

Supplementary Data

Chondroitin Sulfate/Dermatan Sulfate Hybrid Chains from Swim Bladder: Isolation, Structural Analysis, and Anticoagulant Activity

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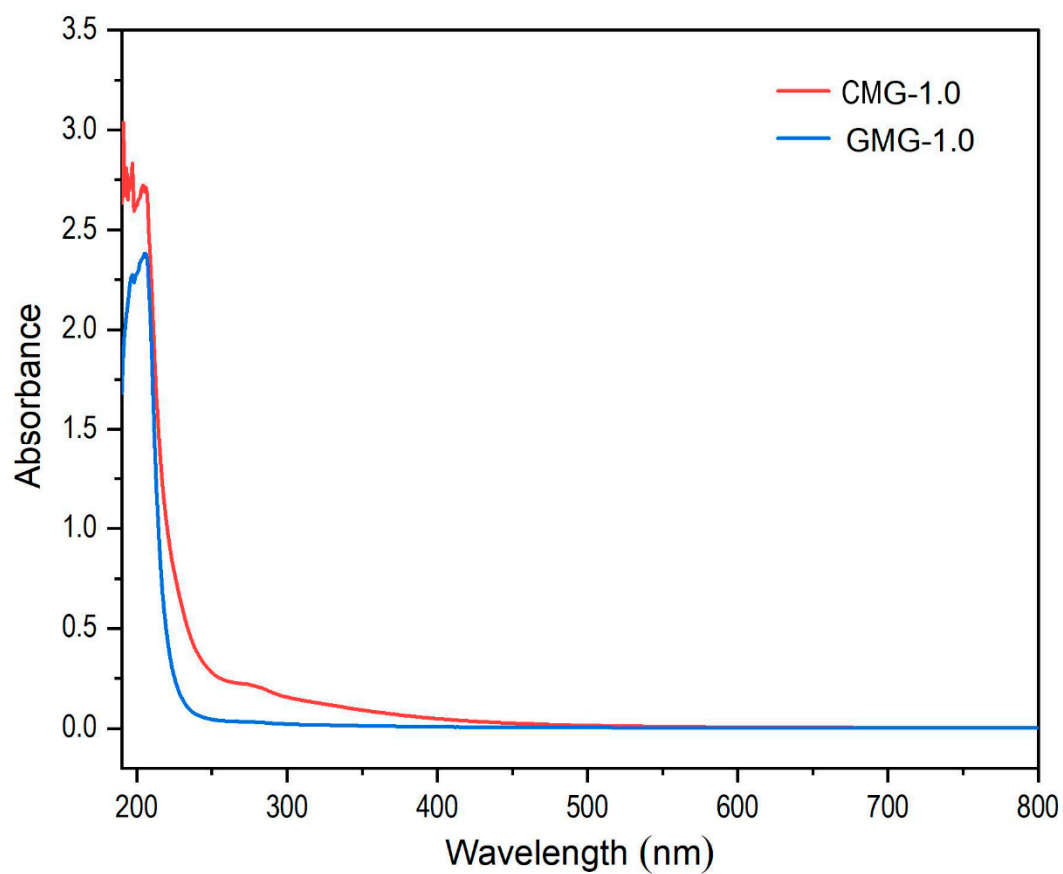


Figure S1. UV spectrum of CMG-1.0 and GMG-1.0

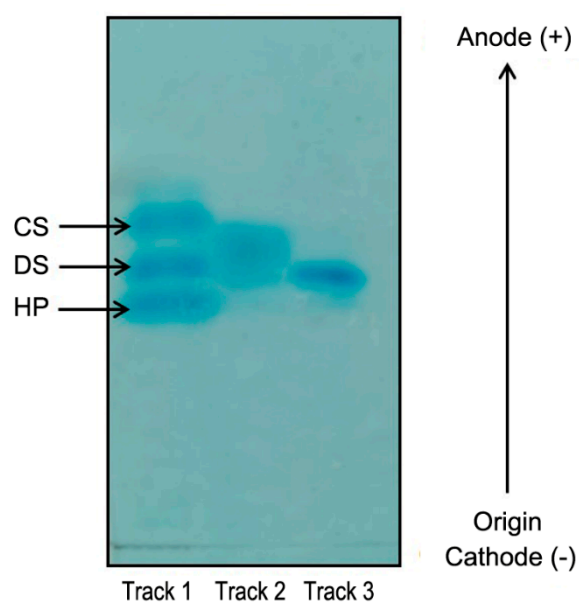


Figure S2. Electrophoretogram of CMG-1.0 (Track 2) and GMG-1.0 (Track 3)

