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Discovery of α-L-Arabinopyranosidases from human gut microbiome expands the diversity within glycoside hydrolase family 42

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Running title: GH42 α-L-arabinopyranosidase subfamily identification

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ABSTRACT
Enzymes of the glycoside hydrolase family 42 (GH42) are widespread in bacteria of the human gut microbiome and play fundamental roles in the decomposition of both milk and plant oligosaccharides. All GH42 enzymes characterized so far have β-galactosidase activity. Here, we report the existence of a GH42 subfamily that is exclusively specific for α-L-arabinopyranoside and describe the first representative of this subfamily. We found that this enzyme (BlArap42B) from a probiotic Bifidobacterium species cannot hydrolyze β-galactosides. However, BlArap42B effectively hydrolyzed paeonolide and ginsenoside Rb2, plant glycosides containing an aromatic aglycone conjugated to α-L-arabinopyranosyl-(1,6)-β-D-glucopyranoside. Paeonolide, a natural glycoside from the roots of the plant genus Paeonia, is not hydrolyzed by classical GH42 β-galactosidases. X-ray crystallography revealed a unique Trp345-X12-Trp358 sequence motif at the BlArap42B active site, as compared to a Phe-X12-His motif in classical GH42 β-galactosidases. This analysis also indicated that the C6 position of galactose is blocked by the aromatic side chains, hence allowing accommodation only of Arap lacking this carbon. Automated docking of paeonolide revealed that it can fit into the BlArap42B active site. The G1ep moiety of paeonolide stacks onto the aromatic ring of the Trp252 at subsite +1 and C4-OH is hydrogen bonded with Asp249. Moreover, the aglycone stacks against Phe421 from the neighboring monomer in the BlArap42B trimer, forming a proposed subsite +2. These results further support the notion that evolution of metabolic specialization can be tracked at the structural level in key enzymes facilitating degradation of specific glycans in an ecological niche.

The complex microbial consortium in the human gastrointestinal tract, referred to as the gut microbiota, has an increasingly recognized vital role in human health (1). Human diet is rich in a wide variety of non-digestible saccharides from plants and animals, and glycan metabolism is a pivotal factor shaping the dynamics and the evolution of gut microbiota (2). Specific taxa gain a competitive edge in fitness in this highly competitive niche through metabolic
specialization, which is reflected by their enzymatic machinery being fine-tuned for specific glycans (3). Glycans containing β-galactoside are abundant in human infant and adult nutrition (4–6), and hydrolysis of the β-galactoside bond by β-galactosidases is a prerequisite for their utilization.

Key enzymes in the hydrolysis and utilization of β-galactosides in gut microbes assign into glycoside hydrolase (GH) family 42 in the sequence-based classification system of the Carbohydrate Active enZymes (CAZy) database (7). Genomes of probiotic strains from the Bifidobacterium genus often encode several GH42 enzymes (8) with distinct subfunctionalities matching diversity and abundance of β-galactosides. For example, B. longum subsp. infantis encodes three GH42 β-galactosidases related to the utilization of the human milk oligosaccharide lacto-N-tetraose (LNT), β-galactosides from bovine milk and arabinogalactan, respectively (9). A similar specialization exists in Bifidobacterium breve that encodes two GH42 β-galactosidases, one targeting LNT (10) and the other plant galactan (11). Notably, B. bifidum utilizes mucin-derived β-galactosidases from the glycoprotein layer coating the human host in epithelial colonocytes (12), which is proposed to be possible through a key GH42 β-galactosidase (13).

The genome of B. animalis subsp. lactis BI-04 encodes two GH42 enzymes (14). Galactooligosaccharides (GOS) were shown to up-regulate gene locus balac_0848 (15), experimentally verified to be a β(1,6)/β(1,3) galactosidase (BldGal42A) (13). The second GH42 (BldArap42B) gene with locus tag balac_0053 was not differentially upregulated by GOS (15), and belongs to a distinct, not previously characterized clade of bifidobacterial GH42 enzymes (16).

This distinct clade is here shown to form a novel GH42 subfamily present throughout the bacterial kingdom, which seems to have exclusive α-L-arabinopyranosidase specificity as evaluated for the soluble intracellular BldArap42B using a panel of pNP-substrates and oligosaccharides. BldArap42B effectively hydrolyzed paconolide (Figure 1A), a plant glycoside which contains a non-reducing end α-L-arabinopyranoside and is found in the roots of the widespread plant genus Paeonia (17). This apparent metabolic specialization could be tracked at the structural level, as the crystal structure of BldArap42B suggested GH42 members with α-L-arabinopyranosidase activity recognize their substrates through an active site Trp345-Trp358 motif as compared to a Phe-His motif in classical GH42 β-galactosidases.

