Screening of Microorganisms Isolated from Different Environmental Samples for Extracellular Lipase Production

Haliru Musa and Bukola Christianah Adebayo-Tayo

Department of Microbiology, University of Ibadan, Ibadan, Oyo State, Nigeria E-mail: <haliru2@yahoo.com; bukola_tayo@yahoo.com>

Abstract

Lipases are hydrolytic enzymes that hydrolyse triglycerides to free fatty acids and glycerol and those from microbes have occupied a prominent position as industrial biocatalysts. Microorganisms isolated from oil polluted environmental samples were screened for their lipase producing ability. A total of thirty seven bacteria and seventeen fungal strains belonging to the genera Trichoderma (16 spp.) and Aspergillus (1 sp.) were obtained from the samples. Acinetobacter sp. had the highest frequency of occurrence (37.8%). The lipolytic activity of the bacteria when screened on solid agar ranged within 3.0^m - 15.5^a mm, 3.0^n - 15.5^a mm and 3.0 - 16^a mm at 24, 48 and 72 hours of incubation, respectively. Acinetobacter sp. (OG3) had the highest activity at different hours of incubation. Eight isolates did not show any activity throughout the incubation period. On submerged fermentation, the growth of the lipolytic bacteria ranged within 0.093 - 1.003 in which Acinetobacter sp. had the highest growth while Bifidobacterium sp. had the lowest. Lipase production ranged within 1.25 U/ml - 8.65 U/ml in which Acinetobacter sp. had the highest production. During submerged fermentation, the growth of the selected fungal isolate ranged within $0.00 - 0.200^{a}$, $0.00 - 0.25^{a}$ and $0.00 - 0.25^{a}$ 0.3190^a in which T. FISO1 had the highest at 3 and 7 days of incubation while T. virens FSU/AW3 had the highest at 14 days of incubation. There was a significant difference in lipase production by the fungi, it ranged within $0.70^n - 12.35^a$ U/ml, $1.8^k - 19.15^a$ *U/ml and 2.50ⁿ - 19.8^a U/ml in which Hypocrea patella FAD1, T. stromaticum FSUAW1* and T. virens FSU/AW3 had the highest at day 3, 7 and 14, respectively. The study has shown that the bacteria and Trichoderma strains isolated are potential lipase producers.

Keywords: Lipase, Screening, Bacteria, Trichoderma spp.

Introduction

Lipases are the enzymes capable of catalysing the hydrolysis and synthesis of esters formed from glycerol and long-chain fatty acids (Sharma *et al.* 2001; and Svendsen 2000). Lipases are produced by many microorganisms (Kamimura *et al.* 2001; Elibol and Ozer 2000) and higher eukaryotes. The ease with which enzymes could be isolated from microbes has made both bacteria and fungi predominant sources of lipase. However, fungi are certainly the best lipase sources and are preferably used for industrial applications (Gupta and Soni 2000; Mahadik *et al.* 2002).

Lipases are able to catalyze hydrolysis, esterification, transesterification (Gupta *et al.* 2011) and lactonization (intramolecular esterification) (Jaeger and Eggert 2002).

Lipase producers have been isolated mainly from soil, or spoiled food material that contains vegetable oil. Lipase production from a variety of bacteria, fungi and actinomycetes has been reported in several works (Sztajer *et al.* 1988; Kulkarni and Gadre 2002).

Lipase producing fungi are present on a wide range of substrates in the ambient environment and these results could also provide basic data for further investigations on fungal extracellular enzymes (Griebeler *et al.* 2011). Among the available lipase

producing microorganisms, filamentous fungi belonging to various species of genera Aspergillus, Rhizopus Penicillium and Trichoderma are described as the most prospective lipase producers (Karanam and Medicherla 2008; Lima et al. 2003; and Kashmiri et al. 2006). Lipases find promising applications in organic chemical processing, formulations, detergent synthesis of biosurfactants, the oleochemical industry, the dairy industry, the agrochemical industry, paper manufacture, nutrition, cosmetics, pharmaceutical processing and the development of lipase-based technologies for the synthesis of novel compounds (Gupta and Soni 2000). However, one limiting factor is a shortage of lipases having the specific required processing characteristics. Because of the numerous potential uses of lipase enzyme and the need to discover new lipase with specific processing characteristics, this study was undertaken to isolate, characterize and screen lipase producing microorganisms from vegetable oil polluted environmental samples.

