

β -Lactam Antibiotics: The Past, Present, and Future

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ABSTRACT In 1928, the discovery of penicillin revolutionized the field of medicine. As the first reported β -lactam antibiotic, penicillin laid the foundation for modern antibiotics. β -lactams, 4-membered cyclic amides, can be used for the prevention and treatment of bacterial infections. Since the discovery of penicillin, many β -lactams have been discovered from natural sources, and modern methodologies in chemical synthesis have powered the design for synthetic β -lactams. This is significant in supplying the continued need for novel antibiotics in the treatment of antibiotic resistant bacteria.

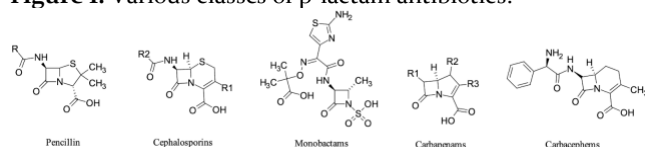
β -LACTAM-HISTORY

Penicillin, a β -lactam antibiotic, was discovered by Alexander Fleming. Fleming was growing a culture of *Staphylococcus* and observed that *Penicillium notatum*, a fungus, had contaminated the dish; a compound secreted by the fungus, later identified as penicillin, inhibited growth of the *Staphylococcus* culture. Years later, the β -lactam was isolated as the active component of penicillin, responsible for its antimicrobial activity. Today, as a result of the discovery of penicillin and the reactivity of β -lactams, many antibiotics contain the β -lactam moiety.[1]

Since the initial discovery of penicillin, others have sought to synthesize, purify, and characterize it. Penicillin continued to advance throughout the twentieth century. Specifically, its antiseptic capabilities, initially discovered by N.G. Heatley using mice were researched and developed.[2] In 1941 during World War II, penicillin's antibiotic capabilities proved to be crucial as it saved millions of lives. Without effective antibiotic treatment, people were dying because of common bacterial infections. At this time, Florey and Heatley enlisted the help of the U.S. government to take on the mass production of penicillin, which was made possible with deep-fermentation tanks.[3]

Following the discovery of penicillin, other β -lactam-containing natural products including penicillin derivatives, cephalosporins, monobactams, carbapenems, and carbacephems have been discovered. The structural features of the different classes of β -lactam antibiotics are shown in Figure 1.

Figure 1: Various classes of β -lactam antibiotics.



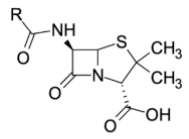
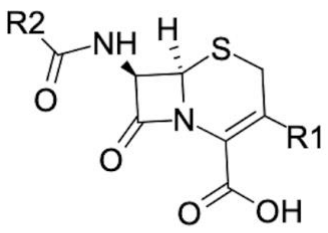
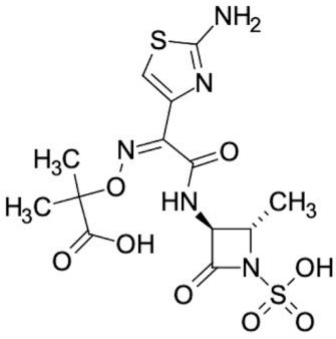
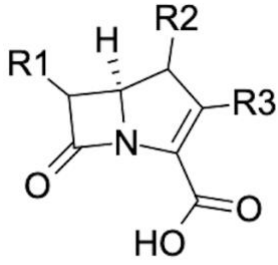
Cephalosporins are β -lactams which have historically been used for treatment against gram-positive bacteria, but recent developments have shown that they can also be effective against gram-negative bacteria. Together with cephamycins, cephalosporins form a β -lactam antibiotic subgroup called cephems.[4]

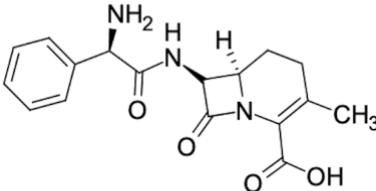
Monobactams are monocyclic, bacterially-produced β -lactam antibiotics that can act against aerobic gram-negative bacteria. In contrast to other β -lactam antibiotics, the β -lactam ring on monobactams is not fused with another ring. Monobactams did not show impressive antimicrobial activity, but the side-chain variation resulted in potent compounds.[5]

Carbapenems are a class of β -lactam antibiotics used for the treatment of severe, high-risk bacterial infections, as they are uniquely resistant to hydrolysis by many bacterial enzymes.

