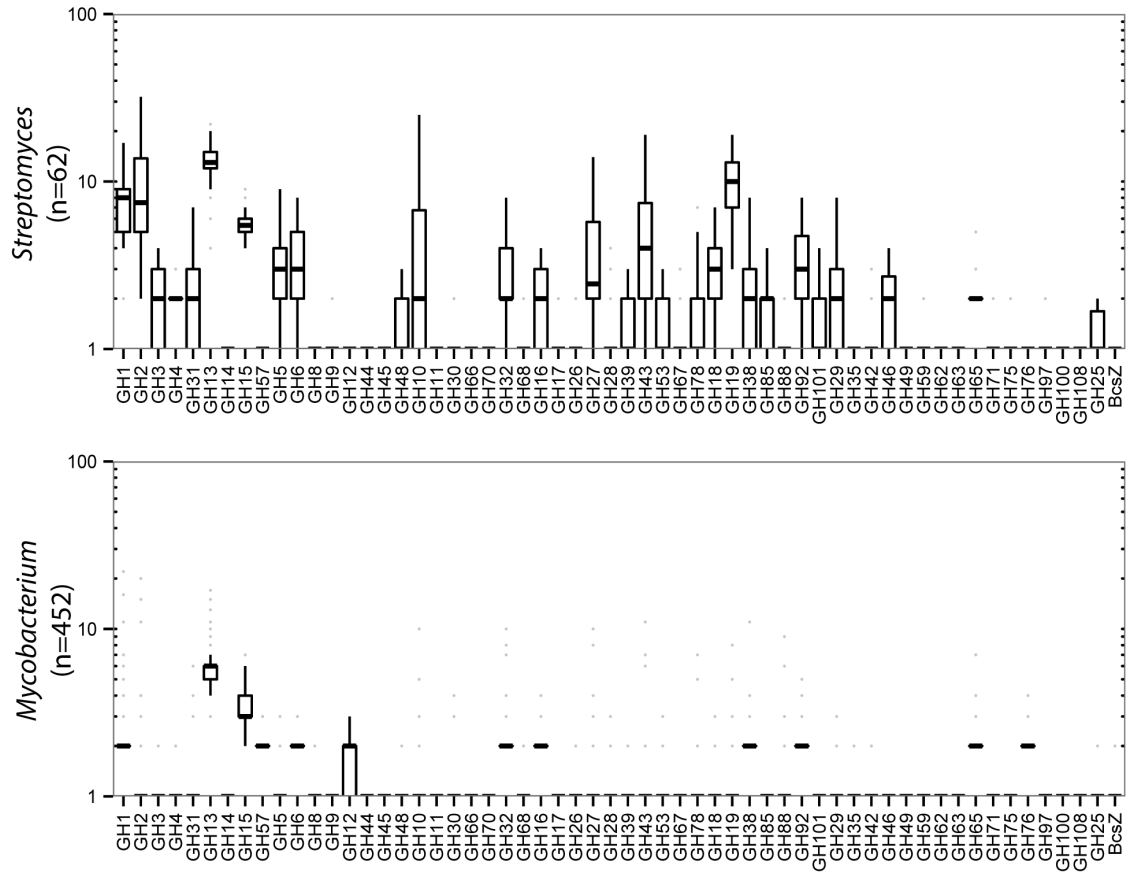


- 1 **Figure S1.** Glycoside hydrolyses (GH) content in *Streptomyces* and *Mycobacteria*.
- 2 The boxes represent the 25-75 percentiles; the bars represent the 2.5-97.5 percentiles.
- 3



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6 **Table S1.** Glycoside hydrolases (GHs) in sequenced bacterial genomes. Pfam
7 accession numbers, substrate specificity of characterized enzymes as stated in the
8 CAZy database, frequency of genomes with specific GH (F), average number of genes
9 for the GH in genomes having the GH (A), and redundancy index (σ).

GH family	Pfam	Substrate	F	A	Redundancy (σ)
GH1	PF00232	Oligosaccharides	0.53	3.1	0.78
GH2	PF00703 PF02836 PF02837	Oligosaccharides	0.61	3.2	0.62
GH3	PF00933 PF01915	Oligosaccharides	0.61	1.7	0.50
GH4	PF02056 PF11975	Oligosaccharides	0.41	2.5	0.68
GH5	PF00150	Cellulose	0.35	1.9	0.44
GH6	PF01341	Cellulose	0.06	1.5	0.25
GH8	PF01270	Cellulose	0.04	1.0	0.05
BCSZ	PF01270	Cellulose	0.02	1.1	0.10
GH9	PF00759	Cellulose	0.05	1.4	0.13
GH10	PF00331	Xylan	0.20	2.7	0.30
GH11	PF00457	Xylan	0.01	1.3	0.24
GH12	PF01670	Cellulose	0.08	1.1	0.05
GH13	PF00128	Starch/Glycogen	0.87	6.6	0.92
GH14	PF01373	Starch/Glycogen	0.004	1.0	0.00
GH15	PF00723	Starch/Glycogen	0.25	1.5	0.35
GH16	PF00722	O. Plant. Polysac.	0.13	2.1	0.49

