

Structures of the Muraymycins, Novel Peptidoglycan Biosynthesis Inhibitors

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Guided by cell-wall specific biological assays,¹ our search for antibacterial agents from natural sources resulted in the discovery of the muraymycins, a family of novel nucleoside-lipopeptide antibiotics with a unique core structure.² The muraymycins are cell-wall biosynthesis inhibitors with *in vitro* activity and *in vivo* efficacy. The compounds show antimicrobial activity against Gram-positive bacteria and excellent activity against a permeable *E. coli* strain. The muraymycins were shown to inhibit *MraY*,³ an enzyme that links UDP-MurNAc-pentapeptide to the C₅₅ lipid carrier during bacterial cell-wall biosynthesis. We report here the structures of the muraymycin family of peptidoglycan biosynthesis inhibitors from a *Streptomyces sp.*⁴ organism.

Nineteen compounds were purified from a crude complex by a combination of adsorption chromatography, ion exchange, and HPLC. These compounds fall into several series, each differing in the amino sugar or one amino acid residue. When hydroxyleucine is present in place of leucine, a variety of fatty acid esters are formed from core structures with different amino sugars. Compounds lacking the amino sugar (A5 and C4) are apparently hydrolysis products formed during purification. The muraymycin core structures were established using data sets comprised of one- and two-dimensional NMR experiments including proton, carbon, COSY, TOCSY, HMQC, HMBC, and NOESY. The final structures were assembled using HMBC, ROESY, and FT-MSⁿ experiments. Figure 1 shows the structure of muraymycin B1, the proton and carbon assignments, and the relevant correlations used in establishing the structure. The structures of the remaining compounds (Figure 2) were established from similar data. High-resolution electrospray ionization Fourier transform ion-cyclotron-resonance mass spectrometry (FT-ICR/MS) and FT-ICR/MSⁿ were used to obtain the elemental compositions for muraymycin B1 and its major diagnostic fragment ions. The computed compositions were consistent with the proposed NMR-derived structure. Doubly and triply charged molecular ions were consistent with the presence of basic groups in the molecule. UV and NMR evidence supported the uracil-uronic acid-ribofuranoside substructures and placed muraymycin B1 in the nucleoside antibiotic family. The closest related structures are liposidomycin⁵ and FR-900493.⁶ The uronic acid, whose relative stereochemistry was established by J-configuration analysis,⁷ is connected to a 2-methoxy-5-amino-5-deoxy-ribofuranoside and to a 3-aminopropyl residue that is juxtaposed to a hydroxyleucyl residue. As evidenced by the production of C1 from B1 via mild base hydrolysis (0.1 N NaOH), the hydroxyleucine β hydroxyl group is esterified by an 8-methyl decanoic acid. The fatty acid confers a degree of lipophilicity to the molecule, apparently contributing to its activity.

An unusual feature of the molecule is the hexahydro-2-imino-4-pyrimidylglycyl moiety, a cyclic guanidino amino acid residue

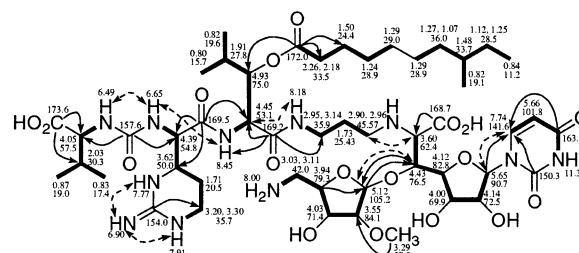


Figure 1. Structure of muraymycin B1 with COSY and TOCSY defined spin networks (bold bonds), select ROESY (dashed arrows), and HMBC (solid arrows) correlations.

