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Fungal feruloyl esterases: Functional validation of genome mining based enzyme discovery including uncharacterized subfamilies

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ABSTRACT

Feruloyl esterases (FAEs) are a diverse group of enzymes that specifically catalyze the hydrolysis of ester bonds between a hydroxycinnamic (e.g. ferulic) acid and plant poly- or oligosaccharides. FAEs as auxiliary enzymes significantly assist xylanolytic and pectinolytic enzymes in gaining access to their site of action during biomass saccharification for biofuel and biochemical production. A limited number of FAEs have been functionally characterized compared to over 1000 putative fungal FAEs that were recently predicted by similarity-based genome mining, which divided phylogenetically into different subfamilies (SFs). In this study, 27 putative and six characterized FAEs from both ascomycete and basidiomycete fungi were selected and heterologously expressed in *Pichia pastoris* and the recombinant proteins biochemically characterized to validate the previous genome mining and phylogenetical grouping and to expand the information on activity of fungal FAEs. As a result, 20 enzymes were shown to possess FAE activity, being active towards *p*NP-ferulate and/or methyl hydroxycinnamate substrates, and covering 11 subfamilies. Most of the new FAEs showed activities comparable to those of previously characterized fungal FAEs.

Introduction

Esterified or etherified to polymers within the lignocellulosic matrix, ferulic acid (FA, 4-hydroxy-3-methoxycinnamic acid) and to a lesser extent *p*-coumaric acid (4-hydroxycinnamic acid) are the most abundant hydroxycinnamic acids in plant cell walls [1,2]. These hydroxycinnamic acids can be linked to arabinoxylans (*O*-5 position of α-L-arabinofuranosyl residues), which are the unique structural components in commelinid monocots (Family Poales, e.g. wheat, rice and barley). They can also be linked to neutral pectic side-chains of rhamnogalacturonan I (*O*-6 position of β-D-galactopyranosyl residues in (arabino)galactan, and *O*-2 or *O*-5 position of α-L-arabinofuranosyl residues in arabinan), which are mainly found in eudicotyledons (Order 'core' Caryophyllales, e.g. sugar beet) [3–8]. FA can form diferulic acids (mainly 5,5′-, 8-*O*-4′-, 8,5′-, 8,8′-diferulic acids) which cross-link two polysaccharide chains or a polysaccharide chain to lignin [7,9–11]. Phenolic cross-links increase the physical strength and integrity of plant cell walls and reduce their biodegradability by microbial invaders and hydrolytic enzymes [2,12].

Feruloyl esterases (or ferulic acid esterases, FAEs) [E.C. 3.1.1.73] represent a subclass of the carboxylic acid esterases (E.C. 3.1.1) and catalyze the hydrolysis of ester linkage between a phenolic acid and a poly- or oligosaccharide releasing hydroxycinnamic acids from plant cell wall polysaccharides [13,14]. FAEs are able to release FAs and other phenolic acids from natural plant sources and agro-industrial byproducts. They facilitate the degradation of complex plant cell wall

Abbreviations: FA, ferulic acid; FAE, feruloyl esterase; SF, subfamily

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polysaccharides by removing the ester bonds between plant polymers providing accessibility for glycoside hydrolases and polysaccharide lyases [15–17]. Apart from being used as accessory enzymes in the saccharification process, FAEs are also potential biocatalysts for synthesis of a broad range of novel bioactive components for use in the food, cosmetics and pharmaceutical industries [18,19]. In 2014, an EU collaborative project 'OPTIBIOCAT' was granted by the 7th Framework Programme (FP7), which aims to use microbial esterases such as FAEs as biocatalysts for synthesis of potential antioxidants for cosmetic products [19]. As these enzymes are relevant for various industries, different types of FAE are required to fit specific conditions such as pH and temperature.

