A review on Microbial production of ferulic acid esterase

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Abstract

Ferulic acid esterases (or feruloyl esterases) are a subclass of carboxylic acid esterases that catalyze the hydrolysis of ester bond between polysaccharides and hydroxycinnamic acids (ferulic acid, p-coumaric acid) on the plant cell walls. The release of hydroxycinnamic acids from agroresdues can be achieved by using either of the following methods: chemical release or enzymatic release. The use of enzymatic system in organic synthesis has become a fundamental tool for selective, efficient and economical transformations with the goal of using less aggressive reagents, less organic solvents, lower temperatures and involvement of shorter pathways. ferulic acid esterases have their potential applications in obtaining ferulic acid from agro-industrial waste materials such as those produced by milling, brewing, and sugar industries. The prospect of broad applications of ferulic acid esterases has fueled much interest in these enzymes, as shown by the increasing number of FAEs discovered in microbial organisms in recent years. This review focuses on the ferulic esterase enzyme isolation and its purification from the culture medium. Extensive search for novel ferulic acid esterase producing microorganisms, by speculating and exploring different environmental niches for their isolation, need an imperative examination. Research is essentially required in order to search for novel ferulic acid esterase producing strain.

Keywords

Ferulic acid esterase, Biotransformation, Screening.

I. INTRODUCTION

The application of FAEs has fuelled much of interest in the enzyme. Microbial enzymes are often more useful than the enzymes released from plant because of the great variety of catalytic activities available, the high yield possible and ease of genetic manipulation. Therefore, it demands for precise, rapid and facile concrete assay method that will benefit in reducing the effort and time required to screen the FAE producers. Many quantitative methods have been developed for screening and detection of FAE activity. These methods include agar plate assay method, spectrophotometric method, capillary zone electrophoresis, gas chromatography and high performance liquid chromatography (Donaghy *et al.* 1998; Donaghy and McKay 1995; Borneman *et al.* 1990; Castanares *et al.* 1992; MacKenzie and Bilous 1988). These all approaches for detection of FAE activity are time consuming, require exorbitant solvents and buffers. Thus, there is a need for a novel detection method which helps to screen out the FAE producers under economic environment within a few hours of culture inoculation.

1. Screening of ferulic acid esterase producing microorganisms

A screening assay method has been developed by Donaghy and McKay (1995) for the detection of phenolic acid esterases using agar medium, but this method experiences some drawbacks like agar medium does not always allow the growth of microorganisms and once the pH sensitive dye is flooded in inoculation plate, it can't be inoculated further. There is another assay protocol which has been developed by Wu *et al.* (2011), based on the pH shift of phenol red. pH shift changed the color from red to yellow because of formation of acid in the reaction, this protocol is not that efficient. Donaghy *et al.* (1998) screened 80 *Bacillus* strains using agar plate supplemented with ethyl ferulate (dissolved in 10% *w/v* dimethylformamide or DMF) in plate pouring stage as we have used in our study. FAEs were first detected in culture of *Streptomyces olivochromogenes* releasing FA from wheat bran (Mackenzie *et al.* 1987), after which a number of microbes have been isolated and characterized with FAE activity such as *Aspergillus awamori* VTT-D-71025, *Aspergillus nidulans, Bacillus subtilis* NCIMB11034, *Clostridium stercorarium* NCIMB 11754 and *Penicillium brasilianum* IBT 20888 (Gong *et al.* 2013; Shin and Chen 2007; Donaghy *et al.* 1998, 2000; Kroon *et al.* 2000) (Table 1).

Table 1 list of reported ferulic acid esterase producing microorganisms (bacteria and fungi).