RESULTS

Biochemical properties—The recombinant BldArap42B was produced and purified to electrophoretic homogeneity. BldArap42B migrated as a single band in SDS-PAGE with the expected theoretically calculated molecular mass of 78.3 kDa. Analytical gel filtration data showed that the protein eluted as a single peak corresponding to 201 kDa. Although this is smaller than the theoretically calculated size for the trimer (235 kDa), GH42 enzymes, which are generally trimeric, usually exhibit similar discrepancy between their size estimations using gel filtration chromatography and crystallography (18). BldArap42B showed significant activity towards p-nitrophenyl (pNP) α-L-arabinopyranoside (α-L-Arap), very low activity towards pNP-β-D-galactopyranoside (pNP-β-D-Galp) and pNP-β-D-fucopyranoside (pNP-β-D-Fucp), and no detected activity on pNP-α-L-arabinofuranoside (pNP-α-L-Araf), pNP-β-D-xylopyranoside (pNP-β-D-Xylp), and pNP-β-D-glucopyranoside (pNP-β-D-Glcp) (Table 1). The kinetics of hydrolysis of pNP-α-L-Arap were best described by Michaelis-Menten kinetics with $k_{cat} = 160 \pm 10 \text{s}^{-1}$ and $K_m = 3.4 \pm 0.4$ mM. RlArap42B, a homologue from Roseburia intestinalis M50/1 (Firmicutes isolated from human gut), sharing 42% sequence identity with BldArap42B (Actinobacteria), has a similar activity profile on aryl substrates (Table 1). BldArap42B displays significant activity towards 2-acetyl-5-methoxyphenyl-α-L-Arap-(1,6)-β-D-Glcp (paconolide, Figure 1A) in a 30 min assay, with complete hydrolysis by overnight incubation as verified by TLC (Figure 1B). We also tested the activity of BldArap42B on plant glycosides containing a terminal α-L-arabinopyranoside group, paconolide, ginsenoside Rb2, and quercetin 3-O-α-L-Arap (Figure 1A), by high-performance anion-exchange chromatography with pulsed amperometric detection (HPAEC-PAD) (Figure 1C). Ginsenoside Rb2 is a triterpene saponin isolated from the root of Panax ginseng (19) while quercetin 3-O-α-L-Arap is a flavonoid isolated
from the aerial parts (leaves) of Alchemilla xanthochlora (Lady's Mantle) (20) and Psidium guajava L. (guava) (21). BlArap42B hydrolyzed paeonolide and ginsenoside Rb2 (Figure 1C) but did not quercetin 3-O-α-L-Arap (data not shown). Kinetic parameters toward the plant glycosides indicate that these substrates exhibit significantly lower $K_m$ (<0.1 mM) and higher catalytic efficiencies (>1500 mM$^{-1}$s$^{-1}$) compared with those of pNP-α-L-Arap (Table 2). By contrast, no activity was observed on an extensive series of β-galactosides from plants and mammals, including human milk (list of substrates in the experimental procedures). Bga42A (Blon 2016), Bga42B (Blon 2123), and Bga42C (Blon 2416) from B. longum subsp. infantis ATCC 15697, and BlGal42A from B. animalis subsp. lactis Bl-04, which are distantly related to BlArap42B (see Figure 4), did not cleave paeonolide, although they were able to slowly hydrolyze pNP-α-L-Arap (Figure 1B).

Three-dimensional structure of BlArap42B—The three-dimensional structure of BlArap42B in its ligand-free form was determined by X-ray crystallography at 2.0 Å resolution with six chains (two trimers) in the asymmetric unit. Data collection, refinement and stereochemical statistics are summarised in Table 3. BlArap42B is homotrimer of a 701 residues subunit, with three subunits related by a 3-fold axis (Figure 2A). Each subunit consists of three domains. Domain A is a ($β$/$α$)$_3$ barrel containing the catalytic residues. Domain B is a structural domain that packs onto Domain A of the adjacent monomer. Domain C, whose role is unknown, adopts an anti-parallel β-sandwich fold. The first seven residues (Met1–Asp7) and the region Pro663–Thr672 in all six chains, as well as a variable number of residues in the C-terminus of each chain (Gly695–Asn701), were disordered and not included in the final model.

BlArap42B active-site architecture and ligand docking—Similar to structures of GH42 β-galactosidases, the active sites and the vicinity encompassing the proposed subsites +1 and +2 are formed at the interface of two adjacent monomers in the BlArap42B trimer (18). It was possible to dock an energetically preferred conformation of paeonolide, the preferred substrate for BlArap42B, into the active site with an estimated affinity of ~8.8 kcal mol$^{-1}$ (Figure 2B). The docked paeonolide molecule makes an intramolecular hydrogen bond between the acetyl oxygen of the aglycon (Figure 1A) and C2-OH of the Glcp. The Arap ring binds at subsite −1, with distances of 3.3 Å between the catalytic nucleophile Glu311 and the anomeric carbon and 2.9 Å between the catalytic acid/base Glu151 and the glycosidic oxygen, respectively. The Glcp ring bound at subsite +1, is stacking onto Trp252, and C4-OH is hydrogen bonded with Asp249. Furthermore, the aromatic ring of the aglycone and Phe421 from the neighboring monomer are almost parallel, making an aromatic stacking at this position, indicative of the presence of a subsite +2.

Comparison with the BlGal42A β-galactosidase structure—The structure of BlArap42B was compared to that of the other GH42 enzyme from the same organism (BlGal42A) that has specificity towards β(1,6)/β(1,3)-galactoside linkages and is one of the best characterized enzymes (both biochemically and structurally) among GH42 β-galactosidases (13). Figure 3A shows superimposition of the structures of BlArap42B and BlGal42A in complex with galactose (PDB: 4UNI). From the structural comparison, Glu151 and Glu311 of BlArap42B were inferred as the acid/base catalyst and the catalytic nucleophile, respectively. Although BlArap42B and BlGal42A only share 25% sequence identity their overall structures are very similar as reflected by the root mean square deviation (RMSD) for C$_a$ atoms of 1.75 Å when chain A (689/695 residues) of BlGal42A is superimposed on chain A (682/701 residues) of BlArap42B.