Recently, we reported a genome mining strategy for FAE discovery, in which more than 1000 putative fungal FAE sequences were identified and, by using a phylogenetical analysis, classified into 13 subfamilies (SFs) [19]. In contrast to the high number of the putative FAE encoding genes, a limited number of fungal FAEs have been characterized in detail and they only cover SF1, 2, 5, 6, 7 and 13. To validate our genome mining strategy and expand the information on activity and properties of fungal FAEs, in this study we report the heterologous expression and biochemical characterization of selected recombinant FAEs discovered through genome mining, and covering the previously uncharacterized SFs.

Materials and methods

Bioinformatics

Genome mining and phylogenetic analysis were performed based on [19]. Signal peptides were predicted using SignalP 4.1 (http://www.cbs.dtu.dk/services/SignalP/; [20]). The gene model correction of selected sequences was performed manually based on BlastX to identify and remove putative introns [21]. Sequence alignment was performed using Multiple Alignment using Fast Fourier Transform (MAFFT) [22]. Theoretical molecular masses and p*I* were calculated by the ExPASy–ProtParam tool (http://www.expasy.ch/tools/protparam.html [23]).

Cloning of fae genes

The genes of the selected FAEs without signal peptide and introns were codon optimized and synthesized for expression in *P. pastoris* by NZYTech (Lisbon, Portugal). The gene products were digested by *Psi*I and *Not*I (Thermo Fisher Scientific), and cloned in frame with α-factor secretion signal in pPNic706 (ProteoNic, Leiden, the Netherlands). The obtained plasmids were purified from *Escherichia coli* DH5α (Invitrogen), transformants selected on Luria Bertani medium supplemented with 50 μg/mL kanamycin, fully sequenced (Macrogen, Amsterdam, the Netherlands), linearised by *Sal*I (Thermo Fisher Scientific), and transformed into *P. pastoris* strain GS115 *his*4 according to the manufacturer's recommendation.

Ten transformants were selected for the enzyme production screening, which was performed in 96 deep-well plates containing 0.8 mL medium. The selected clones were grown first in buffered minimal glycerol medium (1% yeast nitrogen base, 0.1 M potassium phosphate buffer pH 6.5, and 1% w/v glycerol). The plates were sealed with AeraSeal™ (Sigma Aldrich) and incubated overnight at 30 °C, 900 rpm (INFORS HT Microtron, Bottmingen, Switzerland). A volume of cells equal to an OD_{600} of 1.0 was harvested and resuspended in 0.8 mL buffered minimal methanol medium (1% yeast nitrogen base, 0.1 M potassium phosphate buffer pH 6.5, and 0.5% methanol) for induction. The induction was performed at 30 °C, 900 rpm for 72 h before being harvested. The cultures were supplemented with 80 μL of 0.5% (v/v) methanol every 24 h.

Production and biochemical properties of recombinant FAEs

P. pastoris transformants were grown according to [24]. Induction was continued for 96 h at 28 °C with methanol being supplemented to 0.5% (v/v) every 24 h. Culture supernatants were harvested (4000 × g, 4 °C, 20 min), filtered (0.22 μm; Merck Millipore, Darmstadt, Germany) or concentrated (10 kDa cut off; Merck Millipore) and stored at −20 °C prior further analysis. Molecular mass determination and deglycosylation were performed as previously described [24]. Protein concentrations were assessed from SDS-PAGE gels by densitometric method using ImageJ program [25] with bovine serum albumin (Pierce, Thermo Scientific) as a standard.

Enzyme activity assay of FAEs

Activity of the recombinant FAEs towards *p*NP-ferulate (Taros Chemicals, Dortmund, Germany) was performed in 275 μL reaction mixtures adapted from [26]. The *p*NP-ferulate substrate solution was prepared by mixing 10.5 mM *p*NP-ferulate (in dimethyl sulfoxide) and 100 mM potassium phosphate buffer, pH 6.5 containing 2.5% Triton-X (1:9, v/v). The reactions were performed in the presence of 250 μL *p*NP-ferulate substrate solution incubated with 25 μL of culture supernatant at 37 °C. The release of *p*-nitrophenol was spectrophotometrically quantified by following the absorbance at 410 nm for 30 min with a 2 min interval and calculation according to [26]. All assays were performed in triplicate. One unit of FAE activity is defined as the amount of enzyme releasing 1 μmol of *p*-nitrophenol from *p*NP-ferulate per min under the assay conditions.

