppm were observed for the amides of residues in the Ω-loop, including Glu166, which is involved in catalysis.\(^4,43\) The data for BlaC G132S show a major influence of the amino acid substitution on the chemical environment of the backbone amides. CSPs are dispersed throughout the entire protein, with major changes in the active site and around the loop that contains the mutation. Gly132 is part of the BlaC SDG loop that is a conserved SDN loop in other class A β-lactamases. This loop has been shown to play a vital role in the inhibition of BlaC by clavulanic acid, and the introduction of an asparagine on that position allows BlaC to hydrolyze this inhibitor more efficiently.\(^42\)

The crystal structures of BlaC variants A55E, G132S, and D172N were determined to obtain a view of the changes that these mutations cause in the structure. The overall structures are very similar to that of wild-type BlaC with average Cα root-mean-square deviations of 0.29, 0.33, and 0.32 Å, respectively. In the A55E mutant, the γ-carboxy group of Glu55 adds an extra negative charge on the surface of the protein. In the crystal lattice, the γ-carboxyl of Glu55 engages in a hydrogen bond with the symmetry-related side chain of Arg277; notably, the lattice of the A55E mutant deviates from the commonly observed primitive orthorhombic lattice observed for other structures, crystallizing in a closely related but primitive monoclinic lattice, presumably largely because of this mutated

### Table 2. Kinetic Parameters for the Hydrolysis of Nitrocefin and Ampicillin\(^a\)

| BlaC  | \(k_{\text{cat}}\) (SD) (×10^5 s\(^{-1}\)) | \(K_M\) (SD) (×10^2 μM) | \(k_{\text{cat}}/K_M\) (SD) | \(k_{\text{cat}}\) (SD) (s\(^{-1}\)) | \(K_M\) (SD) (×10^2 μM) | \(k_{\text{cat}}/K_M\) (SD) |
|-------|---------------------------------------|------------------------|------------------|------------------------|------------------------|------------------|
| WT    | 2.2 (0.2)                              | 5.6 (0.7)              | 3.9 (0.6)        | 2.1 (0.1)              | 1.3 (0.2)              | 0.17 (0.02)      |
| A55E  | 1.8 (0.2)                              | 3.9 (0.5)              | 4.7 (0.7)        | 2.1 (0.2)              | 0.89 (0.09)            | 0.24 (0.03)      |
| G132S | —                                     | —                      | 0.76 (0.07)*     | 1.7 (0.3)              | 2.7 (1)                | 0.071 (0.04)     |
| D172N | 1.6 (0.2)                              | 4.8 (1)                | 3.5 (0.9)        | 4.5 (1)                | 4.3 (0.7)              | 0.10 (0.03)      |
| G269S | 2.7 (0.4)                              | 5.5 (1)                | 5.0 (1)          | 1.7 (0.4)              | 0.8 (0.2)              | 0.22 (0.09)      |

\(^a\)Nitrocefin measurements for BlaC D172N were performed in duplicate, and all others in triplicate. The reactions were performed in 100 mM NaPi (pH 6.4) at 25 °C. \(^b\)Errors represent the propagated standard deviation. \(^*\)K_M \(\gg\) [S], and \(k_{\text{cat}}/K_M\) was determined from \(v_0/[S]\).

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**Figure 3.** Hydrolyzed nitrocefin in the absence or presence of sulbactam and BlaC after 15 min at 25 °C. Measurements were performed in duplicate in the presence of 125 μM nitrocefin and 2 nM BlaC. The error bars represent one standard deviation.

**Figure 4.** Effect of sulbactam on the hydrolysis of nitrocefin for (A) wild-type BlaC and (B) BlaC G132S. Green lines represent experimental data, and black lines represent fitted values according to model 3. The data were recorded at 25 °C in the presence of 63 μM nitrocefin.
side chain and the new hydrogen bond. The γ-carboxy group also makes three hydrogen bonds involving water molecules.

The changes for D172N are less obvious, as the side chain of asparagine occupies the same space as the aspartic acid in the wild-type protein. The carboxamide group of Asn172 forms two highly favorable hydrogen bonding interactions with the side chain carboxyl of Asp179 and the carbonyl of the peptide bond between residues 178 and 179. These favorable interactions not observed for wild-type BlaC stabilize the 171−180 loop and are likely reflected in the increased thermostability of the D172N mutant.

