



β -Diglycosidases from microorganisms as industrial biocatalysts: biochemical characteristics and potential applications

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Received: 29 May 2018 / Revised: 29 July 2018 / Accepted: 31 July 2018 / Published online: 16 August 2018
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Abstract

Flavonoid glycoside degradation can proceed through two alternative enzymatic pathways: one that is mediated by monoglycosidases, and the other catalyzed by a diglycosidase. β -Diglycosidase performs the flavonoid deglycosylation in a single reaction. The characterized β -diglycosidase activities recognize the following disaccharidic sugar moieties: β -primeverose, acuminose, vicianose, and β -rutinose. The present paper reviews the biochemical characteristics and potential industrial applications of microbial β -diglycosidases that break down plant diglycoconjugated flavonoids.

Keywords β -Diglycosidase · Enzyme catalysis · Fungi · Bacteria · Archaea

Introduction

The major flavonoid glycosides found in plants or fruits are quercetin 3-*O*-rutinoside (rutin), hesperetin 7-*O*-rutinoside (hesperidin), kaempferol-3-*O*-rutinoside, and naringenin 7-*O*-neohesperidoside (naringin) (Mazzaferro and Breccia 2011a). These compounds are involved in the bitter taste or clouding in plant-based foods or beverages, respectively.

Flavonoid glycoside degradation can proceed through two alternative enzymatic pathways: one that is mediated by monoglycosidases, and the other catalyzed by a diglycosidase. Monoglycosidases (e.g., EC 3.2.1.40: α -L-rhamnosidase), the main catalysts for deglycosylation, firstly cleave the glycosidic bond between the monosaccharide moiety and glucose. Subsequently, a β -glucosidase hydrolyzes the link between glucose and the aglycone. In contrast to this, β -diglycosidase performs the flavonoid deglycosylation in a single reaction. Many β -diglycosidases have been identified and characterized from several plants (Imaseki and Yamamoto 1961; Yasuda and Nakagawa 1994; Ogawa et al. 1997; Wirth et al. 2001; Lizotte and Poulton 1988; Mizutani et al. 2002; Suzuki et al. 2002;

Baumgertel et al. 2003; Ahn et al. 2004, 2007; Nakanishi et al. 2005; Chuankhayan et al. 2005). To our knowledge, the crystal structure of β -primeverosidase (EC 3.2.1.149) from plant *Camellia sinensis* has been the only reported β -diglycosidase crystal structure (Saino et al. 2014). There is only one previous review about these enzymes that summarize the functional and biotechnological insights into diglycosidases (Mazzaferro and Breccia 2011a). The present paper reviews the biochemical characteristics and potential industrial applications of β -diglycosidases from microorganisms that break down plant diglycoconjugated flavonoids.

Potential substrate for β -diglycosidases

Quercetin 3-*O*- β -rutinoside (rutin), kaempferol 3-*O*- β -rutinoside, hesperetin 7-*O*- β -rutinoside (hesperidin), diosmetin 7-*O*- β -rutinoside (diosmin), naringenin 7-*O*-neohesperidoside (naringin), and (S)-linalyl β -primeveroside are the major diglycoconjugated flavonoids of some plants (Fig. 1), mainly buckwheat and tea leaves, and fruits, such as apple, grape, and citrus (Mazzaferro and Breccia 2011). Hydroxynitriles, naphthoquinones, isoflavonoids, and terpenoids also consist of a diglycoside moiety. For instance, β -rutosidase (6-*O*- α -L-rhamnopyranosyl- β -D-glucosidase; EC 3.2.1.168) cleaves β -rutinose from rutin, hesperidin, and other rutinose (6-*O*- α -L-rhamnopyranosyl- β -D-glucopyranose)-containing glycoconjugates (Fig. 2).