Activity towards methyl substrates [methyl caffeate, methyl ferulate, methyl *p*-coumarate, and methyl sinapate (Apin Chemicals Limited, Oxon, United Kingdom)] was assayed in 250 μL reaction mixtures according to [24] at 37 °C for 5–30 min. Detection of substrates reduction was performed at 340 nm with a 2 min interval. The activity was determined from the standard curves of the substrates (0.001–0.5 mM). Alternatively, the activities were assayed by HPLC (Agilent 1260 Infinity) using Kinetex 2.6 u C18 100A column (Phenomenex). The quantification was performed by using calibration curves of the methyl substrates and their corresponding acids, and the detection was performed at 320 nm for methyl caffeate, methyl ferulate and methyl sinapate, and at 308 nm for methyl *p*-coumarate. The 1 mL reaction mixtures contained 850 μL MOPS buffer (pH 6.0), 100 μL enzyme and 50 μL substrate (1 mM). The reactions were stopped by adding 1 vol 0.1% trifluoroacetic acid:acetonitrile solution (80:20). Chromatographic separation was performed by isocratic method with 80% 0.1% trifluoroacetic acid and 20% acetonitrile as solvents. The culture supernatant of *P. pastoris* harboring pPicZαA plasmid without insert was used as negative control. All assays were performed in triplicate.

Enzyme activity assay of tannases

Methyl gallate (Sigma Aldrich, St. Louis, MO) was used for the assessment of tannase activity [27]. The reactions were performed in 125 μL reaction mixtures containing 6.25 μL of 100 mM methyl gallate stock solution (in dimethylformamide), 31.25 μL of 100 mM phosphate buffer, pH 6.0, and 25 μL water incubated with 62.5 μL of culture supernatant at 30 °C for 15 min. To detect the release of gallic acid, 75 μL of 0.667% rhodanine (in methanol) (Sigma Aldrich) was added to the reaction mixture followed by 5 min incubation at 30 °C, addition of 100 μL of 0.5 M KOH, further incubation at 30 °C for 5 min, and addition of 1 mL water prior to quantification by measuring the absorbance at 520 nm. The activity was determined from the standard curves of the substrates (0.006–0.6 mM). Alternatively, tannase activity was assayed by the HPLC method described above by detecting methyl gallate at 280 nm and using InfinityLab Poroshell 120 SB-AQ column (Agilent).

Enzyme activity assay of lipases

For assessment of the lipase activity, *p*NP-palmitate (Sigma Aldrich) was used as a substrate. Ten mM *p*NP-palmitate stock solution was prepared in isopropanol and diluted in 100 mM potassium phosphate buffer, pH 6.5. The reaction was performed in 1 mL reaction mixtures containing 900 µL of 0.2 mM *p*NP-palmitate in 100 mM potassium phosphate buffer, pH 6.5, and 100 µL of culture supernatant at 40 °C. The release of *p*-nitrophenol was spectrophotometrically quantified by following the absorbance at 410 nm for 30 min with a 2 min interval and calculation according to [26].

Results and discussion

Discovery of novel fungal FAEs

A genome mining strategy was previously conducted by BLAST analysis with characterized FAEs against published fungal genomes to identify the putative fungal FAEs [19]. In the current study, four additional genomes from *Aspergillus* spp., i.e. *Aspergillus sydowii*, *Aspergillus wentii* DTO 134E9, *Aspergillus carbonarius* ITEM 5010 and *Aspergillus tubingensis* [28], were added to the analysis (A.1 in Supplementary materials). Over 1000 putative fungal FAE sequences were identified, which were classified into 13 SFs. Of these, 33 FAE sequences (six previously characterized and 27 putative FAEs) from both ascomycetes and basidiomycetes, which covered five previously uncharacterized FAE subfamilies (SF3, 8, 9, 10, 12), were selected for biochemical characterization (Table 1). The enzymes from SF11 were not included in this study because they most likely possessed tannase activity.

