Correction

BIOCHEMISTRY

Correction for "Discovery of novel carbohydrate-active enzymes through the rational exploration of the protein sequences space," by William Helbert, Laurent Poulet, Sophie Drouillard, Sophie Mathieu, Mélanie Loiodice, Marie Couturier, Vincent Lombard, Nicolas Terrapon, Jeremy Turchetto, Renaud Vincentelli, and Bernard Henrissat, which was first published March 8, 2019; 10.1073/pnas.1815791116 (*Proc Natl Acad Sci USA* 116: 6063–6068).

The authors wish to note the following: "We have found small errors in Table 2 and Table 3; these errors do not change the main conclusions of the paper, except that one additional novel family is now listed. A protein was wrongly assigned to GH42_dist in the original Table 2. This protein and its orthologs actually form a family completely different from GH42. The orientation of the glycosidic bond cleaved by this protein is different from that of bona fide GH42 proteins. The protein in question is now removed from corrected Table 2 and is listed as GH164 in corrected Table 3. Additionally, a typo and an incorrect GenBank accession number were also corrected in Table 3. The corrected paper reports on an additional novel GH family of proteins. We apologize for the errors." The corrected Table 2 and Table 3 appear below.

Table 2. Activity of enzymes distantly related to the described GH or PL (GH/PLxx_dist) families

Distant CAZy family	GenBank accession no.	Substrate	Organism
GH2_dist	WP_029427454.1	pNP-β-D-xylopyranoside (new)	*Bacteroides cellulosilyticus* WH2
GH2_dist	WP_029428707.1	Tamarind gum (new)	*Bacteroides cellulosilyticus* WH2
GH2_dist	WP_029428765.1	pNP-β-D-glucuronide	*Bacteroides cellulosilyticus* WH2
GH2_dist	WP_018628801.1	pNP-β-D-glucuronide	*Niabella aurantiaca* DSM 17617
GH3_dist	AJG33435.1	pNP-β-D-NAc-glucopyranoside	*Rickettsia rickettsii* str. R
GH5_dist	ZP_06241352.1	pNP-β-D-mannopyranoside	*Victivallis vadensis* ATCC BAA-548
GH10_dist	EMS72420.1	pNP-β-D-xylopyranoside (weak)	*Clostridium termitidis* CT1112
GH16_dist	ZP_02063674.1	pNP-β-D-glucopyranoside (new)	*Bacteroides ovatus* ATCC 8483
GH20_dist	AEV99795.1	pNP-β-D-NAc-6Sulf-glucopyranoside	*Niastella koreensis* GR20-10
GH20_dist	AHF94523.1	pNP-β-D-NAc-glucopyranoside	*Opitutaceae* bacterium TAV5
GH31_dist	EIY61740.1	pNP-α-D-galactopyranoside	*Bacteroides salyersiae* CL02T12C01
GH36_dist	EIY66649.1	pNP-α-D-galactopyranoside	*Bacteroides salyersiae* CL02T12C01
GH36_dist	ACS99969.1	pNP-α-D-galactopyranoside	*Paenibacillus* sp. JDR-2
GH36_dist	ACS99975.1	pNP-α-D-galactopyranoside	*Paenibacillus* sp. JDR-2
GH36_dist	ZP_06242255.1	pNP-α-D-galactopyranoside	*Victivallis vadensis* ATCC BAA-548
GH49_dist	EDY96541.1	*Chaetomorpha* sp. CWP (new)	*Bacteroides plebeius* DSM 17135
GH49_dist	EDY96565.1	*Chaetomorpha* sp. CWP (new)	*Bacteroides plebeius* DSM 17135
GH51_dist	WP_084555785.1	Lichenan (new)	*Alkaliflexus imshenetskii* DSM 15055
GH76_dist	ADO68190.1	pNP-α-D-maltopyranoside (new)	*Stigmatella aurantiaca* DW4/3–1
GH106_dist	WP_018627535.1	pNP-α-L-rhamnopyranoside	*Niabella aurantiaca* DSM 17617
GH106_dist	ACT02314.1	pNP-α-L-rhamnopyranoside	*Paenibacillus* sp. JDR-2
GH117_dist	WP_010134686.1	pNP-β-D-galactofuranoside	*Flavobacteriaceae* bacterium S85

This set encompasses enzymes that fall outside of established subfamilies or that are only distantly related to biochemically characterized enzymes. "New" designates novel specificity in the family. CWP, cell wall polysaccharide.

Table 3. Substrate specificity of new CAZy families

New family	GenBank accession no.	Substrate	Activity	Organism
GH147	WP_029428318.1	β-galactan	Endo-β-(1,4)-galactanase	*Bacteroides cellulosilyticus* WH2
GH147	EFI37897.1	β-galactan	Endo-β-(1,4)-galactanase	*Bacteroides* sp. 3_1_23
GH148	AGN79260.1	Konjac glucomannan	Endo-β-(1,4)-glucosidase	*Pseudomonas putida* H8234
GH148	ACR13278.1	Konjac glucomannan	Endo-β-(1,4)-glucosidase	*Teredinibacter turnerae* T7901
GH157	WP_029429093.1	CM-curdlan	Endo-β-(1,3)-glucanase	*Bacteroides cellulosilyticus* WH2
GH158	ZP_06243608.1	CM-curdlan	Endo-β-(1,3)-glucanase	*Victivallis vadensis* ATCC BAA-548
GH159	WP_007210837.1	pNP-β-D-galactofuranoside	β-galactofuranosidase	*Bacteroides cellulosilyticus* WH2
GH160	AEI51087.1	EPS *Nostoc commune* (new)	Endo-β-(1,4)-galactosidase	*Runella slithyformis* DSM 19594
GH164	EIY59668.1	PNP-α-D-mannopyranoside	α-mannosidase	*Bacteroides salyersiae* CL02T12C01
PL30	WP_029426181.1	Hyaluronan	Endo-hyaluronan lyase	*Bacteroides cellulosilyticus* WH2
PL31	ABD82242.1	β-glucuronan	Endo-β-(1,4)-glucuronan lyase	*Saccharophagus degradans* 2–40
PL31	AGF62897.1	β-glucuronan	Endo-β-(1,4)-glucuronan lyase	*Streptomyces hygroscopicus* subsp. *jinggangensis* TL01
PL32	EIY62149.1	β-mannuronan	Endo-mannuronan lyase	*Bacteroides salyersiae* CL02T12C01
PL33	ALJ61728.1	Hyaluronan	Endo-hyaluronan lyase	*Bacteroides cellulosilyticus* WH2
PL33	AHF90976.1	Gellan (new)	Endo-gellan lyase	*Opitutaceae* bacterium TAV5
PL33	AHF90672.1	Chondroitin sulfate	Endo-chondroitin sulfate lyase	*Opitutaceae* bacterium TAV5
PL33	AHF90411.1	Gellan (new)	Endo-gellan lyase	*Opitutaceae* bacterium TAV5
PL34	AHF91913.1	Alginate	Endo-alginate lyase	*Opitutaceae* bacterium TAV5
PL35	ZP_06241351.1	Chondroitin	Endo-chondroitin lyase	*Victivallis vadensis* ATCC BAA-548
PL36	WP_026728881.1	β-mannuronan	Endo-mannuronan lyase	*Flavobacterium denitrificans* DSM 15936

The substrate and the modality of substrate degradation are specified. "New" designates novel specificity not reported previously. Note that families GH147 and 148 were reported by other groups during the course of our work (30, 31). CM, carboxymethyl.

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