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Understanding the longevity of the β -lactam antibiotics and of antibiotic/ β -lactamase inhibitor combinations

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ABSTRACT

Microbial resistance necessitates the search for new targets and new antibiotics. However, it is likely that resistance problems will eventually threaten these new products and it may, therefore, be instructive to review the successful employment of β -lactam antibiotic/ β -lactamase inhibitor combinations to combat penicillin resistance. These combination drugs have proven successful for more than two decades, with inhibitor resistance still being relatively rare. The β -lactamase inhibitors are mechanism-based irreversible inactivators. The ability of the inhibitors to avoid resistance may be due to the structural similarities between the substrate and inhibitor.

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1. Introduction

The discovery of the β -lactam antibiotics in the early twentieth century represented a turning point in the struggle against pathogenic bacteria. These relatively inexpensive and highly efficient semi-synthetic products have been the mainstay of anti-infective chemotherapy for the past sixty years. However, the appearance and accelerating evolution of hydrolytic enzymes, the β -lactamases, now threaten these drugs, thus necessitating the genomic search for new bacterial targets and new classes of drugs. However, as we undertake this quest, it may be useful to review the successful countermeasures that have been so effective in the β -lactam antibiotic arena. Such strategies may be instructive in our efforts to forestall resistance to future antibiotic classes.

The two most common forms of resistance to β -lactam antibiotics are the production of (one or more) β -lactamases and the development of an altered target PBP (penicillin-binding-protein), such as PBP2a of methicillin-resistant

Staphylococcus aureus (MRSA). Despite recent structural information on PBP2a [1], the former are the better understood (from a structural and mechanistic perspective) and more commonly observed of the resistance mechanisms, and will thus be the focus of this review. There are four different classes of β -lactamases, A through D. Classes A, C, and D β -lactamases are serine enzymes, while class B are zinc metalloenzymes. Their origin is ancient, presumably evolved to combat β -lactams of natural origin, but their development has undoubtedly been influenced by clinical administration of β -lactam antibiotics. The serine β -lactamases are believed to have evolved from the antibiotic target PBP's [2–4], through inclusion of water and other requisite hydrolytic machinery in the active site. β -lactamases are capable of hydrolyzing only activated carboxylic acid derivatives (e.g. structurally appropriate β -lactams and esters) while leaving more stabilized amide bonds unscathed. The precise structural and mechanistic reason for this selectivity is the subject of some speculation. Ambler [5] first proposed this sequence based

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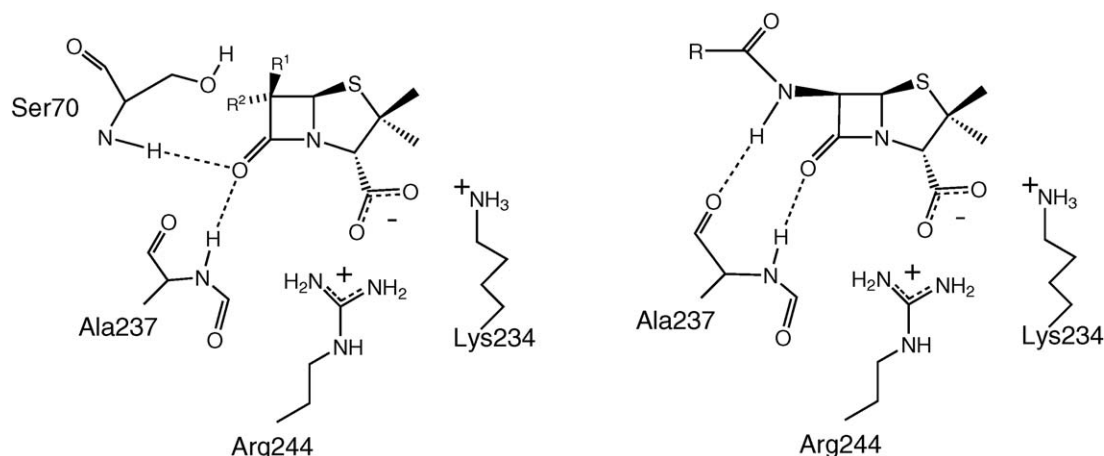


Fig. 1 – Simplified visualization of key interactions in the binding site of TEM-1 β -lactamase (two structures shown for clarity).

classification scheme, which initially involved dividing the known β -lactamases into the class A serine- β -lactamases and into class B metallo- β -lactamases, based on the then available sequences of only four enzymes. Within a few years, two new classes of serine β -lactamases, the class C cephalosporinases [6] and then the class D oxacillinases [7] were identified. Class A enzymes are usually plasmid-mediated, are known as penicillinases (since they tend to prefer penicillins over cephalosporins as substrates), and representative enzymes include (among others) TEM, SHV, and PC subclasses. Some class A β -lactamases have evolved to accept expanded spectrum cephalosporins as substrates and have become known as extended spectrum β -lactamases (ESBL's). Class B metallo- β -lactamases typically have an extremely broad substrate specificity, that includes not only penicillins and cephalosporins, but also the (usually β -lactamase resistant) carbapenems. These zinc metalloenzymes are typified by (among others) the IMP and VIM β -lactamases. Class C serine β -lactamases tend to be chromosomal (although several plasmid-borne class C β -lactamases have now been observed), are often referred to as AmpC β -lactamases, and tend to prefer cephalosporins as substrates. Class D β -lactamases have an unusually high substrate preference for oxacillin and related penicillins are thus referred to as oxacillinases. Functional classification schemes are also utilized [8].