Carbacephems are a class of synthetic antibiotics based on the structure of cephalosporins. Carbacephems are similar to cephalosporins, but with a carbon substituted for the sulfur.[6] All of these antibiotics were results of the discovery of penicillin and contain the β -lactam ring first found in penicillin. A representative overview of the different classes of β -lactam antibiotics is illustrated in Table 1.

Table 1: Overview of the classes of β -lactam antibiotics.

Chemical Structure	Year of Discovery	Common Antibiotics	Significance	Species
 <p>Penicillin</p>	1928	Penicillin, Ampicillin, Azlocillin	Prevents peptidoglycan from cross-linking properly in the last stages of bacterial cell wall synthesis	Penicillium mold
 <p>Cephalosporins</p>	1948	Kefazol, Ancef, Cefitin, Zinacef	Effective against gram-negative bacteria	Fungus Acremonium
 <p>Monobactams</p>	1985	Aztreonam, Tigemonam, Nocardicin A, and Tabtoxin	Effective against aerobic gram-negative bacteria	Chromobacterium
 <p>Carbapenams</p>	1976	Imipenem, Panipenam, Doripenam	Largely resistant to hydrolysis by bacterial enzymes	E. coli, Klebsiella pneumoniae, Enterobacter cloacae, Citrobacter freundii, Proteus mirabilis, & Serratia marcescens

 <p>Carbacephem</p>	1967	Cefixime, Cefdinir, Cefotaxime	Prevents bacterial cell division by inhibiting cell wall synthesis	E. coli, K. pneumoniae, and Enterobacter
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β-LACTAM MECHANISM OF ACTION

A discovery in 1949 by Cooper and Rowley showed the irreversible binding of penicillin to the penicillin-binding proteins, or PBPs, of sensitive bacteria.[7] The crystal structure of penicillin complexed with a PBP is shown in Figure 2A, and Figure 2B shows penicillin covalently acylating the active site of a PBP.

Figure 2A: Crystal structure of PBP₄ (dacB) from *Escherichia coli*, complexed with penicillin-G [opened] (PDB: 3PTE).

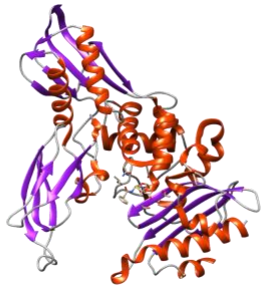
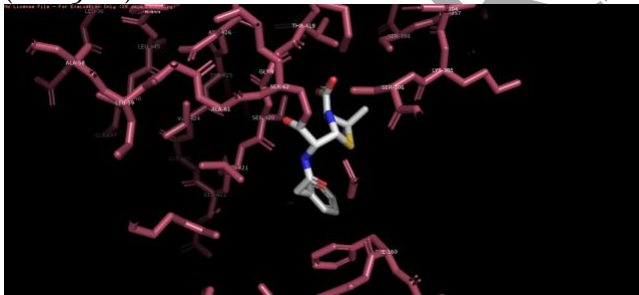
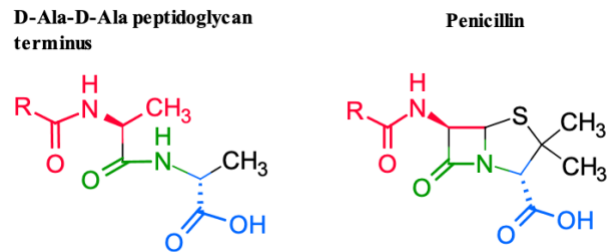


Figure 2B: Penicillin covalently acylates Serine-62 at the active site of a PBP, thus acting as a permanent inhibitor (PDB: 3PTE).