Microorganisms	FAE	References
Schizophyllum commune ATCC 38548	FAE	Johnson *et al.* 1989
Fibrobacter succinogenes S851	FAE	McDermid *et al.* 1990
Aspergillus oryzae VTTD 85248	FAE	Tenkanen *et al.* 1991
Aspergillus phoenicis IMI 211395	FAE	Smith *et al.* 1991
Aspergillus terreus VTT-D-82209	FAE	Tenkanen *et al.* 1991
Neocallimastix	FAE-I, II	Borneman *et al.* 1992
Panicillium pinophilum CMI 87160ii	FAE	Castanares *et al.* 1992
Aspergillus niger I-1472	FAE	Faulds *et al.* 1993
Pseudomonas fluorescens	FAED	Ferreira *et al.* 1993
Aspergilus niger	FAE-I, II	Kroon *et al.* 1996
Aspergilus niger	FAE-B	Kroon *et al.* 1996
Aspergillus tubingensis	FAE-A	de Vries *et al.* 1997
Penicillium expansum	Possible B	Donaghy *et al.* 1997
Aspergillus awamori IFO4033	FAE	Koseki *et al.* 1998
Bacillus substilis NCIMB11034	FAE	Donaghy *et al.* 1998
Lactobacillus fermentum NCFB1751	FAE	Donaghy *et al.* 1998
Clostridium stercorarium NCIMB 11754	FAE	Donaghy *et al.* 2000
Orpinomyces sp PC-2	FAEA	Blum *et al.* 2000
Penicillium finiculosum	FAEB	Kroon *et al.* 2000
Penicillium funiculosum IMI-134756	FAE	Kroon *et al.* 2000
Streptomyces olivochromogenes	FAEA, B, C	Donaghy *et al.* 2000
Aspergillus pullulans NRRLY 2311-1	FAE	Rumbold *et al.* 2003
Aureobasidium pullulans	FAE-B	Rumbold *et al.* 2003
Fusarium proliferatum	FAEB	Rumbold *et al.* 2003
Neurospora crassa	FAEB, D	Crepin *et al.* 2003
Streptococcus thermophile ATCC 34628	FAE	Topakas *et al.* 2003
Streptomyces avermitilis CECT 3339	FAE	Bartolome *et al.* 2003
Fusarium oxysporum	FoFAE-A, B	Nikos *et al.* 2004
Fusarium oxysporum F3	FAE	Topakas *et al.* 2004
Neurospora crassa	FAE-I (FAEB)	Crepin *et al.* 2004
Sporotrichum thermophile	StFAEA	Topakas *et al.* 2004
Talaromyces stipitatus	TsFAEA, B	Garcia *et al.* 2004
Aspergillus awamori VTT-D-71025	FAE	Mathew *et al.* 2005
Aspergillus flavipes	FAE	Mathew *et al.* 2005
Aspergilus niger	FAE-A (III)	Faulds *et al.* 2005
Sporotrichum thermophile	StFAEA, B, C	Vafiadi *et al.* 2005
Streptomyces avermitilis UAH 30	FAE	Faulds *et al.* 2005
Aspergillus niger NRRL3	FAE	Shin and Chen 2006
Fusarium proliferatum NRRL 26517	FAE	Shin and Chen 2006
Fusarium verticillioides NRRL 26517 JSC-3	FAE	Shin and Chen 2006
Aspergillus nidulans	FAE-B	Shin and Chen 2007
Streptomyces sp. S10	FAE	Mukherjee *et al.* 2007
Streptomyces tendae	FAE	Ferreira *et al.* 2007
Aspergillus niger CFR 1105	FAE	Shyamala *et al.* 2009
Aspergillus niger	FAE	Ou *et al.* 2011
Thermobifida sp.	FAE	Huang *et al.* 2011
Chrysosporium lucknowense C1	FAE	Kuhnel *et al.* 2012
Aspergillus flavus	FAE	Zhang *et al.* 2013
Aspergillus usamii	FAE	Gong *et al.* 2013
Pleurotus eryngii	FAE	Nieter *et al.* 2014
Mucor hiemalis NCIM 837	FAE	Singh *et al.* 2015

2. Optimization of process parameters for ferulic acid esterase production

Bioprocess development is an important step for any biotechnological process considering the benefit. It is crucial for large scale production of FAE and it is the primary step towards its commercialization. It may be considered as an important step for cost reduction and increased yield. Industrial scale production of FAE has not been yet successfully achieved due to its low production yield, high recovery and purification cost. Optimization of culture conditions could be one way to increase the yield and development of an economically feasible production process.