Materials and Methods

Sample Collection

Samples were collected from different sites: soils exposed to vegetable oil, palm oil and engine oils for long periods; spoiled food substances and waste materials; and soil from Jatropha-based biodiesel processing plant in Bode-Sa'adu, Moro local government area of Kwara State, Nigeria.

Isolation and identification of lipolytic bacterial and fungal strains

Serial dilution of the collected samples was carried out (Olutiola *et al.* 2000) and 1 ml of the diluents was pour plated on nutrient agar (NA) and Potato Dextrose agar (PDA) supplemented with streptomycin. NA plates were incubated at 37°C for 24 hours while PDA plates were incubated at 28°C for 3 days. Morphological appearances of the inoculated plates (at room temperature) were observed and distinct colonies were subcultured to obtain pure isolates which were then maintained on NA and PDA slants and stored at 4°C for further study. The pure bacterial isolates were further identified by microscopic and biochemical examination, Bergey's Manual of Determinative Bacteriology (Holt *et al.* 1994) was used as a reference for identification based on the result of various biochemical tests. The fungi were identified using information from Barnett and Hunter (1972), the Compendium of Soil Fungi (Domsch *et al.* 1980) and other relevant electronic documents on the identification of the genus *Trichoderma*.

Screening of the bacterial strains for lipase production on solid agar

A plate detection method containing a chromogenic substrate (Congo red) was used to screen the strains for lipase producing ability. The medium used for screening has the following composition in (g/l): peptone 10; NaCl 5; Calcium chloride; 0.1; castor oil, 1ml agar, 50; Congo red, 0.5; and distilled water, 1,000 ml. The sterile medium was pour plated and allows solidifying. The agar plates were spot inoculated with the bacterial and fungal isolates and the plates were incubated at 30°C for 24-48 hours for bacterial isolates and 3-5 days for fungal isolates. Lipolysis was indicated by the appearance of clear zone of inhibition around the spot of inoculation. The diameters of the colonies and clearance zones were measured after 24, 48 and 72 hours for bacteria isolates and 3, 7 and 14 days for fungal isolates.

Screening of the selected isolates for lipase production using submerged fermentation

All the isolates were screened for lipase submerged production in fermentation medium. This was carried out using the modified method of Gupta et al. (2004). The sterile basal medium was inoculated with seed cultures of the bacterial and fungal isolates, respectively. Fermentation was carried out at room temperature $(27\pm2^{\circ}C)$ for 24, 48 and 72 hours for bacterial strains and 3, 7 and 14 days for fungal strains, respectively. Lipase production was determined by assaying lipase activity in crude culture filtrate at standard assay conditions (Harrigan and McCance 1966; Gupta et al. 2003; Shukla and Gupta 2007). One unit (U) of lipase activity was defined as the amount of enzyme capable of releasing one milligram of oleic acid per minute.

Dry Cell Weight Determination

The mycelium from each flask was filtered and then washed. The washed mycelium was dried in British-made Gallenkamp oven at 110°C to a constant mass and the mass was determined using an automatic electronic balance.

Statistical Analysis

Experiments were performed in triplicate and the results were analysed statistically. The treatment effects were compared and the significant difference among replicates has been presented as Duncan's multiple range tests in the form of probability values.

Results and Discussion

Microorganisms isolated form environmental samples such oil as contaminated soils, spoilt food substances and waste materials were screened for their lipase ability producing on solid agar and submerged fermentation. A total of 37 bacteria (Acinetobacter sp., Yersinia sp., *Bifidobacterium* Arthrobacter sp., sp., Brevibacterium Staphylococcus sp., sp., Streptococcus Lactobacillus sp., sp., Citrobacter sp., Serratia marcescens, Bacillus sp., Acetobacterium sp., Acidomonas sp. and Aeromonas hydrophila) 17 and fungi (Trichoderma FAP₂S, minutisporum Trichoderma harziarium FISO6, Trichoderma sp. (1, 2, 3 and 4), Trichoderma longibrachiatum FSU/AW2, Hypocrea neorufa FSU/AW4, Trichoderma polysporum FIS03. Trichoderma ressei FISO14, *Trichoderma* stromaticum FSU/AW1. Trichoderma virens FSU/AW3, Hypocrea stilbohypoxyli Trichoderma FISO10. pleuroticola FISO12, Hypocrea patella Trichoderma fertile FOG1 FAD1. and Aspergillus sp. FISO11) were isolated from different environmental samples and screened

on solid agar as well as submerged fermentation for lipase production.