One reasonably effective strategy for countering β -lactamase-mediated penicillin resistance has been the co-administration of the β -lactam antibiotic together with an inhibitor of one or more of the hydrolytic β -lactamase enzymes [9–18]. Current commercial inhibitors are effective only against the class A serine β -lactamases. Countering recent pharmaceutical product trends toward extremely tight binding reversible inhibitors, the known β -lactamase inhibitors are mechanism-based irreversible inactivators. Structurally, the relative successfulness of this approach probably stems from the resemblance of the inhibitors to the natural substrates themselves, thus making it difficult for the enzymes to mutate non-recognition of the inhibitors and still retain their full hydrolytic capability [19]. It should be noted that current commercial inhibitors share the bicyclic fused four-five membered ring system of the penicillins and also sp^3 -

hybridized nature of the C3 carbon, thus potentially explaining their preferential inactivation of class A penicillinases.

Key recognition elements of class A serine β -lactamases are illustrated in Fig. 1, which depicts the TEM-1 β -lactamase active site with a generic substrate. Such elements include a positively charged pocket to recognize the carboxylate, an oxyanion hole to recognize the β -lactam carbonyl oxygen and to accelerate formation of the tetrahedral intermediate, and well as a key hydrogen bonding interaction with the C6 acylamino group.

The serine β -lactamases operate via a multistep process involving the formation and hydrolytic destruction of an intermediate acyl-enzyme. Most β -lactam inhibitors of the serine β -lactamases function through the formation of a hydrolytically stabilized ester. Depending on the specific inhibitor, this acyl-enzyme may be stabilized electronically (i.e., by favorable resonance interactions that improve the stability of the acyl-enzyme ester bond to the serine), stabilized by covalently bonding to a second nucleophilic residue in the active site, or stabilized due to its position in the active site (e.g., the carbonyl of the bound inhibitor may be removed from the oxyanion hole and/or the hydrolytic water). This last type of stabilization may result from movement of the inhibitor or from a conformational change in the enzyme itself. β -lactam-containing compounds that inactivate serine β -lactamases are typically also substrates of the enzyme, with partitioning of the two processes (turnover and inhibition) at the acyl enzyme stage. For any particular inhibitor, the substrate/inhibitor (turnover) ratio can range from below 10 to nearly 10,000.

2. Commercial β -lactamase inhibitors

Current commercial inhibitors include clavulanic acid, sulbactam and tazobactam, shown below which are administered in the antibiotic/inhibitor combinations: AugmentinTM (amoxicillin/clavulanic acid) [20,21], TimentinTM (ticarcillin/clavulanic acid) [22], UnasynTM (ampicillin/sulbactam) [23], and ZosynTM (piperacillin/tazobactam) [24] (Fig. 2). In particular, these commercial combinations are effective against

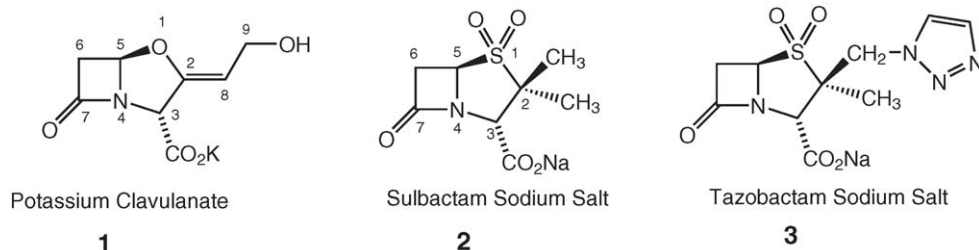


Fig. 2 – Current commercial β -lactamase inhibitors.

susceptible organisms expressing Ambler class A enzymes [25], which remain the most commonly encountered. These inhibitors are all unsubstituted at C6 and have related inhibitory mechanisms.

2.1. Clavulanic acid

The amoxicillin/clavulanate combination represents a broad-spectrum antibacterial, that has been in use for more than 20 years and continues to be widely utilized. The mechanism of inactivation of β -lactamases by clavulanic acid was initially studied by the Knowles group [26,27], and further refined by the Mobashery group [28]. Initial crystallographic studies were performed, on the class A PC1 β -lactamase from *Staphylococcus aureus*, by Chen and Herzberg [29], and ESIMS studies were performed by the Schofield group [30]. A scheme for this inhibition is shown in Scheme 1.

2.2. Sulbactam

Knowles also studied sulbactam [31] and proposed a nearly identical inhibitory mechanism, using the sulfone sulfur as a (sulfinate) leaving group in place of the enol ether oxygen of clavulanate as shown. Mobashery added data solidifying and elaborating this mechanism [32]. One should note the similarities between Schemes 1 and 2, in particular the formation of two structurally related iminium ions 4 and 15, respectively, as well as their partitioning into transient (7 and 16, respectively) and irreversibly inhibited (11 and 18, respectively) species.