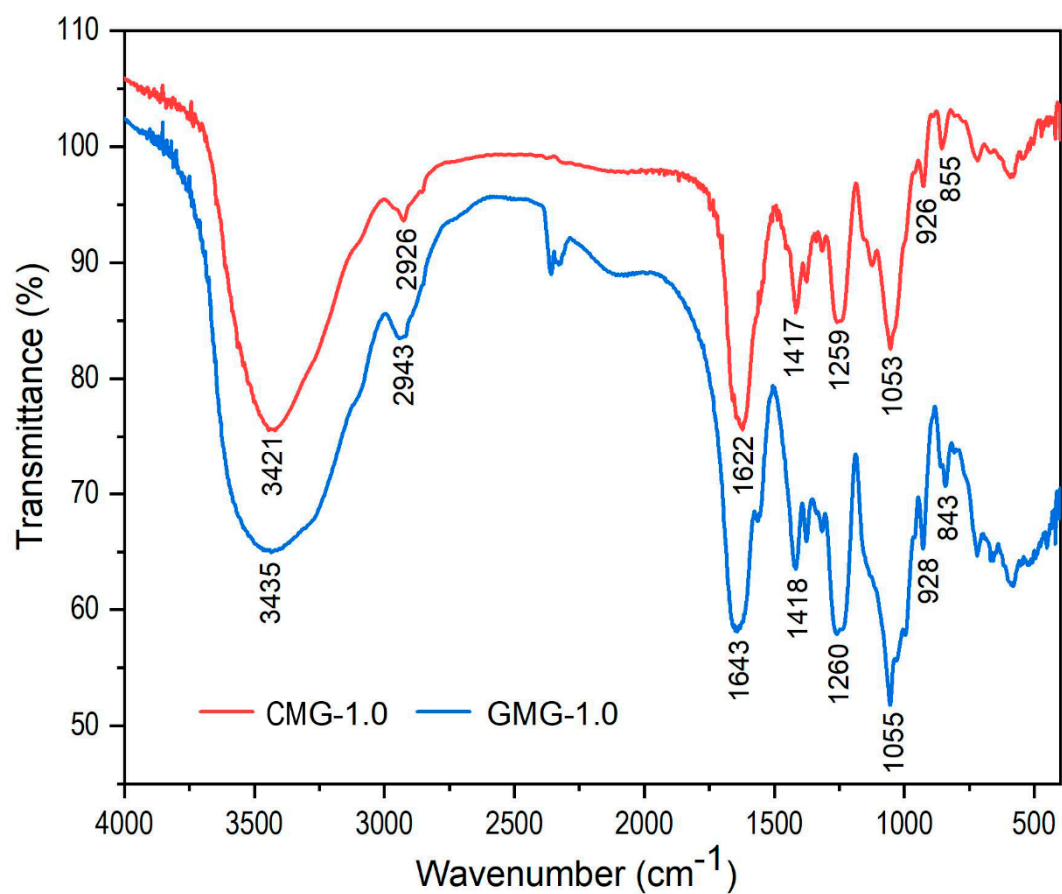
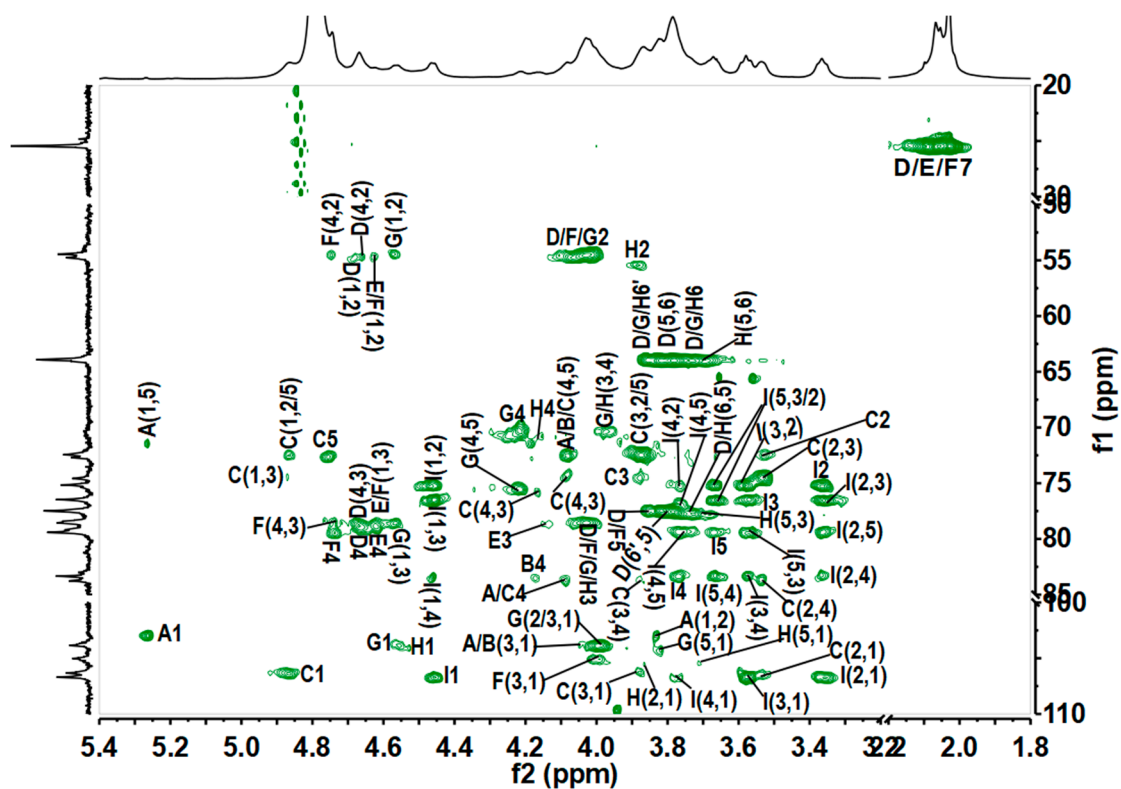