Remarkably, three residues at the substrate binding site are either variant or spatially differently located in BlArap42B as compared to BlGal42A (Figure 3A). Trp345 is phenylalanine in BlGal42A (Phe362) and the aromatic side chain is involved in substrate recognition in subsite −1 by forming a hydrophobic platform for the C4 side of the arabinono- or galactopyranoside. The change of a histidine in BlGal42A (His375) to Trp358 restricts the space in subsite −1 around the C6-O6 hydroxymethyl group of galactoside, which is not present in arabinopyranoside (Figure 3B). Moreover, Trp332 of BlGal42A makes a hydrogen
bond to the C6-OH of galactose, and is also proposed to mediate aromatic stacking to substrate at subsite +1 in GH42 β-galactosidases. In contrast, the conformation of the loop containing Trp332 is different in BlArap42B and locates a tryptophan at the corresponding position in the sequence (Trp320, not shown in Figure 3A), distinctly from the active site in space. Instead, a differently located Trp252, which is not conserved in previously characterized GH42 enzymes, is taking the role of stacking platform at subsite +1 in BlArap42B. Additionally, Met268 in BlGal42A replaces Asp249 that in the docked structure of BlAra42B forms a hydrogen bond to the Glcp C4-OH in paeonolide.

**Mutational analysis**—From the structural comparison with BlGal42A, two non-conserved residues (Trp345 and Trp358) are identified in subsite −1. To examine the role of these residues in relation to substrate specificity, these single residues were replaced using site-directed mutagenesis with those found in the β-galactosidase (Phe or His). Table 1 shows specific activities of the single (W345F and W358H) and double (W345F/W358H) mutants towards pNP-substrates, the single mutants having more than 10-fold reduced activity on pNP-α-L-Arap and the double mutant being almost inactive. W358H was slightly active on pNP-β-D-Fucp, but none of the mutants showed detectable activity on pNP-β-D-Galp or any of the other pNP-substrates. Clearly, the substrate specificity of the GH42 α-L-arabinopyranosidase was not changed to β-galactosidase by these simple mutations.

**Phylogeny and active site motifs of GH42—** A phylogenetic and active site sequence motif analysis of GH42 α-L-arabinopyranosidases (subfamily A) and β-galactosidases (subfamily G), divides GH42 into two subfamilies, respectively (Figure 4). BlArap42B assigns into a distinct uncharacterized clade, group one (G1) in the phylogenetic tree. Based on sequence analysis, it is evident that the two tryptophan residues (Trp345 and Trp358) in BlArap42B are conserved in G1 and subfamily A, and comprise a unique Trp-X-Trp sequence motif through the active site as compared to subfamily G that includes G2–G4. All of the G2–G4 groups of subfamily G contain at least one characterized β-galactosidase that has a Phe-X-His motif. Trp252 of BlArap42B in subsite +1 is conserved in G1 but not in G2–G4 (data not shown).

**DISCUSSION**

BlArap42B is a novel GH42 α-L-arabinopyranosidase—The GH42 family has been assumed very homogenous since all hitherto characterized members exhibited β-galactosidase activity despite representing broad diverse taxa. This further indicated active site conservation within the family, where evolution of the molecular machinery was driven towards subtle changes in the plus subsites for fine-tuning specificities, e.g. for β(1,6), β(1,4), or β(1,3)-linked galactosides or N-acetyl-glucosides (22–24).

While GH42 BlArap42B from *B. animalis* subsp. *lactis* Bl-04 was unable to hydrolyze synthetic β-galactosides and those from plants, mammalian milk and host mucin, so far demonstrated as substrates for GH42 β-galactosidases, it was able to hydrolyze, the different yet structurally similar, α-L-arabinopyranosides (Tables 1, 2 and Figure 1). BlArap42B effectively released α-L-arabinopyranose from paeonolide and ginsenoside Rb2, both containing an aglycone conjugated to α-L-Arap-(1,6)-β-D-Glc, but was unable to hydrolyze quercetin 3-O-α-L-Arap. The subsite +1 is apparently specific for the β(1,6)-linked glucoside with Trp252 as a sugar-stacking residue (Figure 3A), and aromatic residues surrounding this site (Trp358, Phe354, and Phe421) probably make steric clash with the large flavonoid group of quercetin 3-O-α-L-Arap. Thus, BlArap42B have the capabilities to discriminate substrates beyond subsite −1 and demonstrate the potential existence of different α-L-arabinopyranoside specificities. Previously characterized bifidobacterial GH42 β-galactosidases tested here, did not cleave paeonolide, although they were able to hydrolyze pNP-α-L-Arap (Figure 1B). BlArap42B is clearly a GH42 α-L-arabinopyranosidase, distinctly different from previously characterized GH42 enzymes. The *k*<sub>cat</sub> (240 s<sup>−1</sup>) and *K*<sub>m</sub> (0.074 mM) values of BlArap42B towards its preferred substrate, paeonolide, are in the same range as those of previously characterized GH42 enzymes towards their preferred substrates (13, 24).
Structural specificity determinants in GH42 α-L-arabinopyranosidases—The residues creating the spatial and chemical environment at subsite −1 are invariant in characterized GH42 β-galactosidases (13, 18, 22, 26, 27). However, the change from a histidine residue in classical GH42 β-galactosidases to Trp358 in BI/Arap42B limits the space at subsite −1, which would cause clashing with C6 of galactose in accordance with BI/Arap42B being unable to hydrolyze β-galactosides (Figure 3B). A similar structural change is observed between GH27 α-D-galactosidases and β-L-arabinopyranosidases, the only other similar described activity. In GH27 β-L-arabinopyranosidases, a mutagenesis study revealed that the single substitution from an aspartic acid to the slightly larger glutamic acid in the catalytic pocket around the C-6 of galactose as compared to GH27 α-D-galactosidases is critical for modulating the enzyme activity (28). However, a similar attempt to change the specificity of BI/Arap42B from α-L-arabinopyranosidase to β-galactosidase through the single and double mutations of Trp345 and Trp358 failed (Table 1). This may suggest that the active site of this enzyme is optimized to α-L-arabinopyranoside through accumulation of other substitutions around subsite −1 during the molecular evolution after it diverged from the β-galactosidases.