2.3. Tazobactam

Tazobactam is structurally related to sulbactam, the sole structural difference being the addition of a triazole group on the C2 β -methyl group. This modification improves activity against several β -lactamases (IC_{50} 2–100-fold better) and microorganisms (MIC values 4–64-fold lower). The partition ratios, against representative class A β -lactamases for clavulanate, sulbactam and tazobactam are 160, 10,000, and 125, respectively. Tazobactam also has modest activity against some class C β -lactamases, but not enough to be clinically useful. Crystallographic [33,34] and ESIMS [35,36] studies support a mechanism closely related to that of sulbactam and clavulanic acid.

A number of groups have continued to report improvements in β -lactamase inhibitory activity by substitution at (penicillin) C2' [37,38]. Buynak et al. [39] have recently reported

a C3 homologue of sulbactam with improved activity against class C β -lactamases.

3. Carbapenems

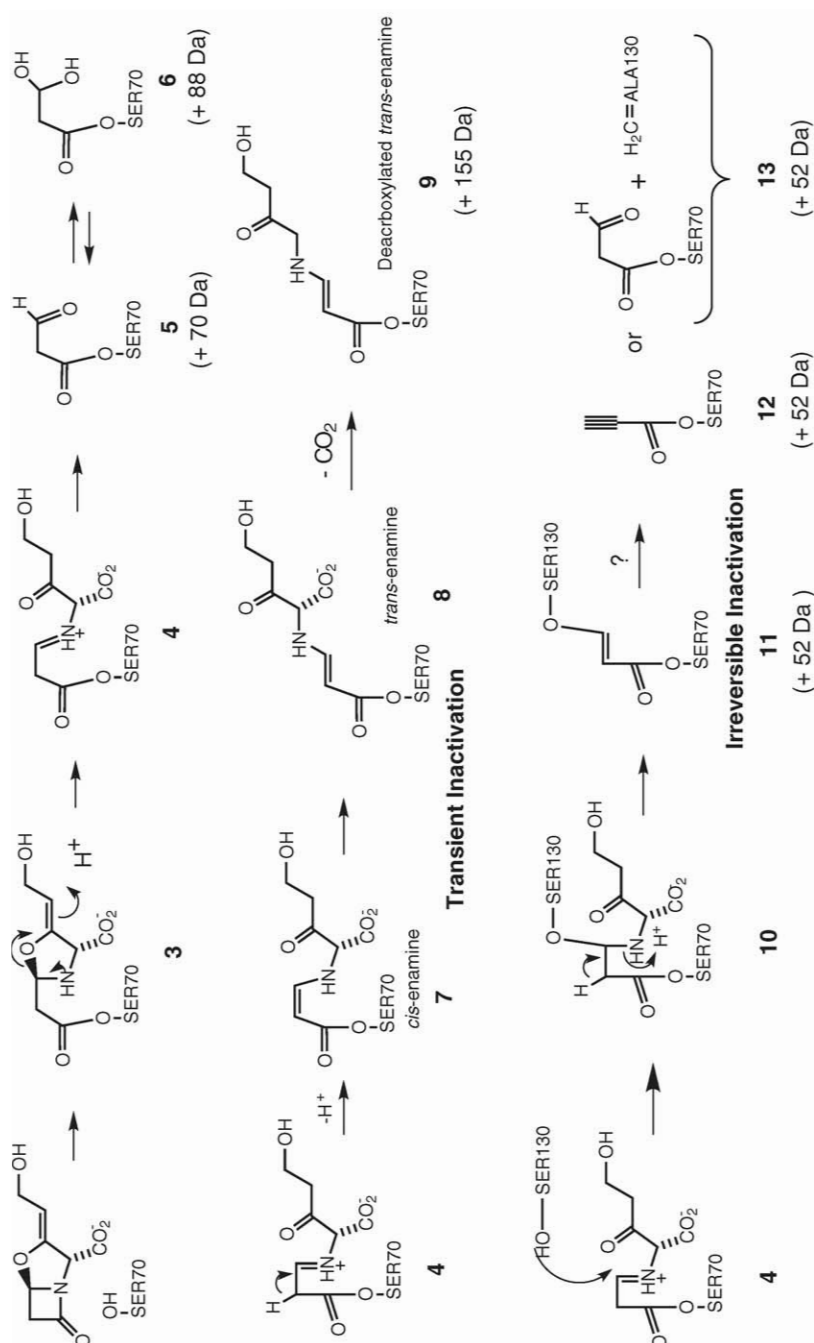
While most β -lactamase inhibitors lack significant antibacterial activity, the carbapenems, having a C6 hydroxyethyl side chain, are recognized as both broad-spectrum antibiotics and also as either very poor substrates or as competitive inhibitors of many serine β -lactamases. Commercial carbapenems include imipenem (19) /cilastatin (PrimaxinTM), Panipenem (20), Biapenem (21), Meropenem (22) (MerremTM), and Ertapenem (23) (InvanzTM) (Fig. 3). The cilastatin is included in the imipenem mixture as an inhibitor of the renal metabolic enzyme, dehydropeptidase (DHP-1), whereas the C1 β -methyl group of later carbapenems renders the molecules poorer substrates of DHP.