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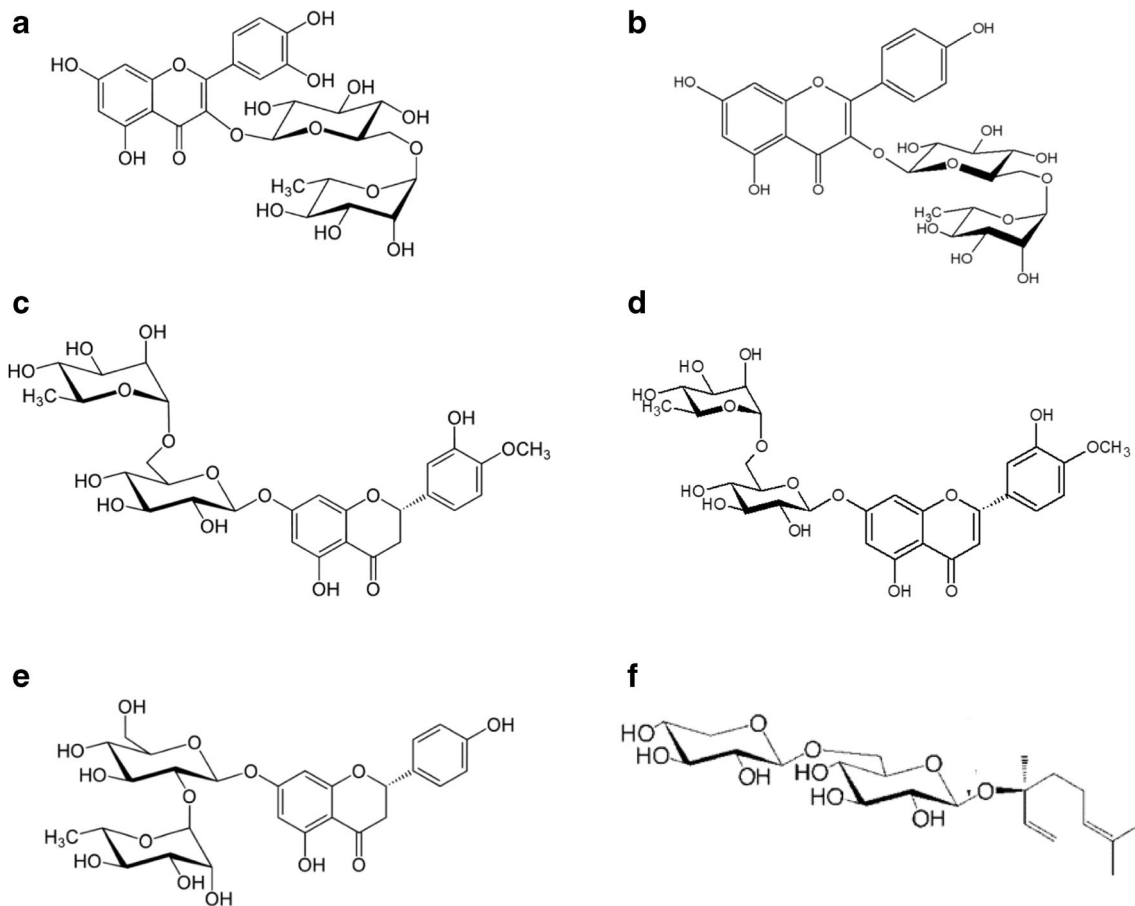


Fig. 1 Chemical structures of potential substrates for β -glycosidase activity. **a** Quercetin-3-*O*-rutinoside (Rutin). **b** Kaempferol-3-*O*-rutinoside. **c** Hesperetin-7-*O*-rutinoside (Hesperidin). **d** Diosmetin-7-*O*-