Recombinant enzyme production of selected fungal FAEs

Heterologous expression of putative FAEs was performed using *P. pastoris* as a host organism. FAE sequences from both ascomycetes and basidiomycetes were produced as active enzymes in *P. pastoris*. Three of the selected enzymes, i.e. An09g05120 (*A. niger*), CsFae3 (*Ceriporiopsis subvermispora*) and ShFae1 (*Stereum hirsutum*), were produced at a concentration greater than 1000 mg/L and five, namely GmFae1 (*Galerina marginata*), OrpFAE (*Orpinomyces* sp.), AnFaeJ, An11g01220 (*A. niger*) and CsFae1 (*C. subvermispora*), were produced at a concentration greater than 100 mg/L. However, the production level of eight and 12 of the enzymes was less than 100 mg/L and 10 mg/L respectively, and five of them were not produced. Almost half of the recombinant enzymes showed higher molecular masses compared to the calculated ones, but the molecular mass reduced to the expected size after treatment with Endoglycosidase H indicating glycosylation by *P. pastoris*.

Activity and substrate preference among the selected fungal FAEs

To screen for FAE activity, *p*NP-ferulate was used as a substrate. Among 27 enzymes, 20 were active, with GmFae1 (*G. marginata*) showing the highest activity (Table 1). With respect to the substrate specificity, four methyl substrates (methyl *p*-coumarate, methyl caffeate, methyl ferulate, and methyl sinapate) were used. In agreement with the previous reports [29–31], AnFaeB (*A. niger*) and AsFaeF (*A. sydowii*) from SF1 hydrolyzed three methyl substrates: methyl *p*-coumarate, methyl caffeate and methyl ferulate (Table 2). Docking simulation of methyl sinapate on a structure of a member of SF1, AoFaeB (from *A. oryzae*, PDB: 3WMT), indicated that its narrow active site hindered the binding of the bulky structure of methyl sinapate [32]. AsFaeI (*A. sydowii*) from SF13 was also able to hydrolyze three methyl substrates similarly to the enzymes from SF1, whereas the other FAEs from SF13 showed either low or no activity towards methyl ferulate. The majority of the active FAEs from SF5 and SF6 hydrolyzed all four substrates, except FoFae2 (*Fusarium oxysporum* from SF6) and CcFae2 (*Coprinopsis cinerea* from SF6), which did not hydrolyze methyl sinapate, and Settu1|102085 (*Setosphaeria turcica* from SF5), which was only active towards methyl caffeate and methyl sinapate. Because Settu1|102085 as well as some other esterases (see below) were not detected to hydrolyze methyl ferulate, they were referred to as hydroxycinnamoyl esterases (HCE) instead of FAEs.

AnFaeA (*A. niger*) from SF7 hydrolyzed only methyl ferulate and methyl sinapate, which is consistent with the previous reports [29,31,33]. The crystal structure of AnFaeA showed a long and narrow cavity displaying hydrophobic residues that stabilize the aromatic moiety of the substrate [34], and replacing the bulky aromatic residues (Tyr80 or Trp260) to smaller residues broadened the substrate specificity of the enzyme [35].