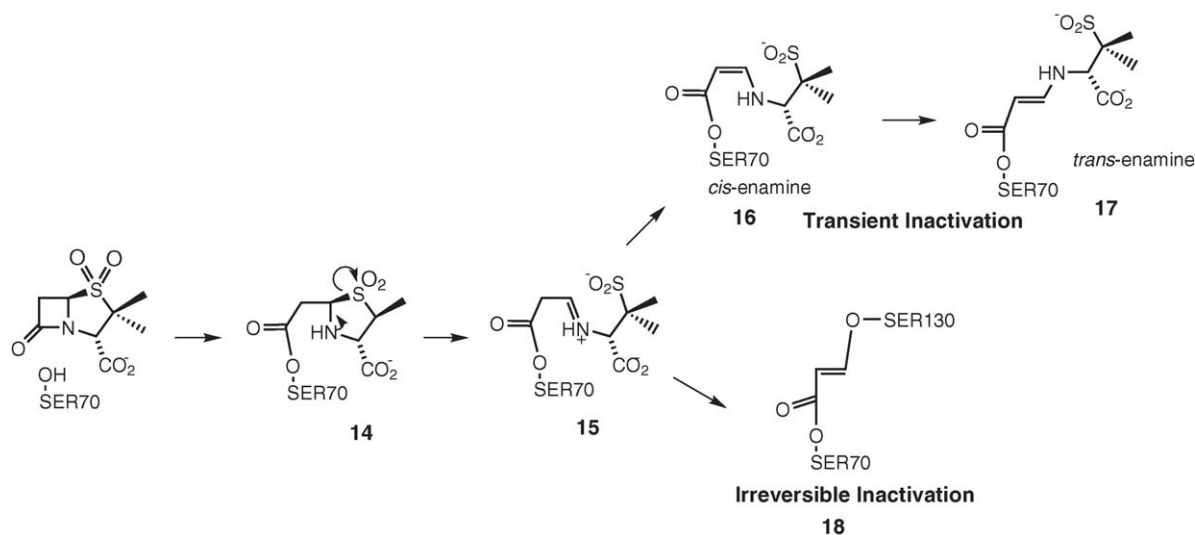
The carbapenems are regarded as the β -lactam class with the broadest spectrum of antibacterial activity, with resistance being relatively rare. These antibiotics are also inhibitors (or very slow substrates [40]) of most serine β -lactamases. However, carbapenems are substrates of class B metallo- β -lactamases [41,42] and also substrates of a few specific serine β -lactamases [43,44]. All carbapenems of current commercial interest retain the C6 α -hydroxyethyl side chain of thienamycin.

Kinetic investigations [40,45–48] and three crystallographic studies, including complexes of imipenem with TEM-1 (class A) [49] and AmpC (class C) [50], and a complex of meropenem with OXA-13 (class D) [51], have been published. In both imipenem structures, the reason for inhibition appears to be that the carbonyl oxygen of the resultant acyl-enzyme has been displaced from the oxyanion hole. In the case of the meropenem structure with the class D oxacillinase, the carbonyl oxygen is in the oxyanion hole, but a conformational change of the enzyme has displaced the hydrolytic water to a distance of nearly 5 Å from the carbonyl carbon. The C6 α -hydroxyalkyl side chain may play a role in the positional movements that occur subsequent to enzyme acylation.

4. 6-(Hydroxyalkyl)penicillanates

Given the potent dual (antibiotic/inhibitor) activity of the carbapenems, a number of researchers have investigated incorporating similar C6 functionality into the penicillins and

Scheme 1 – Mechanism for inhibition of class A β -lactamases by clavulanic acid.



Scheme 2 – Mechanism for the inactivation of class A β -lactamases by sulbactam.

their corresponding sulfones. Early researchers discovered that C6 hydroxyalkyl derivatives, such as 24, were stabilized toward β -lactamase, with the loss of some antibacterial activity [52,53]. DiNinno et al., working at Merck, first prepared simple 6-(hydroxyethyl)penicillanates 25 (lacking the acylamino group; the hydroxyethyl group being analogous to the carbapenem side chain) and showed these compounds to be of modest antibacterial activity [54]. Subsequently, a number of companies simultaneously filed patents describing the generation of C6 hydroxyalkyl penicillanates, such as sulfide 26, and sulfone 27, and claimed their usefulness as inhibitors of β -lactamase [55,56] (Fig. 4). The Pfizer group attempted to further develop benzimidazole-substituted (hydroxymethyl)penicillanates, such as 28, which display both antibacterial activity (against Gram-positive and a few Gram-negative strains) as well as β -lactamase inhibitory activity [57]. Recently, Mobashery designed [58] and, with Samama [59], provided structures of the class A TEM-1 β -lactamase from *E. coli* inhibited with the C6 α -hydroxymethylpenam 29, the NMC-A class A carbapene-