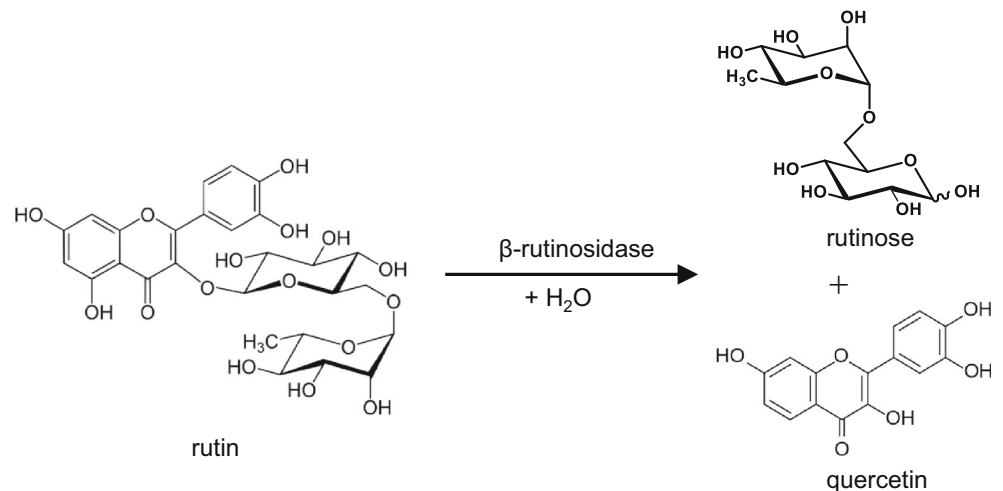
rutinoside (Diosmin). **e** Naringenin-7-*O*-neohesperidoside (Naringin). **f** (S)-Linalyl β -primeveroside

Microbial β -diglycosidases

The β -diglycosidases acting on glycoconjugated flavonoids have been predominantly reported in plants. Recently, β -diglycosidases were also described from microorganisms such as fungi, bacteria, and archae (Narikawa et al. 2000;

Yamamoto et al. 2002; Tsuruhami et al. 2006; Nam et al. 2012; Šimčíková et al. 2015; Neher et al. 2016; Ishikawa et al. 2018). These diglycosidases hydrolyze β -rutinoside (6-*O*- α -L-rhamnopyranosyl- β -D-glucopyranoside) or β -primeveroside (6-*O*- β -D-xylopyranosyl- β -D-glucopyranoside). It was found that *Acremonium* sp. SES201, *Penicillium rugulosum*

Fig. 2 Reaction scheme of the rutin hydrolysis catalyzed by β -rutinosidase



IFO7242, and *Aspergillus niger* K2 produced β -rutosidase when 0.5% hesperidin, 2% rutin, 0.5% rutin, respectively, were used as the sole carbon source (Mazzaferro et al. 2010, 2011b; Narikawa et al. 2000; Šimčíková et al. 2015). It has also been reported that the production of *Aspergillus oryzae* β -1,3-exoglucanase (ExgA) was highest when *A. oryzae* was grown with a carbon source containing flavonoids, such as quercetin and rutin (Riou et al. 1998). Moreover, β -primeverosidase from *Aspergillus fumigatus* AP-20 and *Penicillium multicolor* IAM7153 are extracellular inducible enzymes that uses β -primeveroside-containing substances as the carbon source and inducer (Yamamoto et al. 2002; Tsuruhami et al. 2006). At first, the β -rutosidase (6-*O*- α -rhamnopyranosyl- β -glucosidase)-encoding gene was identified from *A. niger* K2 (Šimčíková et al. 2015). However, this gene was annotated in GenBank as having a putative exo- β -1,3-glucanase-encoding open reading frame. Proximately, the β -rutosidase-encoding gene was also reported in *A. oryzae* RIB40 (Ishikawa et al. 2018). The β -rutosidase from *A. oryzae* showed high degree of sequence similarity to the β -rutosidase from *A. niger* K2 (70%) (Šimčíková et al. 2015) and the β -primeverosidase of *Penicillium multicolor* TS-5 (58%) (Tsuruhami et al. 2006). Based on the amino acid sequence similarity, the CAZy database (Lombard et al. 2014) classifies fungal β -diglycosidases into the GH5-subfamily 23 (GH5_23) of the glycoside hydrolases (Aspeborg et al. 2012). Twelve sequences of only fungal origin have been deposited in the CAZy database in GH5_23 section (Fig. 3). Meanwhile, sequences for exo- β -1,3-glucanases, which are fungal cell wall modifying enzymes, have been deposited in the GH5_9. The β -rutosidases from *A. niger* (AnRutA) and *A. oryzae* (AoRut) showed low similarities with the exo- β -1,3-glucanases from *A. oryzae* (ExgA and Exg1) and *Lentinula edodes* (Exg1) (Tamano et al. 2007; Sakamoto et al. 2005). A thermostable β -glucosidase/ β -rutosidase from the archaea *Pyrococcus furiosus* (Nam et al. 2012) involved in the production of quercetin from rutin belongs to GH1, similar to the β -diglycosidases from plants. Moreover, the gene encoding the GH55 family member 6-*O*- α -L-rhamnopyranosyl- β -D-glucosidase was identified from *Actinoplanes missouriensis* 431^T genome. Biochemical analyses of the corresponding recombinant protein purified from *Escherichia coli* showed specificity for 7-*O*-rutosylated flavonoids (Neher et al. 2016). Exo- β -1,3-glucanases from fungi including the genera *Aspergillus* and *Penicillium* have also been deposited in the GH55 section of the database.