Notably, a major change is observed in the positioning of the subsite +1 stacking platform and potential recognition of hydroxyl groups between BI/Arap42B and BI/Gal42A (Figure 3A). Superimposing the docked paeonolide from BI/Arap42B into BI/Gal42A shows the phenyl aglycone clashes with the backbone of Trp332, which is invariant and similarly spatially located in structurally characterized GH42 enzymes (13, 18, 22, 26, 27), and Phe226 of the neighboring monomer in BI/Gal42A, which can explain its lack of activity for paeonolide (Figure 3C). The present findings indicate that GH42 α-L-arabinopyranosidases have evolved from a common scaffold to target specific α-L-arabinopyranosides present in plant oligosaccharides.

BI/Arap42B defines a novel GH42 α-L-arabinopyranosidase subfamily—Applying a phylogenetic and sequence analysis approach links the α-L-arabinopyranoside specificity of BI/Arap42B with a unique Trp-X12-Trp sequence motif at the active site, as opposed to Phe-X12-His in classical bifidobacterial GH42 β-galactosidases (Figure 4). The Trp-X12-Trp sequence motif is present in enzymes with a GH42 catalytic domain from more than 150 different bacterial species and subspecies of various phyla, and uncovers a novel α-L-arabinopyranosidase subfamily (subfamily A) distinct from GH42 β-galactosidases (subfamily G). As a confirmation that the subfamily division reflects specificity, we have shown that RI/Arap42B, a homologue and subfamily A member from a human gut bacterium, Roseburia intestinalis M50/1 (29), shows the same activity profile on pNP-derivatized substrates, hydrolyzing pNP-α-L-Arap, but not pNP-β-D-Galp (Table 1), supporting the exclusive activity towards α-L-arabinopyranoside of this subfamily. Noticeably, BgaA from Clostridium cellulovorans (30), belonging to subfamily G, contains a Phe-X12-Trp-mixed sequence motif and is the only α-L-arabinopyranosidase currently assigned to GH42 in the CAZy database. Clostridium cellulovorans BgaA, however, hydrolyzes pNP-β-D-Galp with about 10% activity of pNP-α-L-Arap (30) as opposed to BI/Arap42B that shows <0.15% activity of pNP-α-L-Arap on pNP-β-D-Galp.

Subspecificities within the α-L-arabinopyranosidase subfamily A—Distinct groups clearly exist within subfamily A (Figure 4), with members of different groups organized in different gene landscapes. The gene encoding BI/Arap42B is located adjacent to a gene encoding a putative GH30 enzyme, with no close characterized homologues based on sequence similarity, as well as in the near vicinity of a putative GH3 enzyme (BI/GH3). The closest characterized homologue to BI/GH3 is the GH3 Apy-H1 from B. longum H-1, showing 61% sequence identity and 74% similarity, and dual α-L-arabinopyranosidase / β-galactosidase specificity, releasing α-L-arabinopyranoside from ginsenoside Rb2 found in Panax ginseng (31). Interestingly, BI/Arap42B is also able to release α-L-arabinopyranoside from ginsenoside Rb2 with high efficiency. This gene cluster in B. animalis subsp. lactis BI-04 likely targets α-L-arabinopyranosides found in plants of especially Asian origin (17, 32). Similarly, a GH3
member is encoded adjacent to the gene of RiArap42B in R. intestinalis M501, but it clusters with characterized xylan β(1,4) xylosidases based on a phylogenetic analysis of this family (data not shown).

The genes surrounding the gene encoding a putative GH42 α-L-arabinofuranosidase from Bacteroides uniformis ATCC 8492 (Bu42B) of subfamily A (Figure 4) contains all glycoside hydrolase-encoding genes necessary for complete utilization of xyloglucan oligosaccharides (33), suggesting that α-L-arabinofuranosidases exist in xyloglucan, but this has yet to be identified. Generally, α-L-arabinopyranosidase is sparsely reported in plant oligosaccharides, which is in sharp contrast to the evident appearance of BlArap42B homologues in different gene landscapes found throughout the bacterial kingdom. GH42 α-L-arabinopyranosidases therefore may prove useful in the identification of α-L-arabinopyranosides in plant glycans, oligosaccharides and glycoconjugates.

α-L-Arabinofuranosidase activity in the human gut niche—Recently, the human gut microbe Bacteroides thetaiotaomicron was shown to be capable to completely depolymerise the highly complex pectic Rhamnogalacturonan II, containing buried α-L-Arap-(1,4)-β-D-Galp, through the novel BT0983 GH2 α-L-arabinofuranosidase (34). Additionally, the human gut microbe B. breve K-110, isolated from healthy adults, can utilize ginsenoside Rb2 (35). However, the internal amino acid sequence (VIYLTDA) of the purified α-L-arabinofuranosidase from B. breve K-110 match with an AAA+ family ATPase but not with any GHs in the genome sequences, suggesting that the sequence was derived from a contaminated protein. Since ginsenoside Rb2 was effectively hydrolyzed by BlArap42B, B. animalis subsp. lactis BI-04 is potentially conferred with the ability to utilize this compound. The present study reports the enzymology and structure of a GH42 α-L-arabinopyranosidase from the probiotic B. animalis subsp. lactis BI-04, uncovering the existence of a distinct GH42 subfamily, with novel specificity towards α-L-arabinopyranosides and identifying a unique associated active site sequence motif. The molecular insights together with a deep phylogenetic analysis identify key structural elements discriminating the GH42 α-L-arabinopyranosidases from the classical GH42 β-galactosidases. The phylogenetic analysis uncovered the existence of unexpectedly large number (>150) of potential GH42 α-L-arabinopyranosidases in bacterial genomes. It is noteworthy that the plant glycosides effectively hydrolyzed by BlArap42B, paenonolide and ginsenoside Rb2, are contained in traditional herbal medicines in East Asian countries, such as Cortex Moutan (Mu Dan Pi in Chinese and Botanpi in Japanese) and Asian Ginseng, suggesting that other edible root vegetables may also contain certain amounts of glycosides with an α-L-arabinopyranoside. Altogether, these results indicate that α-L-arabinopyranoside metabolism evolved in different ecological niches and probably is widespread in important probiotic members of the human gut microbiota.