nemase inhibited with the C6 α -[(1'-hydroxy-1'-methyl)ethyl]penam 30 [60] (the corresponding hydroxymethyl analog was a substrate) and the class D Oxa-10 β -lactamase inhibited with the C6 α -[(1'-hydroxy-1'-methyl)ethyl]penam 31 [61]. The Mobashery group has been able to utilize the hydroxyalkylpenicillanates as probes to determine the direction of addition of water to the acyl-enzyme [62]. Wyeth researchers evaluated the epimeric C6-(hydroxymethyl)penicillanates, both as sulfides and as sulfones, presenting data that the best inhibitors in this series were the sulfones (e.g., C6 β -(hydroxymethyl)penicillin sulfone 27 exhibited an IC_{50} value of 8 nM against TEM-1) [63]. They also investigated the potential for the inhibitory activity to be modulated through manipulation of the C2 substituent, with their most active molecule being the acrylonitrile 32 [64]. Recently, the Buynak group has prepared the corresponding mercaptomethyl analogs 33 and has demonstrated their activity as dual inhibitors of both serine- β -lactamases and also certain class B metallo- β -lactamases [65].

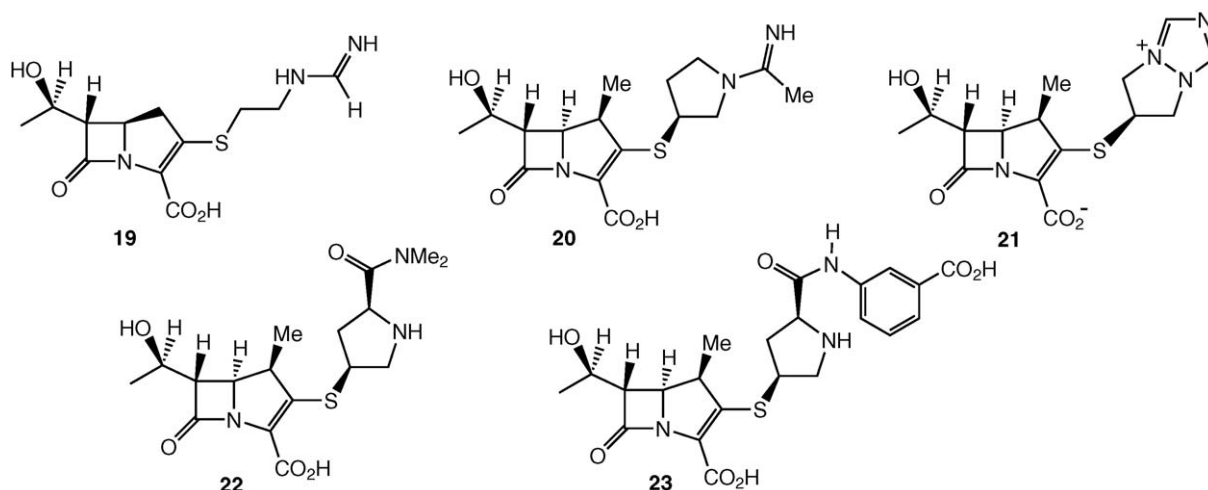


Fig. 3 – Commercial carbapenem antibiotics.

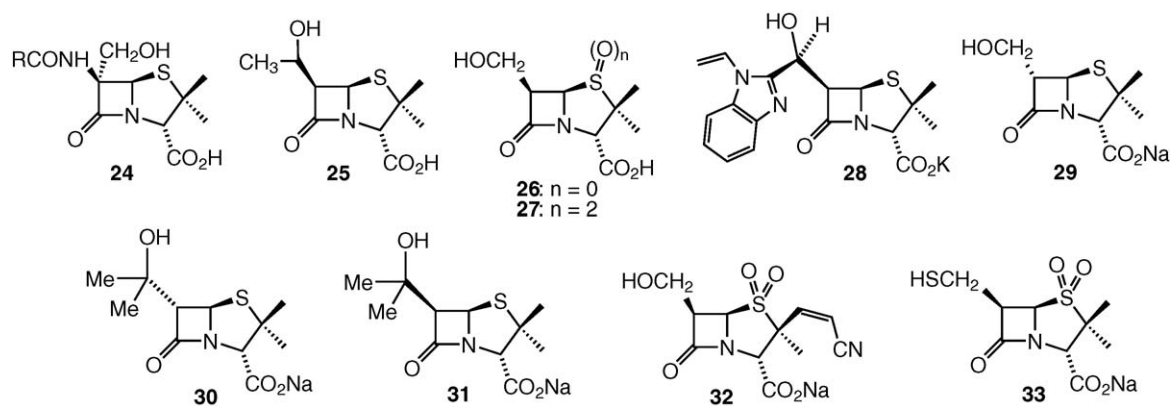


Fig. 4 – 6-(Hydroxyalkyl)penicillanates and corresponding sulfones.