A. oryzae RIB40 and *Oerskovia* sp. Y1 produce isoprimeverose-producing oligoxyloglucan hydrolase (EC 3.2.1.120), a unique β -diglycosidase, that recognizes isoprimeverose (6-*O*- α -D-xylopyranosyl- β -D-glucopyranoside) units from the non-reducing ends of oligoxyloglucans (Kato et al.

1985; Yaoi et al. 2007; Matsuzawa et al. 2016). The enzyme-encoding genes have been identified (Yaoi and Miyazaki 2012; Matsuzawa et al. 2016). Based on the amino acid sequence, isoprimeverose-producing oligoxyloglucan hydrolase has been classified as a member of the GH3 family.

Properties of microbial β -diglycosidases

Data from the studies cited in Table 1 show that the pH and temperature optima of β -rutosidase (α -rhamnopyranosyl- β -glucosidase) and β -primeverosidase from fungi ranged from 2.2–5.0 to 45–70 °C, respectively. The β -rutosidases from *P. rugulosum* and *A. niger*, and β -primeverosidase from *A. fumigatus* are extreme acidophiles (Narikawa et al. 2000; Šimčíková et al. 2015; Yamamoto et al. 2002). Meanwhile, the optimal pH of α -rhamnopyranosyl- β -glucosidase from *A. missouriensis* belonging to the GH55 family was 7.0 (Neher et al. 2016). α -Rhamnopyranosyl- β -glucosidase from *Acremonium* sp. and isoprimeverose-producing oligoxyloglucan hydrolase from *A. oryzae* are thermophilic enzymes (Mazzaferro et al. 2010, 2011b; Kato et al. 1985). Especially, β -glucosidase/ β -rutosidase from archaea *P. furiosus* is an extremely thermostable enzyme (Nam et al. 2012). However, the specific activity for rutin of β -glucosidase/ β -rutosidase from *P. furiosus* was approximately 900- and 15,700-fold lower, respectively, than those for isoquercitrin and *p*-nitrophenyl- β -D-glucoside.

Furthermore, β -rutosidase hydrolyzes several rutinose-containing glycoconjugates including flavonoids, such as hesperidin, rutin, kaempferol-3-*O*-rutoside, and hesperidin methylchalcone. However, the enzyme does not hydrolyze neohesperidose (2-*O*- α -L-rhamnopyranosyl- β -D-glucopyranose)-conjugated flavonoids, such as naringin. The β -rutosidases from *P. rugulosum* and *Arthrobacter* sp. show specificity for 3-*O*-linked rutosides such as rutin, a 3-*O*-rutosylated flavonol (Narikawa et al. 2000; Song-Joon et al. 1990). The catalytic activity of β -rutosidase from *A. niger* was almost ten times higher for rutin hydrolysis than that for hesperidin, a 7-*O*-rutosylated flavanone (Šimčíková et al. 2015). Meanwhile, among the three substrates examined, the catalytic activity of β -rutosidase from *A. oryzae* was highest for kaempferol-3-*O*-rutoside, which is a 3-*O*-rutosylated flavonol, moderate for rutin, and lowest for hesperidin (Ishikawa et al. 2018). In contrast to this, α -rhamnopyranosyl- β -glucosidase from *Acremonium* sp. and *A. missouriensis* hydrolyzes 7-*O*-linked rutosides only, such as hesperidin, but not 3-*O*-linked rutosides such as rutin (Mazzaferro et al. 2010, 2011b; Neher et al. 2016). However, no activity of β -rutosidases from *A. missouriensis* and *A. oryzae* was determined toward diosmin, a 7-*O*-rutosylated flavone. This suggests that the structure of flavonoids also determines enzyme specificity.