Process parameters like pH and temperature have been observed to affect the FAE production. The studies carried on FAE production showed that the optimal pH and temperature for maximum activity ranges from 5.0 to 7.0 and 30 to 60 °C respectively. *Streptomyces olivochromogenes* NRCC 2258 showed 2350 mU/mg FAE activity at 37 °C (Johnson *et al.* 1989) whereas *Sporotrichum thermophile* ATCC 34628 (Topakas *et al.* 2003) showed 156 mU/mg FAE activity at 50 °C. Other microorganisms such as *Schizophyllum Commune* ATCC 38548 (MacKenzie *et al.* 1988), *Aspergillus awamori* IFO4 033 (Koseki *et al.* 1998), *Aspergillus niger* VTTD-77050 (Tenkanen *et al.* 1991), *Bacillus subtilis* ATCC 7661 (Donaghy *et al.* 1998), *Clostridium stercorarium* NCIMB 11754 (Donaghy *et al.* 2000), *Fusarium proliferatum* NRRL 26517 (Shin and Chen 2006) showed their maximum FAE activity at 30 °C.

In addition to the parametric conditions carbon and nitrogen sources are also very essential media components which are required for proper growth and metabolism of the microorganisms, thus, these are required in appropriate amount in media for the enzyme production. Different types of carbon and nitrogen sources have been used by different authors for FAE production (Table 2). *Aspergillus niger* favored FAE production with sugar beet pulp at a concentration of 1.5% (*v*/*v*) whereas brewer's spent grain is reported as the most suitable natural carbon source for FAE production from *Lactobacillus acidophilus* K1 (2.64 ± 0.06 U) and *Lactobacillus rhamnosus* (Szwajgier *et al.* 2011). Other agroresidues such as rice bran, corn pectin and german wheat bran are also reported for FAE production (Szwajgier *et al.* 2011). Topakas *et al.* (2007) and Wong et al. (2013) reported that complex carbon sources viz. wheat bran and sugar beet pulp favors FAE production.

Kumar *et al.* (2011) examined different carbon sources which includes D-glucose, D-fructose, sucrose, lactose, maltose, sorbitol, mannitol, maize starch, and glycerol at 0.5% (*w*/*v*) concentration in his study, for FAE production from *Aspergillus terreus* GA2 strain and observed potato starch (860 U/gds) as the most effective carbon source for FAE production.

Medium optimization or parametric optimization is conducted either by "one variable at a time" or by using different statistical tools such as response surface methodology (RSM). RSM is superior as it exposes all the possible interaction between variables. The "one-variable-at-a-time" approach is subsidiary for estimating opportune operational intervals for consequential inhibitory/stimulatory variables prior to conducting RSM. Optimization of culture conditions by the one factor at a time is not only time consuming but also very often leads to an incomplete understanding of the system, resulting in confusion and failure of predictive replication. To overcome these inhibitions, RSM is employed more often and this technique explores the interactions between numerous illustrative variables and one or more response variables. RSM was introduced by Box and Wilson in 1951. It is an accumulation of statistical techniques for designing experiments, building blocks, assessing the effects of factors probing for the optimal conditions. It has been prosperously utilized in the optimization of bioprocesses (Cui *et al.* 2009; Sarabia and Ortiz 2009; Shukla *et al.* 2007; Chandrika and Fereidoon 2005; Kristo *et al.* 2003; Wejse *et al.* 2003).