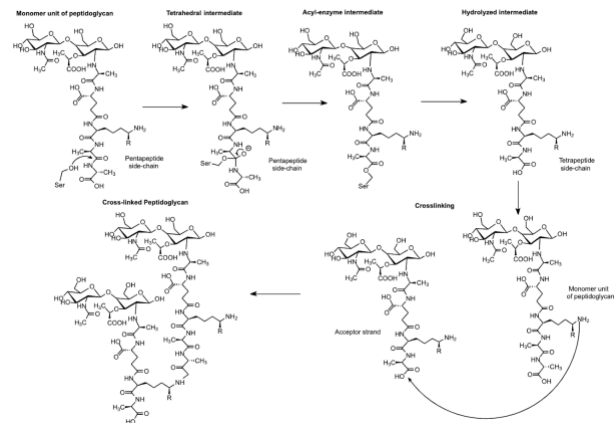
Soon after, in 1956, Lederberg discovered that penicillin converted rod-shaped *E. coli* bacteria into spherical protoplasts, thereby concluding that penicillin interfered with cell wall biosynthesis;[8] further work by Wise, Park, Tipper, and Trominger et al. demonstrated that penicillin targeted the cross-linking of peptidoglycan strands.[9] Ultimately, Timmer and Strominger proposed that the effectiveness of penicillin came from its structural similarity to the D-Ala-D-Ala residue of peptidoglycan, the native substrate of DD-transpeptidase, shown in Figure 3.

Figure 3: Similarities between the D-Ala-D-Ala terminus of peptidoglycan and the penicillin antibiotic.



DD-transpeptidase cross-links peptide side chains of peptidoglycan strands in the cell wall, providing structural rigidity for bacterial cells. This is followed by the breakdown of the acyl-enzyme intermediate and the formation of a new peptide bond between the carbonyl of the D-Ala moiety and the amino group of another peptidoglycan molecule, thereby crosslinking the two peptidoglycan molecules. This mechanism for this process is shown in Figure 4.

Figure 4: DD-transpeptidase catalyzes the cross-linking of peptidoglycan molecules.



β-lactam antibiotics disrupt cell wall biosynthesis via covalent inhibition of the transpeptidase enzyme. The four-membered β-lactam ring is forced into a torsed diamond geometry, as opposed to the natural 109.5° bond angles of a tetrahedral carbon. A four-membered ring has approximately 25 kcal/mol of ring strain, prompting ring opening. As such, β-lactams are often irreversible inhibitors of the enzyme because they permanently acylate the active

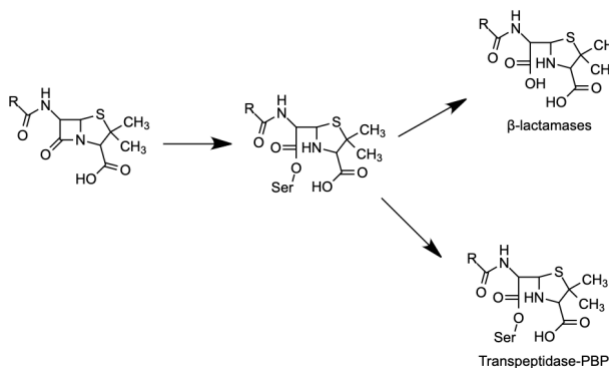
site serine of DD-transpeptidase, effectively preventing the enzyme from interacting with its native substrate, shown in Figure 5. This prevents the formation of the bacterial cell wall and promotes the osmotic lysis of the cell.

β-LACTAM RESISTANCE

Emergence of β-lactamases

From the initial discovery of penicillin as a β-lactam antibiotic, bacterial resistance has trailed closely behind in a molecular arms race between antibiotics and bacteria. Bacterial resistance to β-lactams is conferred by two major mechanisms: (1) inactivation of the β-lactam by hydrolytic enzymes called β-lactamases—shown in Figure 5—and (2) target site alterations to PBPs. Drug-resistant bacteria often express more than one of these mechanisms. The first instances of β-lactam resistance came from β-lactamases, which disrupt the amide bond of the β-lactam. Molecular modeling of various serine β-lactamases and PBP structures have demonstrated three-dimensional similarities with conserved folding patterns and preservation of topology at the active site, suggesting that β-lactamases evolved from PBPs selected for their antibiotic resistance. First found in *E. coli* a year prior to the clinical release of penicillin, β-lactamases have since been found in numerous gram-positive and gram-negative bacteria, often encoded as a mobile genetic element for plasmid-enabling horizontal gene transfer.[10]

Figure 5: β-lactamases hydrolyze the β-lactam ring, preventing β-lactam antibiotics from inhibiting DD-transpeptidase.