Three FAEs from SF2, namely FoFaeC (*F. oxysporum*), AwFaeG (*A. wentii*) and GlFae1 (*Gymnopus luxurians*), showed no obvious substrate specificity pattern. FoFaeC hydrolyzed all tested substrates with low activity on methyl sinapate, which is consistent with the previous report [36]. AwFaeG also showed low activity towards methyl sinapate, but did not hydrolyze methyl *p*-coumarate. GlFae1 showed the highest activity towards methyl sinapate and lower activity towards methyl ferulate, but was not active towards methyl *p*-coumarate and methyl caffeate. The enzymes from SF3 (Aspca3|176503 from *A. carbonarius*), SF9 (Asptu1|30001 from *A. tubingensis*) and SF12 (Galma1|254175 from *G. marginata*) were not active towards methyl ferulate and *p*NP-ferulate, but showed activity towards only one methyl substrate with no specific pattern. Therefore, these esterases were also referred to as HCEs. The enzyme from SF10 (OrpFAE from *Orpinomyces* sp.) was not active towards methyl substrates, but showed activity towards *p*NP-ferulate.

Previously, members of SF1, 2, 5, 6, 7 and 13 were shown to possess FAE activity [19]. In the present study, we reported that enzymes from SF8, 9 and 10 showed limited activity towards synthetic FAE substrates, as well as towards methyl gallate for SF9. Recently, an esterase from *Auricularia auricularia-judae* (EstBC), belonging to SF8 was described that acted efficiently on both artificial cinnamic and benzoic acid esters, but was not active on complex natural FAE substrates [37]. Hence, the enzymes from these subfamilies should be further tested towards feruloylated saccharides or natural substrates, e.g. wheat bran or sugar beet pectin, to confirm their true FAE activity.

Enzymes with other activity

Five enzymes (CsTan1–*C. subvermispora*, AnFaeJ–*A. niger*, Aspsy1|41271–*A. sydowii*, An11g01220–*A. niger*, An09g05120–*A. niger*) were active towards methyl gallate. These enzymes belong to SF9, SF10 and SF13, indicating that the representatives of these SFs may be tannases. Recently, two FAEs from *Schizophyllum commune* were reported to hydrolyse methyl gallate [38]. It is possible that these enzymes are the bridge in the evolution from tannases to FAEs or *vice versa*. Surprisingly, one enzyme (Aspca3|176503 from *A. carbonarius*) was active towards *p*NP-palmitate, although this enzyme does not share amino acid sequence similarity to known lipases.

Conclusions

In the present study, we have confirmed the ability of the genome mining strategy to identify fungal FAE encoding genes, by demonstrating that 20 out of 27 putative fungal FAEs possessed FAE activity towards *p*NP-ferulate and/or methyl hydroxycinnamate substrates. Previously, members of SF1, 2, 5, 6, 7 and 13 were shown to possess FAE activity [19]. In the present study, we also showed that the enzymes from SF8, 9 and 10 are active towards the synthetic FAE substrates. However, it should be noted that most of the enzymes from SF9 possessed tannase activity. Additional experiments are needed to confirm whether the enzymes of these subfamilies are true FAEs. The selected esterases from SF3 and SF12 were active towards methyl caffeate

Table 1
Molecular mass, production level and specific activity (towards *p*NP-ferulate) of characterized FAEs in this study[a].