In the G132S mutant, the side chain moiety of Ser104 is forced away by the side chain of Ser132 (Figure 6A). The side chain of Ser104 is now turned toward the protein surface, and the carbonyl oxygen of its peptide bond with Ile105 engages in a hydrogen bond with the newly introduced hydroxyl group of Ser132 (Figure 6B). This hydrogen bond causes the peptide bond between residues 104 and 105 to assume a cis conformation. A similar effect has been described for the G132N mutation and is unique in the available structures of BlaC enzymes. In the structure of the mutant with the trans-enamine adduct of sulbactam, the different positioning of the residues mediated by the G132S mutation as compared to that in wild-type BlaC is maintained, allowing the hydroxyl of Ser104 to form a hydrogen bond with one of the oxygens of the sulbactam sulfate moiety, not observed in the adduct with wild-type BlaC (PDB entry 6H2K) and BlaC G132S (blue, PDB entry 7A72).

Figure 5. Average CSPs of (A) BlaC G132S and (B) BlaC D172N plotted on the crystal structure of wild-type BlaC (PDB entry 5NJ2). Backbone amides with CSPs of greater than 0.025, 0.05, and 0.1 ppm are colored yellow, orange, and red, respectively; those with no or small CSPs are colored blue, and the ones for which no data are available are colored gray. Mutation sites are indicated, and the side chains of active site residues Ser70, Lys73, and Glu166 are represented as sticks.

Figure 6. Crystal structures of BlaC variants. (A) Superposition of the structures of BlaC G132S (salmon, PDB entry 7A71) and the wild type (gray, PDB entry 5OYO) showing the different orientation of S104 and the active site residues in sticks. (B) Overlay of the structures of wild-type BlaC (gray, PDB entry 5OYO) and BlaC G132S (salmon, PDB entry 7A71), showing the trans and cis peptide bond between residues 104 and 105 in the former and latter. (C) Superposition of the structures with the sulbactam adducts of wild-type BlaC (green, PDB entry 6H2K) and BlaC G132S (blue, PDB entry 7A72).


**DISCUSSION**

A laboratory evolution experiment yielded BlaC variants with several amino acid substitutions that causes enhanced *in vivo* resistance against the inhibitor sulbactam. The increased sulbactam resistance *in vivo* is not observed in a nitrocefin activity test *in vitro* for BlaC AS5E, D172N, and G269S. Mutants that exhibit reduced affinity or faster hydrolysis of the inhibitor will be picked up in the *in vivo* assay, but selection can also be caused by other factors. The ampicillin concentration was kept low, so *E. coli* clones with mutant enzymes that convert ampicillin at a higher rate than wild-type BlaC would be less hindered by sulbactam, enabling growth on selection plates. The D172N mutant showed such an increased ampicillin conversion rate, though the specificity constant \(K_{\text{cat}}/K_{\text{M}}\) was not higher. Differences in the amount of active protein between the mutants, caused by differences in mRNA stability, translation, protein folding, stability, or translocation, could offer another explanation for enhanced resistance against sulbactam *in vivo*. For BlaC D172N, the \(T_m\) is 3 °C higher than that for wild-type BlaC, hinting at increased stability, which we attribute to the increased stability of the \(\omega\)-loop caused by interactions of Asn172 with residues 178 and 179. Substitution of Gly with Ser at position 132 decreases the overall catalytic efficiency of the enzyme and at the same time makes it less susceptible to inhibition by sulbactam. Residue 132 is a Gly in BlaC but an Asn in 95% of class A \(\beta\)-lactamases and has been found to be a serine in only two other class A \(\beta\)-lactamases.\(^{45-47}\) Having a Gly at this position opens up the active site and therefore, purportedly, contributes to the ability of BlaC to convert a broad spectrum of substrates.\(^{42}\) Ser104 assumes a conformation that resembles the one observed for residue 104 in TEM-1 or SHV-1 (PDB entry 1M40\(^{48}\) or 1SHV,\(^{49}\) respectively), in which residue 104 is a Glu or Asp, respectively. The change in the positioning of the loop and the cis peptide bond configuration are induced by the side chain at position 132, because the loop would cause steric collisions with Ser104, were it to take the same position as in wild-type BlaC. These changes affect the entire active site as indicated by the CSPs observed for BlaC G132S. The key structural difference appears to be the position of Ile105, previously termed the gatekeeper residue.\(^{51}\) In the structure of resting state wild-type BlaC, Ile105 partly covers the entrance to the active site, whereas in the adduct with sulbactam, it rotates away, avoiding a steric clash with the adduct.\(^{20}\) In the resting state structure of BlaC G132S, the side chain of Ile105 has moved 1.6 Å, blocking the active side even more, which is caused by the backbone rearrangement due to the introduction of the Ser at position 132 (Figure 6A). In the structure of the mutant with the sulbactam adduct, Ile105 keeps the same position, suggesting that it is more stable in this position in the mutant than in wild-type BlaC. Interestingly, the backbone rearrangement leads to better interactions with the adduct, including a hydrogen bond from Ser104 to the sulfonyl group. This observation seems to be in contrast with the weakened inhibition by sulbactam. However, the structure of sulbactam is very different from that of the adduct. The latter is an elongated molecule without rings, whereas sulbactam has two ring structures, which place the sulfonyl group in a very different position in the active site. The reduced inhibitory effect of sulbactam can be explained by decreased access to Ser70, caused by the rearrangement of the loop containing Ser104 and Ile105 (Figure 7), and is also apparent from the increased \(K_m\) value. Similarly, reduced access of substrate explains the increased \(K_M\) values for nitrocefin and ampicillin (Table 2).