β-lactamases have similar structure to DD-transpeptidase but with one key difference: β-lactams covalently bind to DD-transpeptidase while β-lactamases hydrolyze the β-lactam ring without binding to it. Thus, β-lactamases prevent β-lactams from inhibiting DD-transpeptidase.[11]

Evolution of β-lactamases

Phylogenetic analyses and nucleotide substitution rates have determined that serine β-lactamases are around 2 billion years old, while plasmid encoded OXA β-lactamases are millions of years old, both existing far before the discovery and usage of β-lactam antibiotics.[12] The expression frequencies for these early β-lactamases were low

in bacterial populations and evolved in certain bacterial species as a mechanism for resistance against β-lactam containing compounds produced by fungi. However, the discovery and clinical development of β-lactams as antibiotics resulted in the evolutionary selection for relevant β-lactamases. The evolution of β-lactamases can be divided into four waves as shown in Table 2.

Table 2: The 4 Waves of β-lactamases.

Wave	Characteristics	Susceptible β-lactams	Unaffected β-lactams
1	Narrow-spectrum penicillinases TEM-1 and SHV-1 strands	Penicillin, Ampicillin	Cephalosporins, Carbapenems, Aztreonam
2	Extended spectrum cephalosporinases from point mutations to mutations to TEM and SHV	Cephalosporins	Ampicillin, Carbapenems
3	CTX-M family of β-lactamases	Cephalosporins	Carbapenems
4	Carbapenemases: KPC class β-lactamases, Metallo-β-lactamases, OXA-type enzymes	Carbapenems, Cephalosporins, Penicillin, Ampicillin	Aztreonam (Often ineffective)

Classification of β-lactamases

There are two classifications of β-lactamases: the first of which being the comparatively older classification that distinguished β-lactamases into classes A, B, C, and D based on amino acid sequencing.[13] In a more novel classification, Bush and Jacoby distinguished β-lactamases into Groups 1, 2, and 3, effectively combining classes A and D into a single group based on mechanism and evolutionary lineage.[14] A summary of the Bush and Jacoby classification of β-lactamases is shown in Table 3. The mechanism in which serine β-lactamases hydrolyze β-lactams is shown in Figure 6.

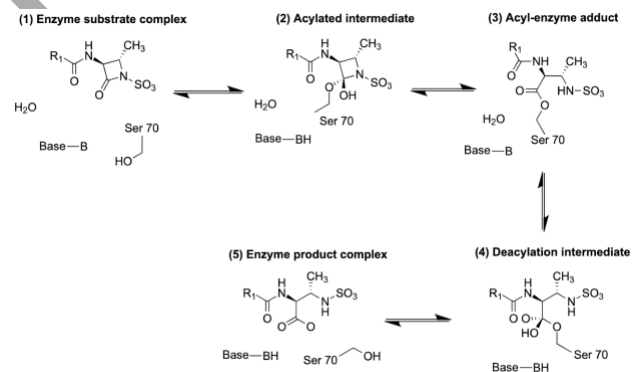
Table 3: Classifications of β-lactamases.