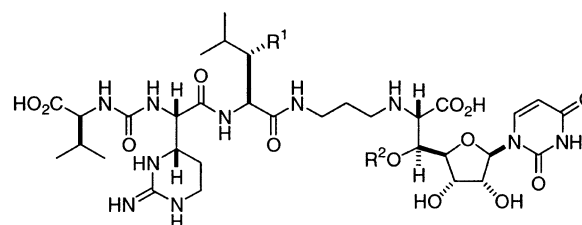


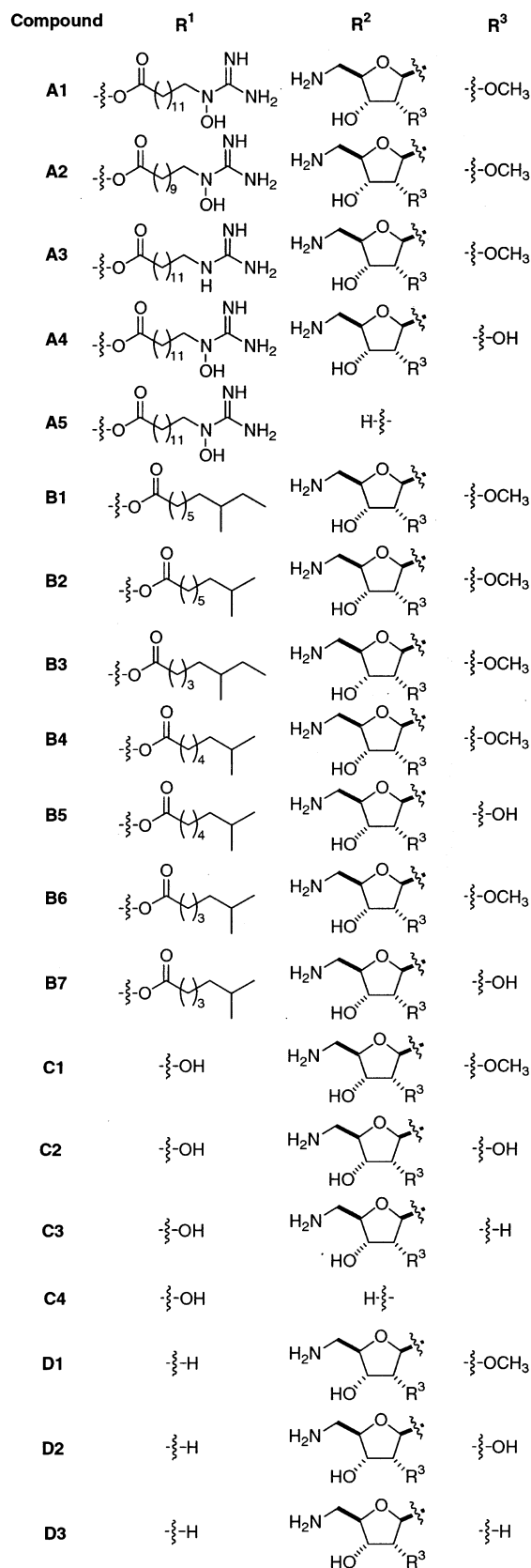
Figure 2. Structure of muraymycins (relative stereochemistry).

that is the source of much of the basicity. The 2*S**,3*S** relative stereochemistry of this residue is the same as that of L-epicapreomycin,⁸ a component of protease inhibitors such as chymostatin⁹ and elastatinal.¹⁰ Similar to those inhibitors, the muraymycins terminate in a basic amino acid-urea-amino acid motif, effectively reversing the directionality of the peptide chain. The muraymycin structures terminate in an epicapreomycin-urea-valine moiety.

All of the muraymycins have a common peptide-appended, glycosylated uronic acid core structure. Members of this family differ primarily in the fatty acid (R¹) and the terminal amino sugar (R²). Compound A1, one of the most active members of the family, showed *Staphylococcal* (MIC 2 to 16 μg/mL), *Enterococcal* (MIC 16 to >64 μg/mL), and Gram-negative (MIC 8 to >64 μg/mL) activity. Very good activity was also observed against an *E. coli* imp mutant (MIC < 0.03 μg/mL). Muraymycin A1 demonstrated efficacy in *Staphylococcus aureus* infected mice (ED₅₀ 1.1 mg/kg). The presence and structure of the fatty acid (R¹) influence activity, and esters were generally more active than nonesters. Esters with charged (guanidino or hydroxyguanidino) fatty acids were most active *in vitro*, with increased potency observed with lengthening of the fatty acid chain.

The muraymycins are structurally and mechanistically related to uridyl peptide antibiotics such as the mureidomycins,¹¹ pacidamycins,¹² napsamycins,¹³ liposidomycins,⁵ and FR-900493⁶ and its derivatives.¹⁴ This compound class reportedly inhibits bacterial translocase,¹⁵ an enzyme that plays a critical role in cell-wall biosynthesis. Translocase, a *MraY* gene product, catalyzes the transfer of the peptidoglycan precursor, phosphoryl-MurNAc-

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pentapeptide, from UMP in the cytosol to the membrane bound C₅₅-undecaprenyl phosphate lipid carrier.¹⁶ Like the mureidomycins and liposidomycins, the muraymycins inhibit translocase,³ thereby inhibiting the transfer and attachment of *p*-MurNAc-pentapeptide to the lipid carrier. Five of the muraymycins tested inhibited MraY (lipid II formation) and peptidoglycan synthesis at the lowest

concentration tested (0.027 $\mu\text{g/mL}$; see Supporting Information). These qualitative data show that the muraymycins are comparable to liposidomycin C and mureidomycin A, which were reported to inhibit *E. coli* translocase in vitro with IC₅₀ values of 0.05 and 0.03 $\mu\text{g/mL}$, respectively.^{17,18}

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Supporting Information Available: Complete NMR data set, table of chemical shifts, and structure determination discussion for muraymycin B1. Data showing inhibition of lipid II and peptidoglycan formation by muraymycins. Proton spectra for each compound (PDF). This material is available free of charge via the Internet at <http://pubs.acs.org>.

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