5. 6-(Hydroxyalkyl)penems

The penems were designed to be a cross between the fused 4- and 5-membered-ring system of the penicillins and the cephalosporins, which have an endocyclic double bond conjugated to the nitrogen [66] (Fig. 5). In terms of structure–activity relationships, penems most closely parallel carbapenems. Further reinforcement of this comparison, is evident in the identical 6S, 8R stereochemistry of the hydroxyethyl side chain, which, as in the carbapenems, was optimized for antibacterial activity [67]. Penems possess both antimicrobial activity and β -lactamase stability. However, several studies also document their β -lactamase inhibitory activity, which seems to be specific for class C cephalosporinases [68–70]. The precise inhibitory mechanism is unknown. Faropenem dioxylate is scheduled (2006) to become the first oral penem available outside Japan.

6. N-sulfonyl- and N-sulfonyloxy- β -lactams

Monocyclic, N-sulfonated- β -lactams, **38**, were first reported as antibacterials in a 1979 Takeda patent [71], and such compounds were the subject of an article from Takeda and an article from Squibb (where the name ‘monobactam’ was suggested), both published in 1981 [72,73] (Fig. 6). Squibb developed this series into the commercial product, aztreonam, **39**. Aztreonam is highly active against Gram-negative aerobic bacteria, but relatively inactive against Gram-positive bacteria or Gram-negative anaerobes [74,75]. It has high affinity for PBP 3. While initially discovered monobactams had poor affinities for class A β -lactamases, and were micromolar inhibitors of

class C β -lactamases, aztreonam was described as forming a covalent complex with the class C P99 enzyme [76] and has been characterized as ‘an efficient transient inactivator’ of class C β -lactamases [77]. More recently, Syn 2190, **40**, a monobactam which is devoid of antibacterial activity, but highly efficient as a selective inhibitor of class C β -lactamases, has been described [78–82].

A structurally related series of compounds are the mono-sulfactams, represented by tigemonam (**41**). These compounds are synthetic in origin and were designed, synthesized, and evaluated at Squibb [82,83]. Structure–activity relationships demonstrate the importance of the substituent at C4 to β -lactamase stability and inhibition [84]. Tigemonam has a spectrum of activity similar to that of aztreonam, but is orally bioavailable. This monosulfactam is resistant to most β -lactamases, and is reported to be an inhibitor of the class C enzymes, such as *Enterobacter cloacae*, P99 [85].

Recently, new series of bridged monobactams [86,87] and bridged sulfactams [88] have been developed as β -lactamase inhibitors by Hoffmann-La Roche. Monobactam Ro 48-1256, **42**, had no antibacterial activity, but acted as a selective inhibitor of class C β -lactamases and displayed synergy with ceftazidime and piperacillin against strains derepressed for the AmpC enzyme [89]. Mechanistically, these compounds were designed to block access of the active site water to the intermediate acyl-enzyme [87]. Previously, the crystal structure of aztreonam bound to the class C β -lactamase from *Citrobacter freundii* [90] indicated that, subsequent to formation of the acyl-enzyme, a 70° rotation about the C3–C4 bond had to occur in order for the hydrolytic water to have access to the ester linkage. (The C4 α -methyl group of aztreonam is believed

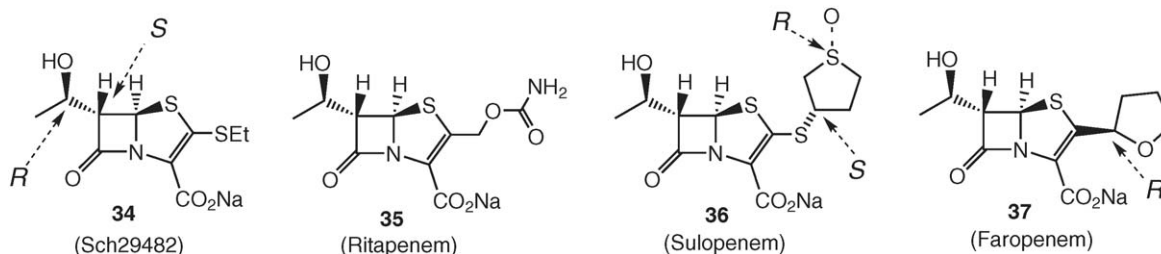


Fig. 5 – 6-(Hydroxyalkyl)penems and 6-(hydroxyalkyl)thioclavams.