Group	Discovery	Description	Mechanism

Group 1 β -lactamases	β -lactamases were first documented in 1940 as the first bacterial enzyme capable of facilitating the breakdown of penicillin.	Group 1 β -lactamases include cephalosporinases, originally derived from <i>Acremonium</i> fungus.[15, 16] The most clinically relevant cephalosporinases are AmpC β -lactamases, mediating resistance to cephalothin, cefazolin, cefoxitin, and most penicillins. Overexpression of the AmpC gene confers resistance to broad-spectrum cephalosporins.[17]	The sequence of the AmpC gene was first recorded in <i>E. coli</i> in 1981,[18] distinct from the genetic sequence of TEM-1 and TEM-2, but still with an active site serine nucleophile.[19, 20]
Group 2 β -lactamases	TEM-1 was first documented in the early 1960s. The TEM-1 enzyme was originally found in a single strain of <i>E. coli</i> isolated from a blood culture from a patient named Temoniera in Greece, hence the designation TEM.	Group 2 β -lactamases include broad-spectrum, inhibitor-resistant, and extended-spectrum β -lactamases. The earliest serine carbapenemases began with the TEM-1 and SHV-1 strands which further evolved into extended-spectrum β -lactamases against aztreonam and oxycillin-hydrolyzing β -lactamases against carbapenem.	As with Group 1 β -lactamases, Group 2 β -lactamases have an active site serine, as shown in Figure 6.
Group 3 β -lactamases	Metallo- β -lactamases were initially discovered	Metallo- β -lactamases have poor hydrolytic capabilities against	In contrast to serine β -lactamases, metallo- β -lactamases

in the 1970s and attracted clinical attention in the 1990s with the spread of the IMP and VIM-type metallo- β -lactamases.	monobactams— β -lactams without fused rings—but have recorded high hydrolytic capabilities towards penicillins, cephalosporins, and carbapenems. Due to its reliance on the zinc cation, metallo- β -lactamases are inhibited by metal ion chelators, such as EDTA.	utilize a zinc+2 cation to hydrolyze the β -lactam ring.
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Figure 6: Serine β -lactamases hydrolyze β -lactams, rendering β -lactams ineffective.



An active site serine hydrolyzes the β -lactam ring, creating a transition acyl-enzyme adduct which undergoes a general base-catalyzed attack by a hydrolytic water molecule to form a second tetrahedral intermediate, which then collapses to form a product complex.[21]

Drug Inactivation by Target-site Alterations: Mutations in PBP

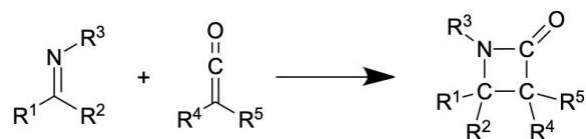
All β -lactams have the same binding target for successful inhibition: bacterial PBPs. This makes the alteration of this binding pocket extremely significant in hindering β -lactam activity. PBPs are membrane-bound DD-peptidases that evolved from serine proteases and are responsible for the crosslinking of peptidoglycan chains in bacterial cell wall formation. Due to the low expression of β -lactamases in *Staphylococcus* bacteria, target site alterations of PBPs are responsible for almost all β -lactam antibiotic resistance. The PBP targets in penicillin-resistant

Streptococci are modified into low-affinity targets for β -lactams, thereby reducing β -lactam inhibitory activity.[22] Meanwhile, certain bacteria such as methicillin-resistant staphylococci express novel PBPs—termed PBP2a—encoded by the *mecA* gene with almost no binding affinity to β -lactams. In the COL52 strain, E→K237 within the non-penicillin-binding domain, along with V→E470 and S→N643 near the SDN464 conserved DNA sequence of the penicillin-binding domain were important for resistance.[23, 24] Thus, research towards inhibitors for PBP2a is of high priority.

B-LACTAM SYNTHETIC ROUTES

The battle against bacterial resistance has necessitated the continued development of new antibiotics and methodologies, thus synthetic access to β -lactams has been of great significance.[25] The first synthetic β -lactam was prepared by Hermann Staudinger in 1907—21 years before Fleming discovered penicillin—by reaction of the Schiff base of aniline and benzaldehyde with diphenylketene in a [2+2] cycloaddition.[26, 27] This reaction, later coined the Staudinger [2+2] cycloaddition—as shown in Figure 7—still remains the most common method of β -lactam synthesis to date.[28, 29]

Figure 7: Staudinger [2+2] cycloaddition, consisting of the reaction between an imine and ketene to form a β -lactam.