Fungal species	Phylum[b]	Accession number	SF[c]	Name[d]	Calculated molecular mass (kDa)	Apparent molecular mass (kDa)	Calculated p*I*	Production (mg/L)	Specific activity[h] (mU/mg)	Remark[i]
Aspergillus niger	Asco	Q8WZI8.1	1	**AnFaeB**	55.8	100 (55)	4.95	55	2	
Aspergillus sydowii	Asco	jgi|Aspsy1| 293049	1	AsFaeF	55.4	55[e]	4.89	< 1	4	
Fusarium oxysporum	Asco	jgi|Fusox1| 5438	2	**FoFaeC**	59.4	70 (61)[f]	6.89	6	Active	
Aspergillus wentii	Asco	jgi|Aspwe1| 156253	2	AwFaeG	56.0	57	4.99	< 1	Active	
Gymnopus luxurians	Asco	jgi|Gymlu1| 46632	2	GlFae1	56.8	58	4.53	3	na	
Aspergillus carbonarius	Asco	jgi|Aspca3| 176503	3	–	56.1	58	5.02	4	na	Lipase activity
Aspergillus sydowii	Asco	jgi|Aspsy1| 901052	3	–	55.8	nd	4.88	np	na	
Aspergillus nidulans	Asco	EAA62427.1	5	**AnidFAEC**	25.8	30 (30)[f]	4.47	30	2	
Aspergillus sydowii	Asco	jgi|Aspsy1| 154482	5	AsFaeC	25.9	30 (30)[f]	4.44	15	2	
Aspergillus sydowii	Asco	jgi|Aspsy1| 48859	5	AsFaeD1	26.6	nd	3.93	np	na	
Setosphaeria turcica	Asco	jgi|Settu1| 102085	5	–	26.9	26	8.90	< 1	na	
Myceliophthora thermophila (*Sporotrichum thermophile*)	Asco	AEO62008.1	6	**MtFae1a**	29.5	35 (30)[f]	4.44	45	3	
Fusarium oxysporum	Asco	jgi|Fusox1 |8990	6	FoFae2	29.6	30	8.44	4	Active	
Aspergillus sydowii	Asco	jgi|Aspsy1| 1158585	6	AsFaeE	29.5	32[e]	4.24	7	4	
Stagonospora nodorum	Asco	jgi|Stano2| 8578	6	–	31.3	30	5.16	12	na	
Coprinopsis cinerea	Basidio	jgi|Copci1| 3628	6	CcFae2	37.7	38	6.63	< 1	Active	
Ceriporiopsis subvermispora	Basidio	jgi|Cersu1| 68569	6	CsFae1	36.9	70	4.58	280	7	
Galerina marginata	Basidio	jgi|Galma1| 144217	6	GmFae1	35.2	42	5.83	600	120	
Aspergillus niger	Asco	CAA70510	7	**AnFaeA**	28.6	40 (35)[f]	4.19	55	4	
Aspergillus clavatus	Asco	jgi|Aspcl1| 3045	8	–	39.1	40[e]	6.34	51	na	
Ceriporiopsis subvermispora	Basidio	jgi|Cersu1| 89153	9	CsTan1	55.0	90 (60)[g]	4.59	np	na	Tannase activity
Aspergillus tubingensis	Asco	jgi|Asptu1| 30001	9	–	57.6	57	4.50	< 1	na	
Aspergillus niger	Asco	An15g05280	9	AnFaeJ	58.6	68 (60)[g]	4.93	500	na	Tannase activity
Aspergillus sydowii	Asco	jgi|Aspsy1| 41271	9	–	57.6	60[e]	4.99	32	na	Tannase activity
Orpinomyces sp.	Neo	AAF70241.1	10	**OrpFAE**	59.0	68	5.06	600	10	
Aspergillus niger	Asco	An11g01220	10	–	55.0	88	4.11	500	na	Tannase activity
Aspergillus sydowii	Asco	jgi|Aspsy1| 194109	10	–	52.7	nd	4.67	np	na	
Dichomitus squalens	Basidio	jgi|Dicsq1| 136925	12	–	56.3	nd	4.78	np	na	
Galerina marginata	Basidio	jgi|Galma1| 254175	12	–	56.0	59	6.90	3	na	
Aspergillus sydowii	Asco	jgi|Aspsy1| 160668	13	AsFaeI	59.4	55[e]	4.90	< 1	4	
Stereum hirsutum	Basidio	jgi|Stehi1| 73641	13	ShFae1	58.1	67	4.40	2160	13	
Aspergillus niger	Asco	An09g05120	13	–	53.1	66	4.79	3400	na	Tannase activity
Ceriporiopsis subvermispora	Basidio	jgi|Cersu1| 150639	13	CsFae2	55.1	nd	4.28	2400	1	