The classical quadratic designs fall into two categories: Box-Behnken designs and Box-Wilson central composite designs. The Box-Behnken design (Box and Behnken 1960) is an independent quadratic design in which it does not contain an embedded factorial or fractional factorial design. In this design the treatment amalgamations are at the midpoints of edges of the process space and at the center. These designs are rotable and require three levels of each factor. The designs have circumscribed capability for orthogonal blocking compared to the central composite designs. It accommodates as a popular cull to fit a second-order replication surface model with good prognostication variance and has been widely utilized in consummately randomized experiments, split-plot experiments and within the robust parameter design setting (Ferreira *et al.* 2007).

A Box-Wilson Central Composite Design, commonly called a central composite design,' contains an imbedded factorial or fractional factorial design with center points that is augmented with a group of 'star points' that sanction estimation of curvature. Statistical optimization of FAE from selected microorganisms has resulted in incremented activity as well as productivity. The mathematical dependences obtained are utilized for presage of the optimum values of the independent variables ascertaining the maximum enzyme activity (Zhang *et al.* 2010; Katapodis *et al.* 2007; Bocchini *et al* 2002; Techapun *et al.* 2002). The statistical implement has been efficiently utilized for optimization of culture conditions (Chapla *et al.* 2010; Jatinder *et al.* 2005) as well as optimization of media components (Fang *et al.* 2010; Dobrev *et al.* 2006).

Table 2 different studies showing microorganism, carbon sources, culture time and activity obtained.

Microorganism	Carbon source	Culture time	FAE activity	Reference
Aspergillus niger NRCC 401127	De-starched wheat bran	4 d	10,580 mU/mg	Johnson *et al.* 1989
Streptomyces C 254	De-starched wheat bran	3 d	80 mU/ml	Johnson *et al.* 1989
Streptomyces olivochromogenes NRCC 2258	De-starched wheat bran	3 d	1200 mU/ml	Johnson *et al.* 1989
Orpinomyces PC 1	Coastal Bermuda grass + Sisal	5 d	220	Borneman *et al.* 1990
Piromyces MC 1	Coastal Bermuda grass + Sisal	5 d	560 mU/ml	Borneman *et al.* 1990
Aspergillus foetidus VTTD 71002	Wheat straw	7 d	12 mU/ml	Tenkanen *et al.* 1991
Aspergillus niger VTTD 77050	Solka-Floc cellulose	7 d	132 mU/mg	Tenkanen *et al.* 1991
Aspergillus oryzae VTTD 85248	Wheat bran	7 d	72 mU/mg	Tenkanen *et al.* 1991
Trichoderma reesei QM 9414	Meadow fescue grass + Glucose	7 d	3000 mU/mg	Smith *et al.* 1991
Penicillium pinophilum CMI 87160ii	Wheat bran+Oat spelt	12 d	156 mU/ml	Castanares *et al.* 1992
Aspergillus niger CBS 120.49	Sugar beet pulp	4 d	10 mU/ml	Faulds *et al.* 1994
Aspergillus awamori IFO 4033	De-starched wheat bran-SFO	3 d	6900 mU/ml	Koseki *et al.* 1998
Bacillus subtilis ATCC 7661	Methyl ferulate	1 d	1.30 mU/ml	Donaghy *et al.* 1998
Bacillus subtilis FMCCDL 1	Methyl ferulate	1 d	19.90 mU/ml	Donaghy *et al.* 1998
Bacillus subtilis NCIMB 3610	Methyl ferulate	1 d	3.40 mU/ml	Donaghy *et al.* 1998
Clostridium stercorarium NCIMB 11754	De-starched wheat bran	3 d	3.40 mU/ml	Donaghy *et al.* 2000
Penicillium funiculosum IMI 134756	Sugar beet pulp	6 d	120 mU/mg	Kroon *et al.* 2000
Aspergillus flavipes	Wheat bran	5 d	33,180 mU/mg	Bartolome *et al.* 2003
Aspergillus niger 1-1472	Corn bran	5 d	-	Crepin *et al.* 2003
Aspergillus niger CS 180	Sugar beet pulp	5 d	10.30 mU/mg	Crepin *et al.* 2003
Aureobasidium pullulans NRRLY 23311-1	Birchwood xylan	2.5 d	347 mU/mg	Rumbold *et al.* 2003
Fusarium oxysporum F3	De-starched wheat bran	3 d	98 mU/mg	Topakas *et al.* 2003
Neurospora crassa STA(74 A)	Wheat bran	3 d	9000 mU/ml	Crepin *et al.* 2003
Sporotrichum thermophile ATCC 34628	Wheat straw	7 d	156 mU/mg	Topakas *et al.* 2003
Streptomyces avermitilis CECT 3339	De-starched wheat bran	2 d	16.80 mU/mg	Faulds *et al.* 2003
Talaromyces stipitatus CBS 375.48	Wheat bran	7d	27 mU/mg	Garcia-Conesa *et al.* 2004
Aspergillus niger NRRL3	Corn bran	5 d	13.90 mU/mg	Shin and Chen 2006
Fusarium proliferatum NRRL 26517	Corn bran	5 d	33.46 mU/mg	Shin and Chen 2006
Penicillium brasilianum IBT 20888	Brewer's spent grain	8 d	1542 mU/ml	Panagiotou *et al.* 2006
Streptomyces avermitilis UAH 30	De-starched wheat bran	4 d	1.75 mU/ml	Wong *et al.* 2006