There are two proposed mechanisms for the Staudinger 2+2 cycloaddition: a stepwise mechanism, wherein the nucleophilic nitrogen atom of the imine first attacks the sp²-hybridized carbon atom of the ketene, followed by nucleophilic addition of the resulting enolate to the iminium; or a concerted mechanism which undergoes a pericyclic transition state to yield the β -lactam ring. Many computational studies have suggested that the mechanism for the [2+2] cycloaddition is stepwise, as reported by Cossio et al., Bachrach and Halzner, and Sordo et al.[30, 31, 32] Similar studies on the related reaction between ketene and alkenes by Burke, Houk and Wang, and Bottoni et al. have shown that the reaction has an asynchronous transition state with appreciable charge separations; however, no intermediates were isolated.[33, 34, 35] Although more than 100 years have passed since the ketene-imine cycloaddition was first reported, the reaction mechanism is still unclear.

Variants of the asymmetric synthesis of β -lactams have incorporated chiral auxiliaries to control enantioselectivity and diastereoselectivity.[36, 37] Asymmetric syntheses of β -lactams yields a mix of *cis* and *trans* isomers; however, stereochemical control is necessary if a particular isomer is desired. Imines, characterized by the C=N functional group, can be prepared via condensation of an amine and aldehyde

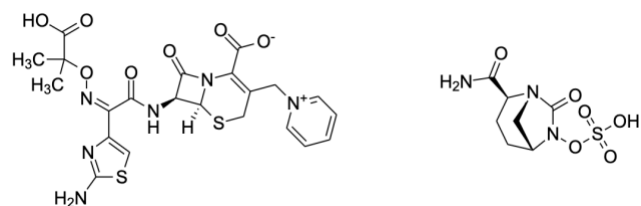
or amine and ketone.[38, 39, 40, 41] Ketenes are a highly reactive species that is characterized by the C=C=O functional group, which can be detected by infrared spectroscopy at around 2100-2200 cm⁻¹. The most common method of ketene preparation involves activation of the carboxylic acid as a leaving group, followed by deprotonation of the α carbon and elimination of the leaving group.

MODERN ADVANCEMENTS

In an effort to produce better yields and improve reaction conditions and results, alternative synthesis methods have been produced in recent years as a substitute for the traditional Staudinger synthesis reaction. As reported by Dong et al., one such method involves a catalytic metal carbene insertion into C-H bonds. Another method consists of the activation of an unsaturated C-C bond in addition to a nucleophilic addition.[42, 43] Transition metal-assisted Staudinger reactions have also been promising alternative synthetic routes devised in recent years.[44]

Recent advancements have also been made to combat β -lactam resistance. In 2015, a novel antibacterial treatment, Ceftazidime-Avibactam (Figure 8), was approved by the U.S. Food and Drug Administration, involving a combination of the β -lactam antibacterial ceftazidime and the novel β -lactamase inhibitor, avibactam. This combination has been shown to have significant activity against β -lactamase-producing Gram-negative pathogens.[45, 46]

Figure 8: The chemical structure of ceftazidime is shown on the left, and the chemical structure of avibactam is shown on the right.



Despite recent advancements in combating resistance to β -lactam antibiotics, resistance to β -lactam antibiotics remains a concern which requires continued research development. Specifically, more needs to be done regarding plasmid-mediated β -lactamases, which transfer easily among groups of organisms and thus contribute to bacterial resistance. Induction of chromosomal β -lactamases is also a continuing problem to be resolved in terms of β -lactam antibiotic resistance.[47]

CONCLUSION

Since the discovery and initial clinical uses of penicillin in the 1900s, β -lactam antibiotics have undergone drastic improvements in order to combat the perpetual problem of bacterial resistance. The β -lactam core moiety of several natural products has attracted the attention of chemists and biologists alike for its prevalence in natural products, structural simplicity and reactivity, and effectiveness in the

mechanism of action against many strains of bacteria. The continued evolution of antibiotic resistant bacteria has made the development of new antibiotics all the more important. The development of new synthetic methodologies in accessing β -lactam-containing compounds has the potential of giving rise to improved β -lactam antibiotics that would be impactful not only in the medical field but also in the health and well-being of billions of people around the world.

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