Synthesis and Biological Activity of Highly Cationic

Dendrimer Antibiotics

Harrison W. VanKoten¹, Wendy M. Dlakic¹, Robert Engel², Mary J. Cloninger^{1*}

¹Department of Chemistry and Biochemistry, 103 Chemistry and Biochemistry Building,

Montana State University, Bozeman, MT 59717, USA.

²Department of Chemistry and Biochemistry, 65-30 Kissena Blvd., Queens College,

CUNY, Queens, NY 11367, USA

Email: Mary Cloninger - mcloninger@chemistry.montana.edu

*Corresponding author

Supporting Information Table of Contents

	Page
General protocol for determining zeta potential	S2
General protocol for determining CMC	S2
Figure S1. Electrophoretic mobility plot	S2
Figure S2. CMC plot	S3
Figure S3. ¹ H and ¹³ C NMR spectrum of 1	S4
Figure S4. MALDI spectra of 1	S5
Figure S5. Hemolysis Data for 1 and 2	S5
Figure S6. Structure of G(4) PAMAM dendrimer	S6
Table S1. MIC values for 1 and 2	S7
Sample calculation for active group MIC	S7
Figure S7. Biofilm Disruption Studies	S8

General procedure for determining charge of C₁₆-DABCO dendrimers.

A 0.01 mM solution of C_{16} -DABCO dendrimers was dissolved in filtered (0.022 µm filter) Millipore water. 100 µL of the solution was placed into Wyatt Technologies' Mobius Dip Cell to perform the electrophoretic mobility experiment. The triangle extending above the y-axis indicates C_{16} -DABCO dendrimers are positively charged. It is noteworthy, that the positive charge appears after the addition of C_{16} -DABCO. Generally speaking, unfunctionalized glycodendrimers are neutral in charge.

General Procedure for Determining Critical Micelle Concentration

Experiments were performed to ensure that C_{16} -DABCO was below the critical micelle concentration (CMC). Several concentrations of C_{16} -DABCO were dissolved in water (Millipore) and filtered through a 0.22 µm syringe filter to ensure no dust or other contaminants were present in the sample. Samples were analyzed on a 90 plus Particle Size Analyzer made by Brookhaven Instruments Corporation. The graph in Figure S4 represents several overlapping data acquisitions. The two regression lines represent the intensity changes as a function of concentration of C_{16} -DABCO. One line shows data prior to micelle formation, and the other line is after formation of micellular aggregates. The intersection point shows the concentration at which micelles begin to form. From this experimental data, the critical micelle concentration was determined to be 0.685 mM. This concentration is well above the concentrations reported throughout this publication for C_{16} -DABCO use in assays.

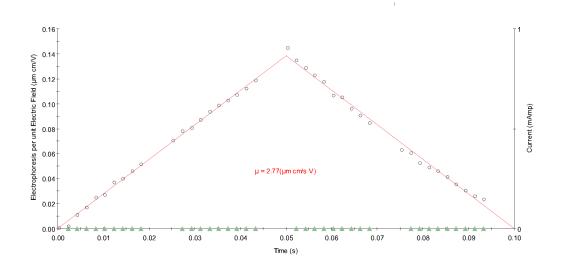


Figure S1. Electrophoretic mobility plot for C₁₆-DABCO dendrimers.