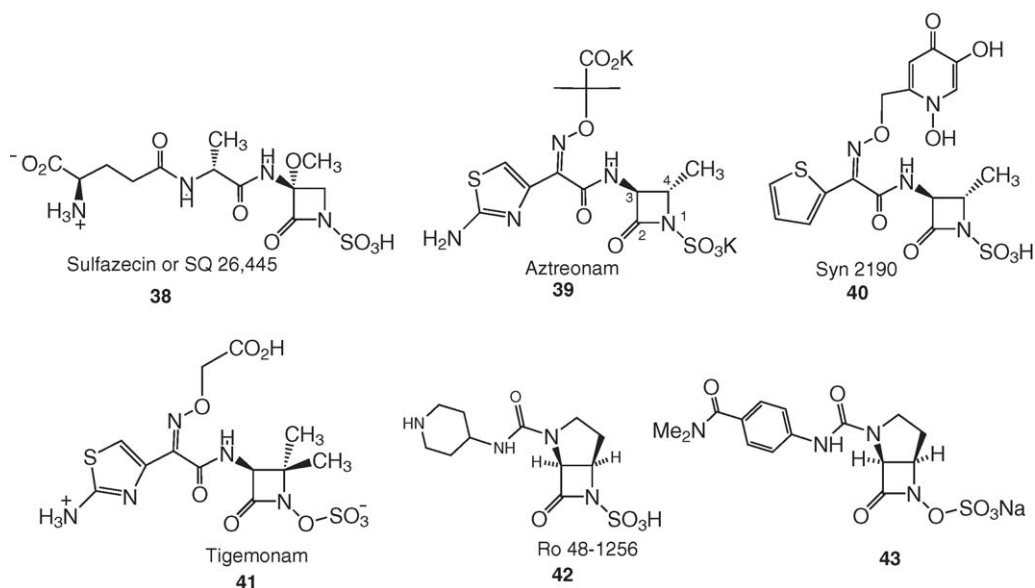


Fig. 6 – Monocyclic N -sulfated- β -lactams (monobactams) and N -sulfonyloxy- β -lactams (monosulfactams).

to interfere with the requisite rotation through a steric interaction with the aryl ring of Tyr150.) By structurally prohibiting this rotation through construction of a bridge between C3 and C4 (i.e., the five-membered ring), they were able to stabilize the acyl-enzyme toward attack of the hydrolytic water and inhibit the enzyme. The corresponding bridged sulfactams **43**, were also potent inhibitors, of both class C as well as class A β -lactamases. Analysis of the inhibition indicated that the inhibition by the bridged sulfactams was due to a high initial affinity for the enzymes and a high rate of acylation. However, the deacylation rate of the sulfactams was also high, rendering the overall synergy with ceftriaxone relatively weak, relative to the corresponding monobactams.

7. Inhibitor resistance

Given the frequency of clinical administration of antibiotic/inhibitor combinations, as well as the high reproduction rate and mutational frequency of bacteria, it is not surprising that inhibitor resistance has developed. The term 'inhibitor-resistant' usually refers to resistance to amoxicillin/clavulanate and does not necessarily imply resistance to other inhibitors. Even the (mechanistically) related penicillin sulfones are observed to have resistance profiles somewhat different from that of clavulanate [91] and no data is currently available on the effect of non-commercial β -lactamase inhibitors on 'inhibitor-resistant' enzymes. Such resistance may occur through hyperproduction of unmodified β -lactamase [92–94], by modification of outer membrane proteins [95], as well as through production of a mutant form of the β -lactamase which is more resilient toward the commercial inhibitors [96–99]. It is this last form that will be discussed.

Since commercial inhibitors target the clinically prevalent, plasmid-mediated class A β -lactamases, it is logical that the

inhibitor-resistant enzymes are also of class A, specifically the inhibitor resistant TEM β -lactamases (IRT's), as well as resistant SHV β -lactamases, close structural relatives of TEM. The frequency of IRT production among resistant strains is a matter of current study. A 1993 French study examined nearly 3000 *E. coli* isolates and found the amoxicillin-clavulanate resistance rate to be 25.0% (hospital) and 10.0% (community). Of these resistant strains, 27.5% (hospital) and 45.0% (community) showed an unusual β -lactam resistance pattern, suggestive of IRT production. Thus, they estimate that the overall IRT production rate, among *E. coli* to be around 4.9%, indicating the IRT producing strains may be beginning to make an important contribution [100]. A recent U.S. study found the overall incidence of amoxicillin/clavulanate resistance was 3–5%, but although IRT-production was detected in some of these resistant strains, the precise frequency of such IRT production was not determined [101]. A study of clinical *E. coli* strains from a Spanish hospital showed that about 7% had reduced susceptibility to amoxicillin/clavulanate, with the major cause (75% of those resistant strains) being probable overproduction of class C β -lactamase, with only approximately 5% of the amoxicillin/clavulanate-resistant strains producing IRT's (i.e., 0.35% of the total resistant strains) [102]. The overall IRT incidence may be higher than recognized, since inhibitor-resistant strains cannot be detected by routine susceptibility tests and are identified by iso-electric points and kinetic investigation of the produced β -lactamases, as well as by molecular biology techniques [103,104]. Obviously, this can lead to discrepancies in determining their current clinical significance.

Several studies of selected inhibitor-resistant enzymes were recently completed and some of these are briefly summarized. In the class A TEM β -lactamases, active site mutations leading to inhibitor resistance include single amino acid substitutions at position 69 (M69I, M69L, M69V), at position 130 (S130G), at position 244 (R244S, R244C, R244H, and R244G), at position 275 (R275L), and at position 276

(N276D). Given the structural similarity between the inhibitors and the substrates, the key mechanistic question involves determining how the enzyme is able to maintain its ability to hydrolyze the antibiotic while reducing the efficacy of inhibitors. Indeed, in most mutations, some attenuation of catalytic efficacy is observed.