**EXPERIMENTAL PROCEDURES**

Substrates—pNP-β-D-galactopyranoside (pNP-β-D-Galp), pNP-β-D-glucopyranoside (pNP-β-D-Glcp), pNP-α-L-arabinofuranoside (pNP-α-L-Araf), pNP-α-L-arabinopyranoside (pNP-α-L-Arap), pNP-β-D-fucopyranoside (pNP-β-D-Fucp), and pNP-β-D-xylolpyranoside (pNP-β-D-XyLP) were purchased from Sigma-Aldrich (St. Louis, MO, USA). 4-β-galactobiose, 6-β-galactobiose, LacNAc were purchased from Dextra Laboratories (Readings, UK). Lacto-N-biose I (LNB) and galacto-N-biose (GNB) were synthesised as described previously (36, 37). Lacto-N-tetraose (LNT) and lacto-N-neotetraose (LNNT) were purchased from Elicityl (Crolles, France). 2-Acetyl-5-methoxyphenyl α-L-Arap-(1,6)-β-D-Glcp (paenonolide), ginsenoside Rb2, and quercetin 3-O-α-L-Arap was purchased from Tokyo Chemical Industry (Tokyo, Japan), Carbosynth (Berkshire, UK), and eNovation Chemicals LLC (Bridgewater, NJ, USA), respectively.

Expression and Purification—The gene encoding a putative GH42 enzyme (locus tag: balac_0053, GenBank accession number ACS45449.1) was amplified from Bifidobacterium animalis subsp. lactis BI-04 genomic DNA by PCR using High-fidelity DNA polymerase (Fermentas, St. Leon-Rot, Germany) with the following primers: 5′-CTA GCT AGC GCC CGC GCA TAC ACC-3′; reverse: 5′-ATA AGA ATG CGG CCG CAT TCA

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**REFERENCES**

TTG TGG GTT GC-3'. Amplified DNA was cloned into pET21(a)+ (Novagen, Darmstadt, Germany) using the NheI and NotI restriction sites (underlined) resulting in BlArap42B with a C-terminal His-tag. *Escherichia coli* BL21 (DE3) ΔlacZ(β-Gal) containing the above expression plasmid was grown at 20 °C in 1 L Luria-Bertani medium containing 50 μg ml⁻¹ ampicillin and 34 μg ml⁻¹ chloramphenicol to an OD₆₀₀ of 0.5, and expression was induced by 100 μM isopropyl-β-thiogalactopyranoside for 36 h at 18 °C. The recombinant enzyme (BlArap42B) was purified using a 5 mL HisTrap HP column (GE Healthcare) with a linear gradient 2.5–100% 400 mM imidazole (20 mM HEPES buffer, 0.5 M NaCl, pH 7.5). The His-purified fractions were pooled and purified by gel filtration (HiLoad 26/60 Superdex G200; GE Healthcare) in 10 mM MES, 150 mM NaCl (pH 6.5) eluted by 1.2 column volume of this buffer at a flow rate of 1 mL min⁻¹. The purity of the enzyme was analysed by SDS-PAGE. The enzyme concentration was determined spectrophotometrically (ε₂₈₀ = 152,890 M⁻¹ cm⁻¹). The W345F and W358H, and double W345F/W358H mutants were constructed using the QuikChange<sup>®</sup> Site-Directed Mutagenesis Kit (Stratagene, California, USA), and the recombinant proteins were prepared and purified as described for the wild-type. The gene with locus tag Roi_37780 from *Roseburia intestinalis* M50/1 (GenBank accession number CBL10553.1) encoding a homologue of BlArap42B was synthesised with a C-terminal His-tag and cloned into pET21(a)+ (GenScript, USA), expressed and the resulting recombinant protein (RiArap42B), was purified as described above for BlArap42B. Bga42A, Bga42B, and Bga42C from *B. longum* subsp. *infantis* ATCC 15697, and BlGal42A from *B. animalis* subsp. *lactis* BI-04 were prepared as previously described (13, 24).