GH18	PF00704	Chitin	0.41	2.9	0.66
GH19	PF00182	Chitin	0.31	2.5	0.29
GH20	PF00728	Oligosaccharides	0.33	3.7	0.74
GH26	PF02156	O. Plant. Polysac.	0.05	1.4	0.27
GH28	PF00295	O. Plant. Polysac.	0.09	4.4	0.92
GH29	PF01120	Mixed	0.13	2.5	0.51
GH30	PF02055	Xylan	0.12	1.7	0.41
GH31	PF01055	Oligosaccharides	0.30	1.8	0.56
GH32	PF08244 PF00251	Fructan	0.52	1.6	0.35
GH35	PF01301	Mixed	0.10	1.4	0.29
GH38	PF01074 PF07748	O. Ani. Polysac.	0.28	1.4	0.25
GH39	PF01229	O. Plant. Polysac.	0.005	1.2	0.16
GH42	PF02449 PF08533 PF08532	Mixed	0.11	1.4	0.30
GH43	PF04616	O. Plant. Polysac.	0.20	2.5	0.40
GH44	PF12891	Cellulose	0.0002	1.0	0.00
GH45	PF02015	Cellulose	0.0001	3.0	1.00
GH46	PF01374	Mixed	0.01	1.1	0.12
GH48	PF02011	Cellulose	0.01	1.1	0.06
GH49	PF03718	Mixed	0.007	1.8	0.59
GH53	PF07745	O. Plant. Polysac.	0.09	1.1	0.10
GH57	PF03065	Starch/Glycogen	0.14	1.3	0.19
GH59	PF02057	Mixed	0.002	1.3	0.25
GH65	PF03633	Starch/Glycogen	0.48	1.6	0.45

	PF03632				
	PF03636				
GH66	PF13199	Dextran	0.02	1.1	0.10
GH67	PF07477	O. Plant. Polysac.	0.03	2.4	0.85
	PF07488				
	PF03648				
GH68	PF02435	Fructan	0.04	1.1	0.10
GH70	PF02324	Dextran	0.03	1.0	0.03
GH71	PF03659	Mixed	0.004	1	0.00
GH75	PF07335	Mixed	0.001	1.0	0.08
GH76	PF03663	Mixed	0.15	1.4	0.17
GH78	PF05592	O. Plant. Polysac.	0.39	1.7	0.40
GH85	PF03644	Chitin	0.07	1.6	0.50
GH88	PF07470	O. Ani. Polysac.	0.36	2.2	0.43
GH92	PF07971	O. Ani. Polysac.	0.18	2.2	0.27
GH97	PF10566	Mixed	0.06	1.8	0.40
GH100	PF12899	Mixed	0.05	1.0	0.04
GH101	PF12905	O. Ani. Polysac.	0.08	1.1	0.11
GH108	PF05838	Mixed	0.05	1.1	0.11

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11 **Table S3.** Overall GH-based functional dissimilarity (Bray-Curtis) in group of
 12 genomes with specific 16S rDNA distance.

16S rDNA distance	Functional dissimilarity (Bray-Curtis)		Fraction of pairwise comparison
	Median	Mean	
0	0.062	0.086	0.58%
<0.001	0.066	0.090	0.79%
<0.005	0.088	0.103	1.29%
<0.010	0.100	0.124	1.63%
<0.025	0.183	0.227	2.74%
<0.050	0.308	0.284	3.86%
<0.075	0.385	0.367	5.27%
<0.100	0.454	0.442	8.06%
all	0.733	0.719	100%

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15 **Table S4.** Spearman correlations between potentials (genes/genome) for
 16 polysaccharides hydrolysis in sequenced bacterial genomes (all significant
 17 $P_{\text{Spearman}} < 0.05$)

	Oli	Cel	Xyl	Chi	Sta	Dex	BcsZ
Oligosaccharides (Oli)							
Cellulose (Cel)	0.22						
Xylan (Xyl)	0.48	0.14					
Chitin (Chi)	0.44	0.48	0.20				
Starch/Glycogen (Sta)	0.60	0.23	0.42	0.39			
Dextran (Dex)	0.46	-0.15	0.22	0.21	0.44		
Fructan (Fru)	0.52	0.16	0.21	0.14	0.30	0.27	
BcsZ	0.41	-0.14	0.32	0.12	0.36	0.45	0.06

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