Humicola grisea	Brewers' spent grain	>8 d	0.47 ± 0.01 mU/g	Mandalari *et al.* 2008
Humicola grisea	Wheat bran	10 d	0.33 ± 0.00 mU/g	Mandalari *et al.* 2008
Aspergillus niger CFR 1105	Wheat bran	>4 d	32.5 mU/g	Hegde *et al.* 2009
Bifidobacterium animalis Bi30	Methyl-*p*-Coumarate	36 h	14.95 mU/g	Szwajgier *et al.* 2010
Bifidobacterium longum KN29	Methyl-*p*-Coumarate	36 h	13.53 mU/g	Szwajgier *et al.* 2010
Aspergillus niger ATCC 16404	Wheat bran	72 h	3.8 ± 0.12 mU/g	Ou *et al.* 2011
Aspergillus terreus GA2	Potato starch	7 d	860 U/gds	Kumar *et al.* 2011
Lactobacillus acidophilus K1	Methyl Ferulate	60 h	23.32 ± 0.05 mU/g	Szwajgier *et al.* 2011
Lactobacillus rhamnosus OXY	Methyl-*p*-Coumarate	36 h	3.64 ± 0.84 mU/g	Szwajgier *et al.* 2011

3. Ferulic acid esterase purification

The various purification procedures have been employed for obtaining pure FAE enzyme from the crude extract obtained from different bacteria, fungi and plant sources. PeFAE from *Pleurotus eryngine* has been purified using cation exchange hydrophobic interaction (HIC) and finally size exclusion chromatography (SEC) (Nieter *et al.* 2014). Kuhnel *et al.* (Kuhnel *et al.* 2012) purified an extracellular enzyme FeaA2 from culture filtrate produced from *Chrysosporium lucknowense* C1 and FAEB2 by hydrophobic interaction chromatography followed by anion exchange chromatography using an AKTA explorer 100 preparative system (GE healthcare) (Table 3).

Ammonium sulphate precipitation (ASP) method is the most common type of protein precipitation techniques. Different types of salts such as sodium sulphate and ammonium sulphate are widely used to precipitate out proteins. Among which, ammonium sulphate is the most widely used salt for the precipitation of proteins as it is inexpensive, highly soluble and easily available in highest purity level and moreover in most of the cases it does not denature proteins. Ammonium sulphate can be used for precipitation of protein to approx. 90% saturation or for differential precipitation level of proteins using different saturation of salts. Various reports are available where FAE has been purified using ammonium sulphate precipitation method followed by chromatographic methods like AnFAE and AaFAE (Hegde and Muralikrishna 2009 and Koseki *et al.* 1997).