Figure S3. FT-IR spectra of CMG-1.0 and GMG-1.0



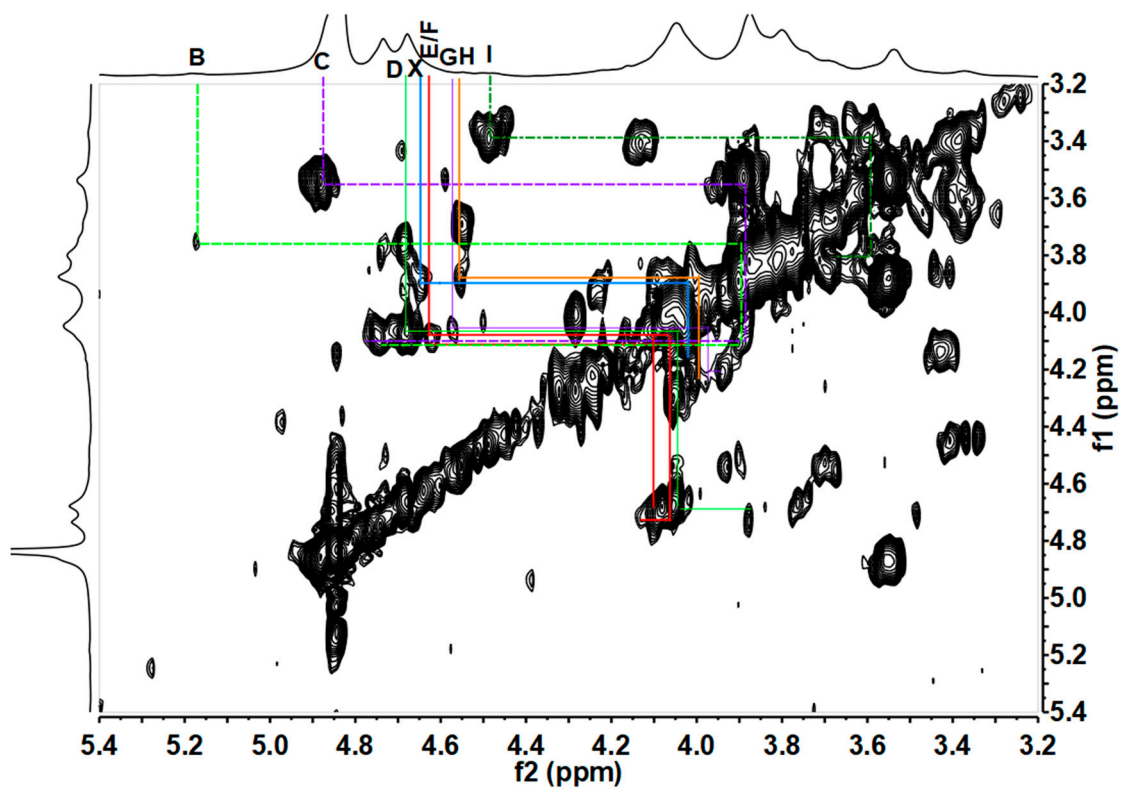


Figure S5. ^1H - ^1H COSY spectrum of GMG-1.0

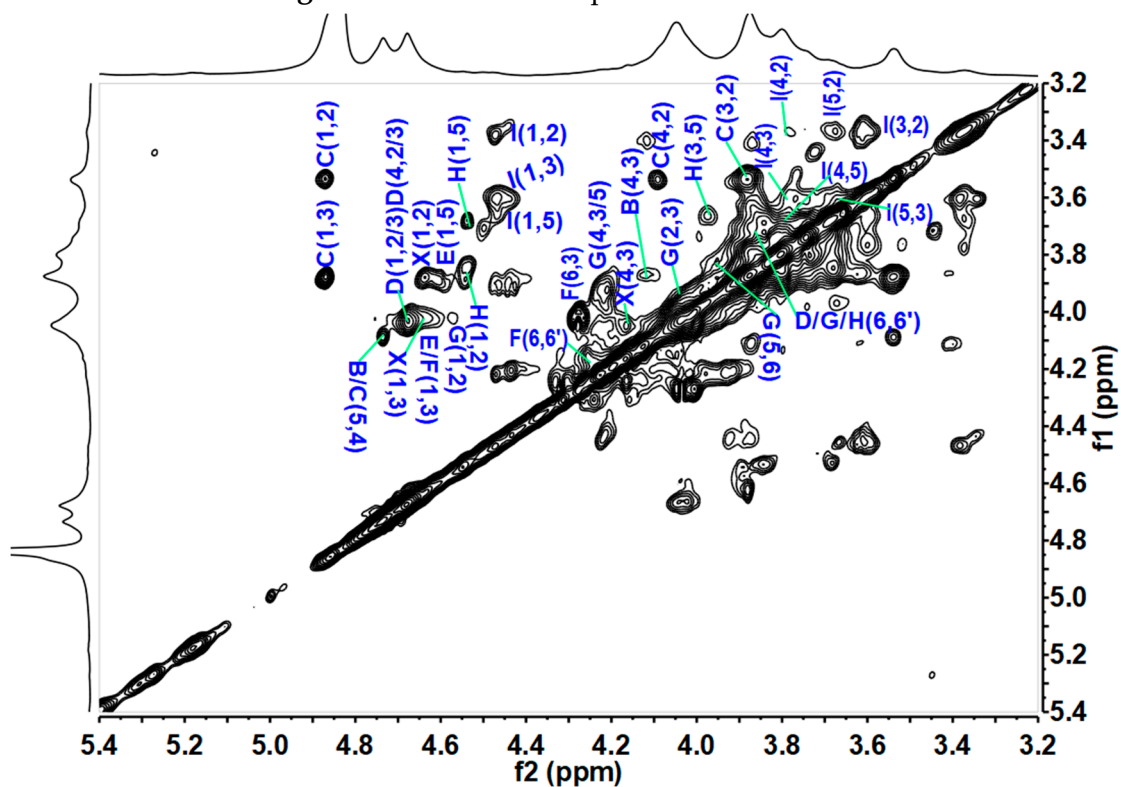


Figure S6. ^1H - ^1H TOCSY spectrum of GMG-1.0

Table S1. Assignment of ¹H and ¹³C NMR signals of GMG-1.0.

Residues	H/C	Chemical Shifts (δ,ppm) ^a							
		1	2	3	4	5	6	7	8
A	H	5.27	<u>3.85</u> ^b	n.d.	4.10 ^c	4.76			
α-D-IdoA _{2S}	C	103.6	<u>79.0</u>	n.d.	83.0	72.4	176.8		
B	H	5.18	<u>3.76</u>	3.87	4.12	4.74			
α-D-IdoA _{2S}	C	103.2	<u>79.1</u>	73.5	83.7	72.7	176.8		
C	H	4.87	3.54	3.89	4.08	4.74			
α-D-IdoA	C	106.2	72.4	74.5	83.7	72.7	176.8		
D	H	4.67	4.08	4.04	<u>4.68</u>	3.87	3.74/3.84		2.08