[a] na, no activity detected; nd, no protein band detected; np, no protein produced or the protein level was lower than detection limit.
[b] Asco, ascomycete; Basidio, basidiomycete; Neo, Neocallimastigomycete.
[c] According to [19].
[d] Name in bold indicates the previously reported FAEs [19]. The abbreviation of the enzyme code is based on the convention protein names for different species and not on the types of FAEs.
[e] indicates the protein band was visible only after deglycosylation by Endoglycosidase H.
[f] indicates molecular mass after deglycosylation by Endoglycosidase H.
[g] indicates molecular mass after deglycosylation by PNGase F.
[h] One unit of enzyme activity is defined as the amount of enzyme releasing 1 μmol of *p*-nitrophenol from *p*NP-ferulate per min under assay conditions. Active indicates the enzyme was active but the specific activity could not be calculated.
[i] Tannase and lipase activities were evaluated using methyl gallate and *p*NP-palmitate as substrate, respectively.

Table 2
Relative FAE activity towards four methyl substrates[a].

Fungi	SF[b]	Name[c]	Relative activity (%)[d]			
			Methyl *p*-coumarate	Methyl caffeate	Methyl ferulate	Methyl sinapate
Aspergillus niger	1	**AnFaeB**	100	77	59	na
Aspergillus sydowii	1	AsFaeF	100	66	60	na
Fusarium oxysporum	2	**FoFaeC**	100	67	29	9
Aspergillus wentii	2	AwFaeG	na	100	88	29
Gymnopus luxurians	2	GlFae1	na	na	18	100
Aspergillus carbonarius	3	–	na	100	na	na
Aspergillus nidulans	5	**AnidFAEC**	98	42	100	46
Aspergillus sydowii	5	AsFaeC	91	45	100	40
Aspergillus sydowii	5	AsFaeD1	na	na	Low[e]	na
Setosphaeria turcica	5	–	na	100	na	91
Myceliophthora thermophila	6	**MtFae1a**	100	77	90	36
Fusarium oxysporum	6	FoFae2	100	60	16	na
Aspergillus sydowii	6	AsFaeE	95	53	100	60
Stagonospora nodorum	6	–	na	na	na	na
Coprinopsis cinerea	6	CcFae2	100	41	23	na
Ceriporiopsis subvermispora	6	CsFae1	na	na	na	na
Galerina marginata	6	GmFae1	Low[e]	Low[e]	Low[e]	Low[e]
Aspergillus niger	7	**AnFaeA**	na	na	100	81
Aspergillus clavatus	8	–	na	na	Low[e]	na
Aspergillus tubingensis	9	–	na	100	na	na
Aspergillus niger	9	AnFaeJ	na	Low[e]	Low[e]	Low[e]
Aspergillus sydowii	9	–	na	na	na	na
Orpinomyces sp.	10	OrpFAE	na	na	na	na
Aspergillus niger	10	–	Low[e]	Low[e]	Low[e]	Low[e]
Galerina marginata	12	–	100	na	na	na
Aspergillus sydowii	13	AsFaeI	100	65	60	na
Stereum hirsutum	13	ShFae1	na	na	Low[e]	na
Aspergillus niger	13	–	na	Low[e]	Low[e]	Low[e]
Ceriporiopsis subvermispora	13	CsFae2	na	na	na	na

[a] na, no activity detected.
[b] According to [19].
[c] The abbreviation of the enzyme code is based on the conventional protein names for different species and not on the types of FAEs. Name in bold indicates the previously reported FAEs.
[d] The relative activity was calculated as a percentage of the highest activity for each enzyme that was set to 100%.
[e] Low indicates activity which was lower than the reliable detectable range.

and methyl *p*-coumarate, respectively, but not towards methyl ferulate. In comparison with the previously characterized fungal FAEs, most of the new FAEs showed similar levels of specific activity. Thus, they may potentially be eligible candidates for related biotechnological applications.

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at https://doi.org/10.1016/j.nbt.2017.11.004.

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