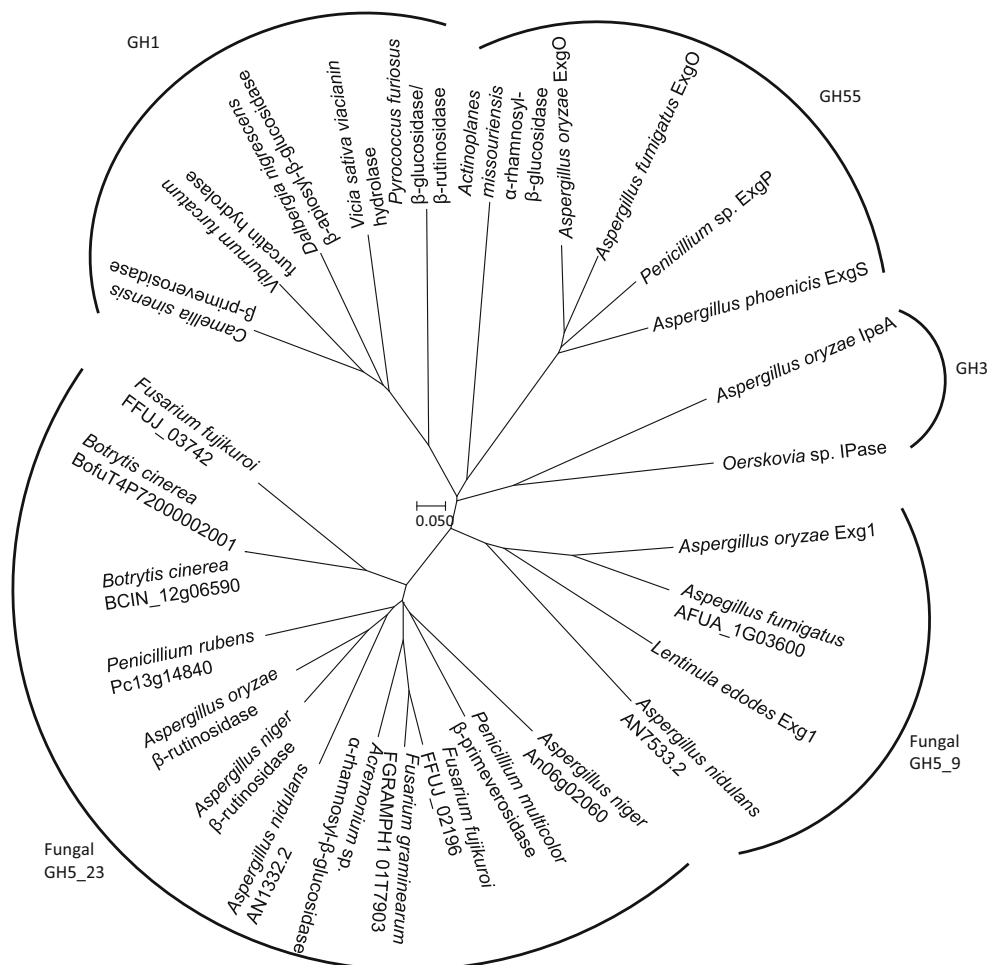


Fig. 3 Phylogenetic trees among β -diglycosidases and exo- β -1,3-glucanases classified as GH1, GH3, GH5_9, GH5_23, and GH55 in the CAZy database. An amino acid sequence alignment was performed using ClustalW (Thompson et al. 1994), and the phylogenetic tree was constructed using molecular evolutionary genetics analysis software version 7.0 (Tamura et al. 2007). The accession numbers are as follows: *Acremonium* sp. α -rhamnosyl- β -glucosidase (AMD11613.1), *Actinoplanes missouriensis* α -rhamnosyl- β -glucosidase (BAL86042.1), *Aspergillus fumigatus* ExgO (CAF32160.1), *Aspergillus oryzae* ExgA (CAC07551.1), *Aspergillus oryzae* ExgO (BAB92972.1), *Aspergillus oryzae* IpeA (BAE62006.1), *Aspergillus oryzae* β -rutinosidase (BAE61018.1), *Aspergillus nidulans* AN1332.2 (EAA65515.1), *Aspergillus niger* β -rutinosidase (CAK39791.1), *Aspergillus niger*

An06g02060 (CAK48049.1), *Aspergillus phoenicis* ExgS (BAB83607.1), *Botrytis cinerea* BofuT4P72000002001 (CCD33736.1), *Camellia sinensis* β -primeverosidase (BAC78656.1), *Dalbergia nigrescens* β -apiosyl- β -glucosidase (A3RF67.1), *Fusarium fujikuroi* FFUJ_02196 (CCT65263.1), *Fusarium fujikuroi* FFUJ_03742 (CCT64988.1), *Lentinula edodes* Exg1 (BAD97445.1), *Oerskovia* sp. IPase (BAM08953.1), *Penicillium multicolor* β -primeverosidase (BAG70961.1), *Penicillium rubens* Pc13g14840 (CAP925533.1), *Penicillium* sp. ExgP (BAH69264.1), *Pyrococcus furiosus* β -glucosidase/ β -rutinosidase (AAC25555.1), and *Viburnum furcatum* furcatin hydrolase (BAD14925.1). The bar represents 0.05 amino acid substitutions per site

The hydrolytic activity of the β -primeverosidase from *A. fumigatus* on the *p*-nitrophenyl β -gentiobioside was greater than that from *P. multicolor* (Yamamoto et al. 2002; Tsuruhami et al. 2006). The substrate specificity of these fungal enzymes also differed appreciably from that of tea β -primeverosidase.

Potential industrial applications

In the citrus processing industry, the deglycosylation of flavonoids plays an important role in improving the product quality,

such as in the reduction of bitterness, clarification of juices, and in enhancing the aroma in wine and tea (Günata et al. 1998; Hemingway et al. 1999; Wang et al. 2001; Ma et al. 2001; Genovés et al. 2005). This process is also used for controlling aroma compounds, such as monoterpene alcohols, in sweet potato shochu which is a traditional Japanese distilled spirit (Sato et al. 2018). A simple enzymatic-spectrophotometric method for hesperidin quantification in citrus-based foods was developed by means of *Acremonium* sp. α -rhamnosyl- β -glucosidase (Mazzafarro and Breccia 2012a).

Rutinose-containing compounds have been demonstrated to have interesting pharmaceutical and medicinal