All chromatographic techniques depend on differences in the distribution of the sundry compounds in the applied mixture between the mobile phase and the stationary phase. Ion exchange chromatography is the most popular method for the purification of proteins and other charged biomolecules based on the reversible interaction between the molecule and oppositely charged chromatography medium. This chromatography helps to speed biomolecules with even a small difference in their surface charge by choosing the optimal buffer pH and ion exchange. DEAE- anion exchange resins have been used for the purification of most of the proteins (Wu *et al.* 2011).

Thin layer chromatography is simple, rapid, and inexpensive method for the separation, tentative identification, and visual semi-quantification of a wide variety of substances. Gel filtration chromatography is a separation technique used to separate proteins on the basis of shape and their size, additionally applicable for the separation of molecular weight of proteins. The main aim of the gel filtration chromatography is fractionation of proteins. Smaller molecules incline to spend more time in the matrix, whereas the higher molecular weight molecule elute from the column before the minute molecules. Matrixes used to purify esterases from the microbes are sepharose, sephacryl, and sephadex etc. FAE was purified from *lactobacillus acidophilus* by gel filtration chromatography utilizing sephacryl S-300 (Szwajgier *et al.* 2010)

Table.3 comparison of consecutive steps of ferulic acid esterase purification from Individual microorganisms

Microorganisms	Purification steps	FAE activity (U/mg protein)	Yield (%)	Purification (fold)	References
Aspergillus awamori IFO4033	Culture supernatant	0.6	100	1.0	Koseki *et al.* 1997
	Ammonium sulphate precipitation fractions (40 ± 80%)	1.1	74.5	1.8	
	DEAE-5PW	2.6	49.0	4.3	
	G-2000SW	4.3	38.7	7.2	
	Phenyl-5PW	13.2	20.3	22.0	

Fusarium oxysporum	Culture filtrate	1.7	100.0	1.0	Topakas *et al.* 2003
	SP-Sepharose	2.3	80.0	1.4	
	1st t-butyl-HIC	4.3	46.0	2.5	
	2nd t-butyl-HIC	5.4	23.0	3.2	
	Sephacryl S-200	22.5	21.0	13.2	
Aspergillus niger CFR1105	Crude	3.23	100	1.0	Hegde and Muralikrishna 2009
	Ammonium sulphate precipitation fraction (30-60%)	11.9	66.7	3.7	
	DEAE cellulose, FAE-1 and FAE-2 respectively	21.5, 30.1	10.0, 8.4	7.6, 9.3	
	Sephacryl 100-HR, FAE-1 and FAE-2 respectively	35.9, 80.0	4.3, 2.5	11.11, 24.8	
Lactobacillus acidophilus K1	Crude enzyme solution	1.58	100.00	1.0	Szwajgier *et al.* 2010
	Ultrafiltration	1.6	5.82	1.01	
	Dialysis	7.81	12.62	4.94	
	Vacuum concentration	13.2	11.39	8.35	
	Ion exchange chromatography	17.62	5.45	11.15	
	Size exclusion chromatography, Sephacryl S-300	48.97	2.25	30.99	

4. Purity criteria of Ferulic acid esterase

Different methods are in use to assure the homogeneity of enzyme which includes Polyacrylamide gel electrophoresis (PAGE), which separates molecules according to their size and charge. During electrophoresis there is an interaction of samples, gel matrix buffers, and electric current resulting in separate bands of individual molecules. Empirically the pore size providing optimum resolution for proteins is that which results in the relative mobility (Rf) value between 0.55-0.6. R*f* values for categorical proteins is calculated as follows:

$$Rf = \frac{\text{Distance migrated by protein of interest}}{\text{Distance migrated by ion front}}$$

Almost all analytical electrophoresis of proteins are carried out with SDS PAGE (sodium dodecyl sulfate polyacrylamide gel electrophoresis). SDS PAGE was carried out under conditions that ascertain dissociation of proteins into their individual polypeptide subunits and that minimize aggregation. The Laemmli buffer system is a discontinuous buffer system that incorporates SDS, a vigorously anionic detergent in buffer (Laemmli 1970). The proteins are separated according to their molecular weight, making this system astronomically subsidiary for calculating molecular weight and to assure purity.