β-D-GalNAc _{4S}	C	105.0	54.3	78.1	<u>78.9</u>	77.4	63.8	178.1	25.0
X	H	4.64	<u>3.89</u>	4.02	4.16	3.85	<u>4.17/4.84</u>		2.08
β-D-GalN _{2S6S}	C	105.3	<u>55.0</u>	78.9	70.8	77.4	<u>70.0</u>	178.1	25.0
E	H	4.62	4.10	4.08	<u>4.65</u>	3.88	3.73/3.84		2.05
β-D-GalNAc _{4S}	C	105.0	54.7	78.6	<u>79.1</u>	77.7	63.9	177.9	25.5
F	H	4.61	4.08	4.04	<u>4.73</u>	4.15	<u>4.17/4.25</u>		2.04
β-D-GalNAc _{4S6S}	C	105.0	54.3	78.9	<u>79.4</u>	75.7	<u>70.0</u>	177.9	25.5
G	H	4.56	4.02	3.96	4.21	3.93	3.74/3.84		2.04
β-D-GalNAc	C	105.0	54.5	78.6	70.3	77.4	63.9	177.4	25.5
H	H	4.54	<u>3.88</u>	4.00	4.19	3.69	3.70/3.80		
β-D-GalN _{2S}	C	105.4	<u>55.0</u>	78.4	70.8	77.4	63.8		
I	H	4.48	3.36	3.59	3.78	3.67			
β-D-GlcA	C	106.5	75.1	76.4	83.3	79.1	177.4		