Table 1 Properties of β -diglycosidases from microorganisms

Organism	Enzyme	EC number	Molecular mass (kDa)	pHopt	Topt (°C)	pHsta	Tsta (°C)	Main substrate	Accessions	Reference
Fungi										
<i>Acremonium</i> sp. DSM24697	α -rhamnosyl- β -glucosidase	3.2.1.168	46	5.0	70			hesperetin 7-O- β -rutinoside	AMD11613.1	Mazzafarro et al. 2010; 2011
<i>Aspergillus fumigatus</i> AP20	β -primeverosidase-like endo-manner β -glycosidase	3.2.1.149	47	2.5–3.0	55	7.0–8.0		<i>p</i> -nitrophenyl β -primeveroside		Yamamoto et al. 2002
<i>Aspergillus oryzae</i> RIB40	β -rutinosidase	3.2.1.168	65–75	4.0	45	45		kaempferol-3-O- β -rutinoside	BAE61018.1	Ishikawa et al. 2018
<i>Aspergillus oryzae</i> RIB40	isoprimeverose-producing oligoxyloglucan hydrolase	3.2.1.120	115	5.0	60	5.0–7.0	50	oligoxyloglucan	BAE62006.1	Kato et al. 1985; Matsuzawa et al. 2016
<i>Aspergillus niger</i> K2	β -rutinosidase	3.2.1.168	~75	3.0	50			quercetin-3-O- β -rutinoside	CAK39791.1	Šimčiková et al. 2015
<i>Penicillium multicolor</i> IAM7153	β -primeverosidase-like enzyme	3.2.1.149	50	4.5–5.5	55			<i>p</i> -nitrophenyl β -primeveroside	BAG70961.1	Tsuruhami et al. 2006
<i>Penicillium rugulosum</i> NBRC7242	β -rutinosidase	3.2.1.168	65	2.2	50	2.0–11.0	40	quercetin-3-O- β -rutinoside		Narikawa et al. 2000
Bacteria										
<i>Actinoplanes missouriensis</i> 431 ^T	α -rhamnosyl- β -glucosidase	3.2.1.168	62	7.0	55		50	hesperetin 7-O- β -rutinoside	BAL86042.1	Neher et al. 2016
<i>Arthrobacter</i> sp.	β -rutinosidase	3.2.1.168	42					quercetin-3-O- β -rutinoside		Song-Joon et al. 1990
<i>Oerskovia</i> sp. Y1	isoprimeverose-producing oligoxyloglucan hydrolase	3.2.1.120	105	4.5	55	3.5–7.5	45	oligoxyloglucan	BAM08953.1	Yaot et al. 2007; 2012
Archaea										
<i>Pyrococcus furiosus</i> DSMZ3638	β -glucosidase/ β -rutinosidase	3.2.1.21		5.0	95			<i>p</i> -nitrophenyl β -D-glucoside	AAC25555	Nam et al. 2012

applications (Robinson et al. 2004; Knaup et al. 2007). Rutinose-containing flavonoids have been shown to be absorbed in the intestines only after rhamnose hydrolysis and catalyzed by human gut microflora (Nielsen et al. 2006). The transglycosylation potential of the fungal β -rutosidase has been explored. The biocatalyst has been shown to have broad acceptor specificity toward aliphatic, aromatic, and arylalkyl alcohols using α -rhamnosyl- β -glucosidases from *Acremonium* sp. (Minig et al. 2011; Mazzaferro et al. 2012b) and *A. niger* (Šimčíková et al. 2015; Bassanini et al. 2017). Bassanini et al. (2017) have developed two-step two-enzymatic synthesis of coniferin using the α -rhamnosyl- β -glucosidase and *A. terreus* α -L-rhamnosidase. It has also been reported that rutosylation of various phenolic acids can increase their antiviral activity against feline calicivirus, more than the respective aglycone (Katayama et al. 2013).

Conclusions

In conclusion, we present here the biochemical characteristics and potential industrial applications of β -diglycosidases from archaea, bacteria, and fungi that breakdown plant diglycoconjugated flavonoids. Eukaryotic β -diglycosidases are effective catalysts when food technology for aroma modulation and pharmaceutical and medicinal applications are envisioned. Because of their retaining mechanism, transglycosylation activity is to be expected. The synthetic potential of β -diglycosidases from fungi and plants has also been demonstrated, which can glycosylate alkylic, phenolic, and arylalkyl alcohols and phenolic acids in vitro (Mazzaferro et al. 2012b; Šimčíková et al. 2015; Katayama et al. 2013; Bassanini et al. 2017).

Funding information This work was supported by the Japan Society for the Promotion of Science KAKENHI (Grant Number JP26450117).

Compliance with ethical standards

Conflict of interest The authors declare that they have no competing interests.

Ethical approval This article does not contain any studies with human participants or animals performed by any of the authors.

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