Soroka and colleagues previously reported that substituting residue 132 with asparagine, thus restoring the SDN motif as present in most \(\beta\)-lactamases, results in an enzyme that can hydrolyze clavulanic acid yet is more sensitive to avibactam.\(^{42,50}\) Introducing a glycine in class A \(\beta\)-lactamases that have the SDN motif, BlaMab and KPC-2, improves inhibition by clavulanic acid.\(^{50,51}\) Interestingly, while we found BlaC G132S is also more sensitive to avibactam, the mutation does not lower resistance to clavulanic acid when compared to that of the wild type (Figure S13). Elings et al. found that BlaC G132N exists in two forms in solution that are in exchange \(\sim\)88 s\(^{-1}\).\(^{44}\) Clearly, the residue at position 132 is critical for the substrate and inhibitor specificity of BlaC. The research question of this work was whether additional resistance against sulbactam could readily be obtained. A single-point mutation is already able to increase resistance. However, our study and the work of Soroka et al.\(^{42,50}\) demonstrate that mutation of critical residues often comes at the cost of activity loss or larger sensitivity to other inhibitors, suggesting that judicious choice of inhibitor combinations could slow evolutionary adaptation and resistance of Mtb against a \(\beta\)-lactam/inhibitor treatment. It should be noted...
though that bacteria of the Mycobacteriaceae family have a cell wall that differs significantly from the cell wall of Enterobacteriaceae, having high lipid and mycolic acid content, so penetration of the compound into the periplasm can differ between these types of bacteria. Our results relate to the inherent catalytic properties of BlaC, but the efficacy of antibiotics and inhibitors is also dependent on the concentration that can be reached at the point of action in vivo.

ASSOCIATED CONTENT

Supporting Information

The Supporting Information is available free of charge at https://pubs.acs.org/doi/10.1021/acs.biochem.1c00168.

Primers used to introduce mutations into blaC (Table S1), data collection and refinement statistics of crystal structures (Table S2), nonsynonymous and synonymous mutations found during screenings (Table S3), melting temperatures of BlaC mutants (Table S4), kinetic parameters for sulbactam inhibition (Table S5), sequences of BlaC variants (Figures S1 and S2), in vivo activity of Mtb BlaC mutants in E. coli (Figure S3), Michaelis–Menten curves of BlaC mutants for nitrocefin and ampicillin (Figure S4), data showing hydrolysis of nitrocefin after incubation of BlaC with sulbactam at 37 °C (Figure S5), in vivo ampicillin conversion activity of Mtb BlaC mutants in E. coli (Figure S6), TROSY-HSQC spectra of BlaC mutants (Figures S7–S10), chemical shift perturbation of BlaC ASSE and BlaC G269S plotted on the crystal structure (Figure S11), bar chart of the chemical shift perturbation per residue for the backbone amides of the BlaC mutants (Figure S12), and activity of BlaC G132S in the presence of avibactam and clavulanic acid (Figure S13) (PDF)

Accession Codes

Wild-type BlaC, P9WKD3.

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Notes

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