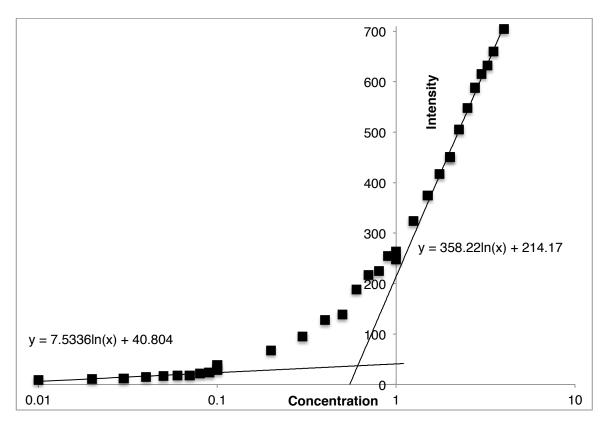
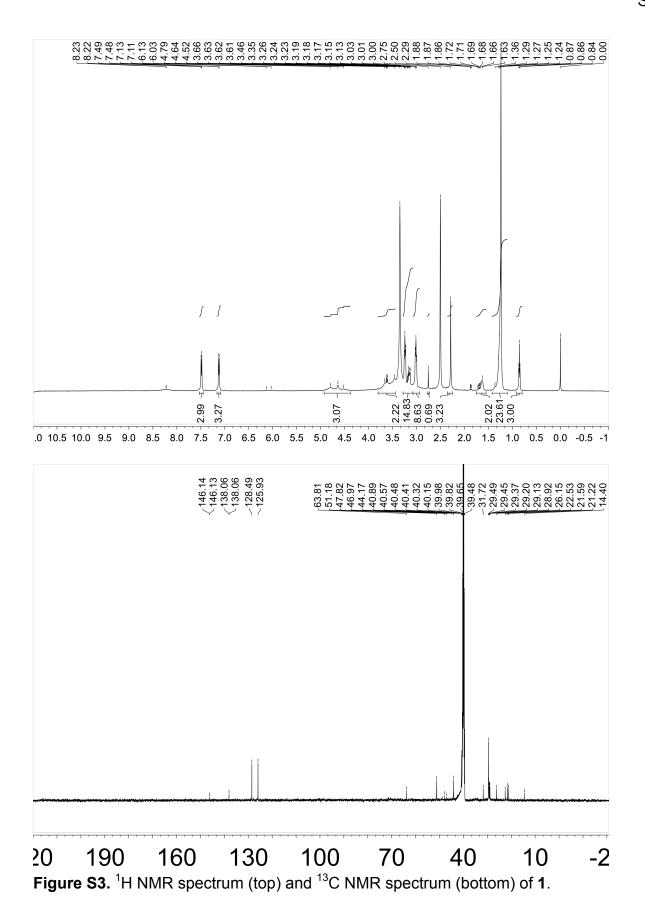


Figure S2. CMC determination for 1.



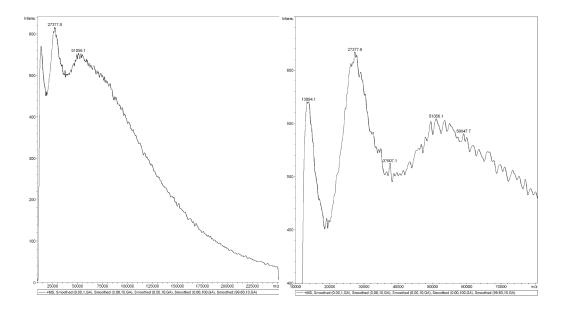


Figure S4. MALDI-TOF MS of 1. Full spectrum on left and zoom view on right.

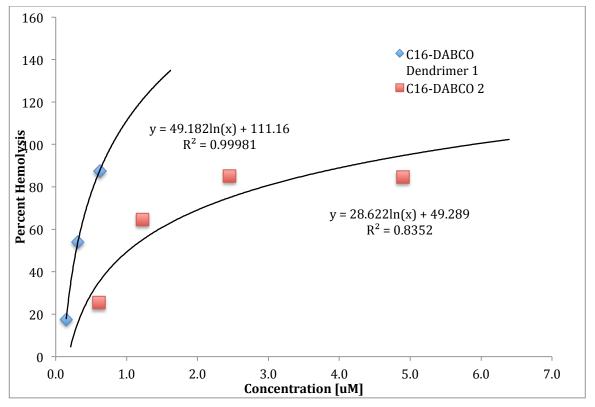


Figure S5. Red blood cell hemolysis for C_{16} -DABCO dendrimer **1** and C_{16} -DABCO monomer **2**.

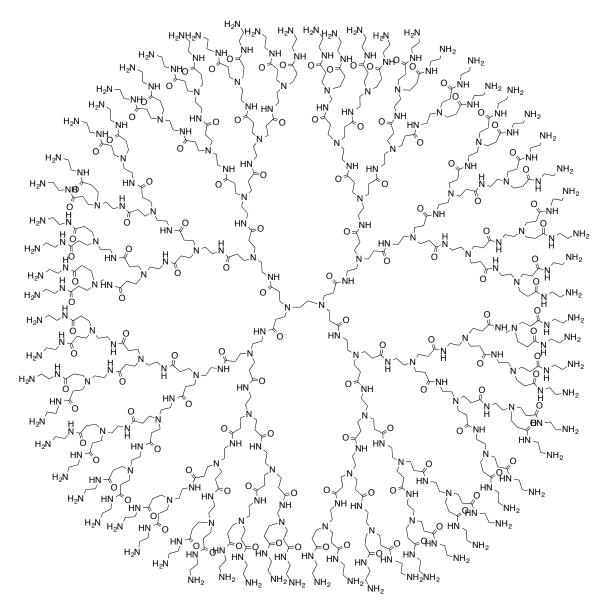


Figure S6. Fourth generation poly(amidoamine) dendrimer, i.e. G(4)-PAMAM.