5. Physiochemical properties of ferulic acid esterases

FAEs have been purified and characterized from different microorganisms named *Penicillium brevicompactum*, *Talaromyces stipitatus* CBS 375.48, *Lactobacillus acidophilus* IFO13951, *Chrysosporium lucknowense* C1 and *Pleurotus eryngii* (Nieter *et al.* 2014; Kuhnel *et al.* 2012; Garcia *et al.* 2004; Donaghy *et al.* 1995). FAE activity was also observed in various *Aspergillus* species such as *Aspergillus niger, Aspergillus awamori*, *Aspergillus flavipes* and *Aspergillus nidulans* (Debeire *et al.* 2012; Shin and Chen 2007; Koseki *et al.* 2005; Mathew *et al.* 2005; Faulds *et al.* 1995). Purified FAEs show significant variation in physical and chemical characteristics such as isoelectric point, molecular weight and optimal hydrolytic reaction conditions. The molecular weight of the purified FAE ranges from the 11-210 kDa. FAEA1 and FAEB2 from the *Chrysosporium lucknowense C1* have been reported with molecular weight (determined by SDS-PAGE) of 29, 36 kDa and isoelectric point 5.5, 5.2, respectively (Kuhnel *et al.* 2012). However the FAEA2 from the same organism was reported to have a molecular weight of 33 kDa and PI of 6.0A. FAE from *Aspergillus niger* CS180 is a heavily glycosylated dimer (Kroon *et al.* 1996). FAE from *Aureobasidium pullulans* was found with 48% glycosylation (Rumbold *et al.* 2003). A glycosylated FAE (TsFAEC) has been isolated from the fungus *Talaromyces stipitatus* (Garcia-Conesa *et al.* 2004) (Table 4).

Microbial FAE has a broad range of temperature and pH dependence. They exhibit optimal activities between temperature 30 to 65 °C and pH 4.0 to 8.0. FAEA1 and FAEB2 from *Chrysosporium lucknowense* C1 have been reported to be highly active in the range of 45 to 60 °C and pH 5.0 to 7.0 respectively, whereas FAEA2 was less stable than FAEA1 and FAEB2, showing the optimum temperature in the range of 35 to 40 °C Kuhnel *et al.* 2012. FAE from *Pleurotus eryngii* showed an optimum pH of 5.0 and showed more than 50% residual activity over a broad pH range from 3.5 to 7.0 and optimum temperature for maximum enzyme activity was 50 °C. The PeFAEA showed good activity at a temperature ranging from 40-50 °C (Table 5).

Table 4 molecular weight, optimum ph and temperature for ferulic acid esterase released from individual microorganisms