**Biochemical Characterization—Activity** was assayed towards pNP-β-D-Galp, pNP-α-L-Arap, pNP-β-D-Fucp, pNP-α-L-Araf, pNP-β-D-Glcp, and pNP-β-D-XyIp (final conc. 5 mM) at 37 °C in 40 mM sodium citrate, 0.005% Triton X-100, pH 6.5 (50 μL) by addition of enzyme (2–2,000 nM) and stopping the reaction after 10 min by 1 M Na₂CO₃ (200 μL) for BlArap42B wild-type and mutants, and RiAra42B. The amount of released pNP was measured spectrophotometrically at A₄₁₀ using pNP (0–2 mM) as standard. One unit of activity was defined as the amount of enzyme that released 1 μmol pNP min⁻¹. The kinetic parameters k₉₅ and Kₙ were determined from initial rates of pNP-α-L-Arap (0.5–7.5 mM) hydrolysis in the above buffer by non-linear regression fit of the Michaelis-Menten model: v = k₉₅ [E] × [S] / (Kₙ + [S]) to data from triplicate experiments (GraphPad Prism 6, La Jolla, USA). Activity of BlArap42B as well as Bga42A, Bga42B, and Bga42C from *B. longum* subsp. *infantis* ATCC 15697, and BlGal42A and *B. animalis* subsp. *lactis* BI-04 (75–125 nM) were measured towards 4 mM pNP-α-L-Arap and 4 mM paeonolide in 50 mM sodium phosphate pH 6.5 at 30°C for 30 min and 24 h and monitored by TLC. HPAEC-PAD experiments were carried out using a Dionex ICS-3000 HPLC system (Chromelone software version 6.80, Dionex) with a Dionex Carbotrap PA20 column. The analytes were separated using 40 mM NaOH in isocratic mode at 0.5 ml min⁻¹. Initial hydrolysis activities were measured using 20 nM BlArap42B at 30 °C in 40 mM sodium citrate (pH 6.5) towards paeonolide, ginsenoside Rb2, and quercetin 3-O-α-L-Arap (100 μM) in 19.2 – 65.2 min assays. The kinetic parameters k₉₅ and Kₙ were determined from initial rates of paeonolide, and ginsenoside Rb2 (7.812 – 1000 μM) using 40 PM BlArap42B at 30 °C in the above buffer at 4 time points by integrating the area of the peaks corresponding to released L-arabinose.

**Crystallization, Data Collection, and Structure Determination of BlArap42B** BlArap42B was concentrated to 12.0 mg ml⁻¹ in 10 mM MES pH 6.5, 150 mM NaCl and screened for initial crystallization conditions at 20 °C with the JCSG core I–IV screens (Qiagen). Crystals were observed in the JCSG core IV screen (1.5 M ammonium sulfate, 12% glycerol (v/v), 0.1 M Tris pH 8.5). The final crystallization condition was 12% glycerol, 1.6 M ammonium sulfate, 0.1 M MES buffer pH 6.5 obtained from optimization in 24-well VDX trays (Hampton Research) in sitting drops containing 1 μL protein stock and 1 μL reservoir at 20 °C. Glycerol (20% final conc.) was added as cryoprotectant before harvesting.

A data set to 2.0 Å resolution was obtained at the BL5A beamline, Photon Factory, Tsukuba,
Japan. Processing and scaling of the data was done with HKL2000 (38). The space group was determined to be P41212 with six molecules in the asymmetric unit. Molecular Replacement was performed using Balbes (39) with a chain of the homotrimer of the PDB entry code 1KWG (18) as the initial search model. ARP/wARP (40) was used to partially build the structure, and refinement was completed using Coot (41) and Refmac5 (42).

The quality of the structures, including Ramachandran statistics, was verified by MolProbity (43), and PyMOL v1.8.5 (Schrödinger, LLC, New York) was used for structural analysis and rendering of molecular graphics.

**Ligand preparation and docking**–Paeonolide was prepared from the PubChem project (CID: 92043525) and PCModel v 9.20 (Serena Software) using energy minimisation with MMX force field. The energy minimised molecule was docked into the active site of BlArap42B using AutoDock Vina 1.1.2 (44) with the grid box (16 Å × 16 Å × 16 Å) centred on the scissile glycosidic bond oxygen. The ligand structure was docked with flexible torsion angles, whereas the protein structure was fixed.

**Bioinformatics analysis**–The amino acid sequences of bifidobacterial GH42 members were extracted from the CAZy database (7) using CAZy Tools (A. H. Viborg, http://research.ahv.dk/cazy) and aligned using MUSCLE v3.8 with default settings (45). The active site sequence motif (WHWHSIHNSFETYW) for group one (G1) and (FQWRQSRGGAEKFH) for group two, three, and four (G2, G3, and G4) were queried against the NCBI nr-database using BLASTP. Non-identical sequences were extracted and the redundancy was decreased by USEARCH (46) to yield approximately 200 sequences from each of the two sequence motifs, which were merged with the bifidobacterial entries and previously characterized GH42 enzymes. Sequence motif logos for the subfamilies were rendered by WebLogo 3 (47). ClustalW2 was used to render a phylogenetic tree with default settings, which was visualised in Dendroscope 3.0 (48).

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**Conflict of interest:** The authors declare that they have no conflicts of interest with the contents of this article.

**Author contributions:** AHV, MAH, and BS conceived the study. AHV conducted most of the experiments and analysed the results. AHV wrote the manuscript with contributions from SF. TK conducted TLC experiments on the hydrolysis of paeonolide. TA and SF assisted in X-ray data collection, structure determination and analysis. SF performed molecular replacement and ligand docking. LLL assisted in preliminary crystallisation trials, structural analysis and verification. TK, MAH, MK and BS assisted in experimental design and analysis of the data. All authors reviewed the results and approved the final version of the manuscript.
REFERENCES


**FOOTNOTES**

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*The atomic coordinates and structure factors (code 5XB7) have been deposited in the Protein Data Bank (http://wwpdb.org/).*

The abbreviations used are as follows: CAZy, Carbohydrate Active enZymes; GH, glycoside hydrolase; GNB, galacto-N-biose; GOS, galacto-oligosaccharide; HPAEC-PAD, high-performance anion-exchange chromatography with pulsed amperometric detection; LNB, lacto-N-biose I; LNnT, lacto-N-neotetraose; LNT, lacto-N-tetraose; pNP, p-nitrophenyl; RMSD, root mean square deviation.
FIGURE LEGENDS

FIGURE 1. (A) Chemical structures of substrates, (B) TLC analysis on the hydrolysis of pNP-α-L-Arap and paenolide by BI/Arap42B and other GH42 enzymes, and (C) HPAEC-PAD analysis on the hydrolysis of plant glycosides containing a non-reducing end α-L-arabinopyranoside by BI/Arap42B.