Microorganism (Gram + or -)	C ₁₆ -DABCO Dendrimer 1 (per C ₁₆ -DABCO group)	C ₁₆ -DABCO Dendrimer 1 (per dendrimer)	C ₁₆ -DABCO Monomer 2	C ₁₆ -DABCO Dendrimer 1 (per dendrimer)	C ₁₆ -DABCO Monomer 2	Ampicillin	Cephalexin	Streptomycin
Streptococcus oralis (+)	>165 μM	>20.0 uM	3033 μM	>600 (μg/mL)	1024 (μg/mL)	N/A	N/A	<34 μM
Staphylococcu s aureus (+)	1.1	0.133	11.8	4	4	<67 μM	<68 μM	<17
Bacillus cereus (+)	1.1	0.133	17.7	4	6	27	41	N/A
Pseudomonas aeruginosa (–)	16	2.00	331.7	60	112	N/A	N/A	<17
Escherichia coli (–)	11	1.09	148.1	40	50	11	22	N/A

 Table S1. Minimum Inhibitory Concentrations (MICs) for Dendrimer 1 and Monomer 2.

Sample Calculation. Determining Concentration of Active Group.

From mass concentration of dendrimer to molar

 $x\frac{mg}{mL}*\frac{1\ mol\ dendrimer}{30,074\ g\ dendrimer}*\frac{1\ g\ dendrimer}{10^3\ mg\ dendrimer}*\frac{1\ mL}{10^{-3}L}*\frac{1\ umol}{10^{-6}\ mol}=y\ \frac{umol}{L}=y\ uM$

Equation 1. Solving for concentration of active group (per dendrimer basis)

(mass of a tosyl group) * (number of tosyl groups) + (mass of a C16DABCO group) * (number of tosyl groups)

= (mass after tosyl and C16DABCO addition

- mass before tosyl and C16DABCO addition)

Equation 2. Determining ratio active group to non-active group vis NMR analysis

 $ratio of tosyl methyl to C16DABCO methyl (NMR) = \frac{number of tosyl groups}{number of C16DABCO groups}$

Two equations with two unknowns.

Solve for one variable in **equation 2** in terms of the other variable; put answer in **equation 1**; solve for the only variable and put answer back into **equation 1** to determine second variable. Variables are the number of tosyl and C16DABCO groups.

<u>Finally</u>,

number of C16DABCO per dendrimer * molarity of dendrimer (y) = molarity of C16DABCO per dendrimer

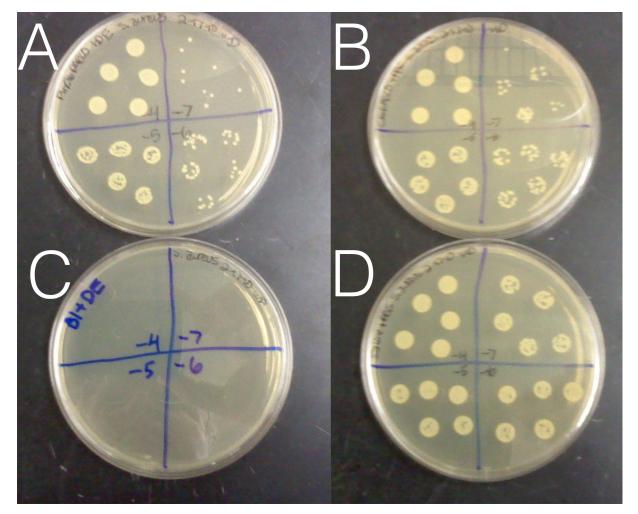


Figure S7. Biofilm Disruption Studies (log-kill platings) for S. aureus.

A) C₁₆-DABCO dendrimer **1.** B) C₁₆-DABCO monomer **2**. C) Bleach. D) Saline.