The mutations of Met69 are commonly observed in inhibitor-resistant enzymes and are poorly understood mechanistically. The three mutations lead to enzymes with an approximate ten-fold increase in the apparent K_i and also an approximate ten-fold decrease in the k_{inact} toward all three commercial inhibitors (and consequent hundred-fold degradation of the inhibitory efficacy, k_{inact}/K_i) and with a comparatively less dramatic effects on either the k_{cat} or K_m of the antibiotics [105,106]. This side chain lies directly behind the oxyanion hole. Recent hypotheses include hydrophobicity and steric constraints [106], a distortion in the conformation of Ser70 [107], and a difference in the dynamic motions of the residues in the vicinity of the active site [108]. It is interesting that replacement of the methionine by less sterically demanding residues (i.e., M69A and M69G) results in an enzyme more susceptible toward inhibitors [109].

Ser130 is currently believed to play key roles in recognition of the C3 (C4) carboxylate of the penams and cepheps, respectively, providing a proton to the departing nitrogen during initial acylation of Ser70, as well as serving as the second nucleophile in irreversible inactivation (attack of the intermediate imine, resulting in double attachment to the enzyme) of the β -lactamase by commercial inhibitors, clavulanate and the penicillin sulfones. Particularly in view of this last factor, it might be anticipated that an S130G mutant would be entirely resistant to inhibitors. The fact that commercial inhibitors still have (albeit diminished) efficacy [110] against such a mutant underscores the importance of the transiently stabilized intermediates (see Scheme 2) on the in vitro inactivation of the enzyme (particularly considering the 20 min replication cycle of the bacterium). A recent structure of an S130G mutant of SHV-1, complexed with tazobactam as the cis-vinylous urethane further emphasizes this fact [111]. In a study of this SHV-1 mutant, it was found that the mutation increased the K_m for the substrate ampicillin (approx. 2-fold) and the apparent K_i values for the inhibitors (approx. 40–300-fold) [112]. The k_{cat} values for ampicillin was decreased (approx. 10-fold), while k_{inact} of the inhibitors was relatively unchanged. As a measure of efficiency, the S130G k_{cat}/K_m value for ampicillin was 3.6% that of the wild type, while the k_{inact}/K_i values for clavulanate and tazobactam, were 0.24 and 1% that of the wild type, respectively. The partition ratios for the two inhibitors were approximately the same for the wild type and the S130G mutant. Thus, the enzyme loses efficiency in the hydrolysis of ampicillin, to enjoy a larger enhancement in inhibitor resistance. In both cases, the dominating factor is the increase in the (apparent) dissociation constants for the preacylation complex of either the inhibitor or the antibiotic. Similar results were obtained in a study of a TEM 1 S130G mutant [113]. In both SHV and TEM S130G mutants, a water molecule is believed to be taking the place of Ser130 in the donation of a proton to the departing nitrogen.

The IRT data obtained thus far seem to indicate that the inhibitors, with their smaller structures and two point

recognition (i.e., C3 (C4) carboxylate and β -lactam carbonyl oxygen, via the oxyanion hole) are more susceptible to mutations affecting these two critical points than are the β -lactam antibiotics, which have additional hydrogen bonding recognition at the C6 (C7) acylamino side chain (see Fig. 1).

8. Conclusion and analysis

β -Lactam antibiotic/ β -lactamase inhibitor combinations are one of the success stories of the anti-infectives area. These drugs have been successful in circumventing the bacterial evolutionary drive toward resistance. There are still several important questions to be addressed, the most important of which remains the identification of a suitable inhibitor which can simultaneously inactivate both class A and class C serine β -lactamases. Additionally, the appearance of class B metallo- β -lactamases, and carbapenem-hydrolyzing class A enzymes now threaten the carbapenems, which represent one of the remaining generally effective β -lactam antibiotics. A key to the success of β -lactamase inhibitors has been their close structural resemblance to the substrate antibiotics themselves. Another, related, feature is the mechanism-based irreversible nature of the inactivation. It is reasonable to suggest that the prerequisite for substrate-like acylation of the enzyme improves their selectivity and that such formation of covalent bonds between the inhibitor and the target enzyme renders it still more difficult for small mutations to lessen the binding efficacy.

Pathogenic bacteria are adaptable and resourceful opponents. Our search for new antibiotics must be relentless, utilizing all available technology. However, given the historical precedent of the appearance of resistance within a few years of the introduction of the antibiotic class, it seems inevitable that the new antibiotics developed to hit novel targets will also encounter resistance. The existing bacterial 'resistome' may be more highly developed than previously recognized, including mechanisms such as efflux, permeability barriers, target modification, and drug inactivation. Bacterial cell wall machinery has proven a useful target, that, due to differences between bacterial and mammalian cells, allows the administration of a number of highly selective (i.e. non-toxic) small molecules. At the present moment, it seems likely that we will be forced to utilize the entire armamentarium of antibiotics (particularly including β -lactams) for the foreseeable future. Knowledge of previous success stories, such as the β -lactams, may assist in the design and development of new classes of drugs.

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