Microorganisms	Enzyme	Enzyme type	Molecular weight (kDa)	pH optimum	Thermo - stability	Reference
Aspergillus oryzae	FAE		30	4.5-6.0	45	Tenkanen *et al.* 1991
Neocallimastix	FAE		69	5.5-6.8		Borneman *et al.* 1992
Penicillium pinophilum	FAE		57	6	55	Castanares *et al.* 1992
Aspergillus niger	FAE	B	29			Faulds and Williamson 1993
Aspergillus niger	FAE	A	36	5	60	de Vries *et al.* 1997
Aspergillus tubigensis	FAE	A	36	5	60	de Vries *et al.* 1997
Penicillium expansum	FAE		65	5.6	37	Donaghy *et al.* 1997
Aspergillus awamori	AwFAE	A	37	7	45	Koseki *et al.* 1998
Aspergillus nidulans	AnFAE	B	56	7	45	Donaghy *et al.* 1998
Aureobasidium pullulans	FAE	B	210	6.7	60	Donaghy *et al.* 1998
Clostridium stercorarium	FAE	C, D	33	8	65	Donaghy *et al.* 2000
Penicillium funiculosum	FAE	B	53			Kroon *et al.* 2000
Streptomyces olivochromogenes	FAE		29	5.5	30	Donaghy *et al.* 2000
Talaromyces stipitatus	TsFAE	A, B, C	35, 35, 65	6.0-7.0	60	Malherbe *et al.* 2002
Aspergillus sp.	FAE		42	4	50	Record *et al.* 2003
Fusarium proliferatum	FAE	B	31	6.5-7.5	56	Rumbold *et al.* 2003
Neurospora crassa	FAE	B, D	35	6	55	Crepin *et al.* 2003
Talaromyces stipitatus	TsFAE	C	66	6.0-7.0	60	Crepin *et al.* 2003b
Fusarium oxysporum	FoFAE	A, B	27, 31	7	45-55	Nikos *et al.* 2004;
Neurospora crassa	FAE	D	32			Crepin *et al.* 2004a
Sporotrichum thermophile	StFAE	C	23	6	55	Topakas *et al.* 2004
Talaromyces stipitatus	TsFAE	A	35			Garcia-conesa *et al.* 2004
Talaromyces stipitatus	TsFAE	B	35			Garcia-conesa *et al.* 2004
Sporotrichum thermophile	StFAE	A, B, C	33, 23	6	55	Vafiadi *et al.* 2005
Aspergillus nidulans	FAE	B	130	7	45	Shin and Chen 2007
Aspergillus niger	FAE	A, B	36	5	55	Zheng *et al.* 2007;
Aspergillus oryzae	AoFAE	B	61	6	55	Koseki *et al.* 2009
Aspergillus oryzae	AoFAE	C	75	6	60	Koseki *et al.* 2009

TABLE 5 OPTIMUM PH AND TEMPERATURE FOR FERULIC ACID ESTERASE ACTIVITY

Microorganism	Optimal pH	Optimal Temperature (°C)	Reference
Aspergillus oryzae	4.5–6.0	Upto 45	Tenkanen *et al.* 1991
Aspergillus niger CBS 120.49	5.0	55-60	Faulds and Williamson 1994
Streptomyces avermitilis CECT 3339	6.0	50	Garcia *et al.* 1998
Fusarium oxysporum	7	45	Topakas *et al.* 2004
Bifidobacterium animalis Bi30	6.3	37	Szwajgier *et al.* 2010
Bifidobacterium catenulatum KD 14	6.3	37	Szwajgier *et al.* 2010
Aspergillus niger (ATCC 16404)	-	36	Ou *et al.* 2011
Lactobacillus acidophilus K_1	6.3	37	Szwajgier *et al.* 2011
Lactobacillus rhamnosus E/N	6.5	37	Szwajgier *et al.* 2011
lactobacillus rhamnosus oxy	6.3	37	Szwajgier *et al.* 2011
Aspergillus flavus CBE 332.1	5.5	58	Zhang *et al.* 2013
Pleurotus eryngii	5.0	50	Nieter *et al* 2014
Mucor hiemalis NCIM 837	5.0	30	Singh *et al.* 2015

CONCLUSION

Microbial production of ferulic acid esterase as biocalyst for release of ferulic acid from agroresidues, suggest that these microorganisms may be useful in ferulic acid esterase production on a large scale. FAEs are highly applicable in pharmaceutical, food and cosmetic industries. Furthermore, the purified enzyme may contribute significantly to the production of ferulic acid, which is applied in production of vanillin; the most flavoring agent. Recently, due to advances in biology and computational approaches, the information can be used to identify and characterize the gene, which are involved in the release of ferulic acid esterase. This will offer new opportunities on a metabolic level to develop more efficient industrial process for production of ferulic acid esterase.

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AUTHOR CONTRIBUTION

SS and AS contributed to the design and implementation of the review article. SS wrote the article under the supervision of AS.

Conflict of interest The authors declare that they have no conflict of interest.

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

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