(A) Structures of pNP-α-L-Arap, pNP-β-D-Fucp, pNP-β-D-Galp, and paenolide, ginsenoside Rb2, and quercetin 3-O-α-L-Arap are shown. pNP-α-L-Arap and pNP-β-D-Fucp differ from pNP-β-D-Galp by lacking C6 and C6-OH, respectively. Non-reducing end α-L-arabinopyranose is found in 2-acetyl-5-methoxynaphthalene-α-L-Arap-(1,6)-β-D-Glc (paeonolide) from Paeonia, ginsenoside Rb2 from Panax ginseng and quercetin 3-O-α-L-Arap from Psidium guajava Linn. (B) Substrate activity screening using TLC of BI/Arap42B (4) and previously characterized bifidobacterial GH42 β-galactosidases, Bga42A (1), Bga42B (2), and Bga42C (3) from B. longum subsp. infantis ATCC 15697 as well as BI/Gal42A (5) from B. animalis subsp. lactis Bl-04. (0) is control without enzyme. BI/Arap42B (4) displayed significant activity towards paenolide by 30 min incubation, with complete hydrolysis overnight. Bga42A, Bga42B, Bga42C, and BI/Gal42A did not show significant activity towards paenolide after 24 h incubation, despite their ability to hydrolyze pNP-α-L-Arap. (C) HPAEC-PAD chromatograms showing activity towards paenolide and ginsenoside Rb2. Paenolide is the de-arabinosylated product of paenolide. Activity was not detected towards quercetin 3-O-α-L-Arap. Peaks corresponding to the substrate ginsenoside Rb2 and its de-arabinosylated product (= ginsenoside Rd) could not be detected in the elution range under the conditions employed (see Experimental Procedures).

FIGURE 2. Overall structure and docking of paenolide into BI/Arap42B.

(A) Top view along the axis of the BI/Arap42B trimer with docked paenolide shown as spheres in one of the three active sites. (B) Active site residues of BI/Arap42B shown with docked paenolide. The Ara moiety binds at subsite −1 with distances of 3.3 Å between the catalytic nucleophile Glu311 and the anomic carbon, and 2.9 Å between the catalytic acid/base Glu151 and the glycosidic oxygen. Glcp participates in an aromatic stacking interaction with the proposed subsite +1 platform Trp252 and C4-OH hydrogen bonds to Asp249. Paenolide in this conformation can form an intramolecular hydrogen bond between its acetyl oxygen and C2-OH of the Glcp. The neighboring monomer participates in determining the substrate specificity by Phe421 engaged in aromatic stacking with the phenyl group of paenolide at a possible subsite +2.


(A) Stereo view of the comparison of the active site with subsites −1 through +2 of BI/Arap42B (green) and the BI/Gal42A β-galactosidase (white and grey) in complex with galactose from B. animalis subsp. lactis Bl-04 (PDB: 4UNI). Trp345 and Trp358 occupy the active site environment in BI/Arap42B, as compared to the smaller side chains of Phe362 and His375 in BI/Gal42A. The subsite +1 aromatic stacking platform is composed of Trp residues from different loops (Trp252 in BI/Arap42B and Trp332 in BI/Gal42A) and are spatially differently located in the two enzymes. (B) The residues of subsite −1 of BI/Arap42B overlaid with galactose from BI/Gal42A (sphere). The Trp358 of BI/Arap42B, which is the smaller His in BI/Gal42A, is clashing with the C6-OH of galactose in complex with BI/Gal42A, explaining lack of activity towards β-galactosides of BI/Arap42B. (C) Active site residues of BI/Gal42A with paenolide docked from BI/Arap42B shown as spheres. Both the side chains of Trp332 and Phe226 at subsite +1 and +2 sterically hinder the docking of paenolide, in agreement with the lack of activity for BI/Gal42A.

FIGURE 4. BI/Arap42B defines a novel GH42 α-L-arabinopyranosidase subfamily.
The phylogenetic tree of GH42 enzymes, divides the family into the two distinct α-L-arabinopyranosidases (subfamily A) and β-galactosidases (subfamily G) subfamilies, respectively. Bifidobacterial GH42 enzymes (black) from the CAZy database reveals four distinct groups, with functional assignment for groups G2, G3 and G4. Group G1 was previously uncharacterized and multiple sequence alignment shows this group is diverse and comprises a unique Trp-X$_{12}$-Trp sequence motif as compared to the Phe-X$_{12}$-His sequence motif of group G2, G3 and G4. Approximately 200 non-identical sequences (grey) found throughout the bacterial kingdom from each of the two Trp-X$_{12}$-Trp and Phe-X$_{12}$-His sequence motifs were merged with the bifidobacterial GH42 sequences and previously characterized GH42 enzymes (grey) to yield the phylogenetic tree.
<table>
<thead>
<tr>
<th>Substrate</th>
<th>BLArap42B</th>
<th></th>
<th></th>
<th>RiArap42B</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Wild-type</td>
<td>W345F</td>
<td>W358H</td>
<td>W345F/</td>
</tr>
<tr>
<td>pNP-α-L-Arap</td>
<td>79.0 ± 0.7</td>
<td>2.7 ± 0.1</td>
<td>5.9 ± 0.1</td>
<td>0.1 ± 0.0</td>
</tr>
<tr>
<td>pNP-β-D-Galp</td>
<td>0.1 ± 0.0</td>
<td>n.d.</td>
<td>n.d.</td>
<td>n.d.</td>
</tr>
<tr>
<td>pNP-β-D-Fucp</td>
<td>1.9 ± 0.0</td>
<td>n.d.</td>
<td>0.7 ± 0.0</td>
<td>n.d.</td>
</tr>
</tbody>
</table>