n.d. -not detected. ^a The 600 MHz NMR spectra were recorded at 298 K. All chemical shifts are relative to TSP at 0 ppm. ^{b,c} Values with underline and in boldface indicate sulfated and glycosylated positions, respectively.

Species Identification Results

Cynoscion microlepidotus was confirmed by the partial sequence of mitochondrial 16S

rRNA gene sequence:

CCTCTACCTAGTTTTTGGTGCATGAGCCGGAATAGTGGGCACAGCTTTGAGCCTTCTG
 ATTCGAGCAGAACTCAGTCAACCAGGCGCACTCCTCGGAGACGACCAGGTTTATAAC
 GTAATCGTTACAGCACACGCCTTTGTTATAATTTTCTTTATAGTAATGCCCATCATGAT
 CGGAGGGTTTGGAAGTGAAGTACTTATCCCGCTAATGATCGGAGCCCCCGACATGGCATT
 CCCCCGAATAAATAATATGAGCTTCTGACTTCTACCACCCTCCTTCCTCCTACTCTTAA
 CCTCATCAGGGGTAGAAGCAGGGGGCCGGAACGGGCTGAACAGTTTATCCCCCACTTG
 CGGGCAATCTAGCACATGCAGGGGCTTCCGTCGACTTAGCCATCTTCTCCCTGCATCT
 CGCAGGTGTGTCCTCGATTCTAGGGGCTATCAACTTCATTACAACCATTATTAATATG
 AAACCTCCCGCTATCTCCAGTATCAGACACCTCTGTTTGTATGGGCCGTCCTAATTA
 CAGCTGTCCTCTTACTGCTCTCGCTCCCTGTCTTAGCTGCCGGTATTACAATACTCCTT

ACAGACCGCAATCTCAACACAACCTTCTTCGACCCCGCAGGAGGGGGGACCCAATT
CTCTATCAACACTTATTC

Gadus morhua was confirmed by the partial sequence of mitochondrial 16S rRNA gene sequence:

CGCCTCTTGCTCCAAAAATATAAGAGGTCCCGCCTGCCCTGTGACTATAAGTTTAACG
GCCGCGGTATTTTAACCGTGCGAAGGTAGCGTAATCACTTGTCTTTTAAATGAAGACC
TGTATGAATGGCATCACGAGGGCTTAGCTGTCTCCCATCTCCAGTCAATGAAATTGAC
CTCCCCGTGCAGAGGCGGGGATAATTACATAAGACGAGAAGACCCCTATGGAGCTTTA
GACCTAAAGTAAGTCACGTTTAACATGCTGTGATAACAGTAAAACTTAGTGATATTT
ACTGAAGTGTCTTTGGTTGGGGCGACCGCGGGGTAAAACACAACCCCCATGTGGACC
GGGGATATTATCCCTAATACTCAGAGCCTCTACTCCAAGTAACAGAAATTCTGACTTT
TCTGATCCGGTATAACCGATCAACGAACCGAGTTACCCTAGGGATAACAGCGCAATC
CCCTCTCAGAGCCCATATCGACGAGGGGGTTTACGACCTCGATGTTGGATCAGGACA
TCCTAATGGTGCAGCCGCTATTAAGGGTTCGTTTGTTCACGATTAAAGTCCT

Based on the National Center for Biotechnology Information (NCBI) Genbank, the BLAST analysis revealed that the sequence similarity with *Cynoscion microlepidotus* and *Gadus morhua* sequence was 100%.