U mg⁻¹ = μmol min⁻¹ mg⁻¹. n.d. not detected (<0.05 U mg⁻¹). The activity was measured at 37 °C in 40 mM sodium citrate (pH 6.5) and 0.005% Triton X-100. All enzymes including the mutants showed no detectable activity towards pNP-β-D-Glc, pNP-α-L-Ara, and pNP-β-D-Xylp.
TABLE 2. Kinetic parameters of BlArap42B on plant glycosides and pNP-α-L-Arap

<table>
<thead>
<tr>
<th>Substrate</th>
<th>$K_m$ (mM)</th>
<th>$k_{cat}$ (s$^{-1}$)</th>
<th>$k_{cat}/K_m$ (mM$^{-1}$ s$^{-1}$)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Paeonolide$^a$</td>
<td>0.074 ± 0.007</td>
<td>240 ± 10</td>
<td>3,200 ± 200</td>
</tr>
<tr>
<td>Ginsenoside Rb2$^a$</td>
<td>0.051 ± 0.018</td>
<td>79 ± 8</td>
<td>1,500 ± 400</td>
</tr>
<tr>
<td>pNP-α-L-Arap$^b$</td>
<td>3.4 ± 0.4</td>
<td>160 ± 10</td>
<td>46 ± 0.3</td>
</tr>
</tbody>
</table>

$^a$ Measured at 30 °C in 40 mM sodium citrate (pH 6.5).

$^b$ Measured at 37 °C in 40 mM sodium citrate (pH 6.5) and 0.005% Triton X-100.
### TABLE 3. Data collection and refinement statistics for BlArap42B

<table>
<thead>
<tr>
<th>Data collection</th>
<th>BlArap42B</th>
</tr>
</thead>
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<tr>
<td>Beamline</td>
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<tr>
<td>Resolution (Å)</td>
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</tr>
<tr>
<td>Space group</td>
<td>$P4_12_2$</td>
</tr>
<tr>
<td>Unit cell parameters (Å)</td>
<td>$a = b = 177.95$, $c = 375.70$</td>
</tr>
<tr>
<td>No. of reflections</td>
<td>5,987,058</td>
</tr>
<tr>
<td>No. of unique reflections</td>
<td>400,874 (19,842)</td>
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<tr>
<td>Mean $I/\sigma$ ($I$)</td>
<td>27.7 (3.8)</td>
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<tr>
<td>R-sym (%)</td>
<td>12.7 (50.2)</td>
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<tr>
<td>Completeness (%)</td>
<td>100.0 (100.0)</td>
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<tr>
<td>Redundancy</td>
<td>14.9 (14.6)</td>
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<tr>
<td>Refinement</td>
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<td>Resolution (Å)</td>
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<td>R-free (%)</td>
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<td>RMSD bond lengths (Å)</td>
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<td>RMSD bond angles (°)</td>
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<td>Average B-factors (Å$^2$):</td>
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<tr>
<td>PDB code</td>
<td>5XB7</td>
</tr>
</tbody>
</table>

Numbers in parentheses are for the highest resolution shell.
Figure 1

A

\[
\begin{align*}
\text{pNP-\(\alpha\)-Arap} & \quad \text{pNP-\(\beta\)-Arap} \\
\text{pNP-\(\beta\)-Galp} & \quad \text{Ginsenoside Rb2} \\
\text{Paenolide} & \quad \text{Quercetin 3-\(\alpha\)-Arap}
\end{align*}
\]

B

\[
\begin{align*}
pNP-Arap & \quad 30 \text{ min} \\
\text{Paenolide} & \quad \text{Paenolide}
\end{align*}
\]

C

\[
\begin{align*}
\text{Retention Time (min)} & \quad \text{Detector Response} \\
0 & \quad 1000 \\
2 & \quad 800 \\
4 & \quad 600 \\
6 & \quad 400 \\
8 & \quad 200 \\
10 & \quad 0
\end{align*}
\]

\[
\begin{align*}
\text{Paenolide} & \quad 125 \mu\text{M} \\
& \quad 19.2 \text{ min} \\
& \quad 34.6 \text{ min} \\
& \quad 49.9 \text{ min} \\
& \quad 65.2 \text{ min}
\end{align*}
\]

\[
\begin{align*}
\text{Ginsenoside Rb2} & \quad 125 \mu\text{M} \\
& \quad 19.2 \text{ min} \\
& \quad 34.6 \text{ min} \\
& \quad 49.9 \text{ min} \\
& \quad 65.2 \text{ min}
\end{align*}
\]
Figure 2
Figure 3
Discovery of \(\alpha\)-L-arabinopyranosidases from human gut microbiome expands the diversity within glycoside hydrolase family 42

Alexander Holm Viborg, Takane Katayama, Takatoshi Arakawa, Maher Abou Hachem, Leila Lo Leggio, Motomitsu Kitaoka, Birte Svensson and Shinya Fushinobu

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