Figure 1 shows the percentage frequency of occurrence of the different bacteria isolated from the samples. Acinetobacter sp. had the highest frequency of occurrence (37.8%), followed in order by Yersinia sp. (10.8%), Bifidobacterium sp (8.1%).Arthrobacter sp (8.1%).Brevibacterium sp (5.4%), Staphylococcus sp (5.4%) and Aeromonas hydrophila (5.4%), Acetobacterium sp., Serratia marcescens, Acidomonas sp., Lactobacillus sp., Bacillus sp., Streptococcus sp and Citrobacter sp (2.7%). Bacteria were the predominant organisms isolated from the samples. The existence of lipase producing microorganisms in diverse environment such as industrial wastes, vegetable oil processing factories, dairies, soil contaminated with oil, oilseeds, and decaying food, compost heaps, coal tips, and hot springs has been studied (Sztajer et al. (1988; Wang et al. 1995).

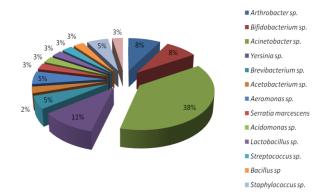


Fig. 1. Percentage frequency of occurrence of the bacterial isolates.

Similar bacteria isolates have been reported by Riaz *et al.* (2010), Barbaro *et al.* (2001), and Pandey *et al.* (1999). Gupta *et al.* (2004) also referenced 38 distinct bacterial sources from which common lipases are derived. Some of the commercially important lipase-producing fungi have been reported by Yadav *et al.* (1998) and Gulati *et al.* (1999). Abdel-Fattah and Hammad (2002) reported the use of tributyrin clearing zone techniques in the production of lipase by certain soil fungi. Table 1 shows the cultural, morphological and microscopic characteristics of the fungal isolates. The most frequently isolated genera were *Trichoderma* with a few being *Aspergillus*.

The screening of bacterial isolates for lipase production on solid agar is shown in Table 2. The lipolytic activity ranged within $3.0^{\text{m}} - 15.5^{\text{a}}$ mm, $3.0^{\text{n}} - 15.5^{\text{a}}$ mm and $3.0 - 16^{\text{a}}$ mm at 24, 48 and 72 hours of incubation, respectively. *Acinetobacter* sp. (OG3) had the highest activity at different hours of incubation. Eight isolates did not show any activity throughout the incubation period.

Table 3 shows lipase production and growth of the bacteria isolates using submerged fermentation. The growth of the bacterial isolates in submerged fermentation ranged within 0.093 - 1.003 in which *Bifidobacterium* sp. had the lowest while *Acinetobacter* sp. had the highest, respectively. Lipase production ranged within 1.25 U/ml - 8.65 U/ml in which *Acinetobacter* sp. had the highest production.

Table 4 shows the screening of the fungal isolates for growth and lipase production using submerged fermentation. The growth of the selected fungal isolate ranged within 0.00 - 0.200a, 0.00 - 0.25a and 0.00 - 0.3190a in which *Trichoderma* sp.1. FISO1 had the highest at 3 and 7 days of incubation while *T. virens* FSU/AW3 had the highest at 14 days of incubation.

It could be inferred from the obtained results that maximum biomass production was attained at the late period of (14^{th} day) of fermentation. This, however, is in contrast with the report of Rashimiri *et al.* (2006) who reported that maximum biomass production by *T. viride* was observed during the early hours of fermentation. There was a significant difference in lipase production by the fungi.

Isolate code	Appearance on Agar	Microscopic spore shape	Examination of Hyphae	Probable Identity	
FAP25	Presenting a whitish green granular colony	Smooth green ellipsoidal conidia	Phialides typically crowded arising from broad cells	Trichoderma nutisporum	
FISO6	Yellow green conidia formed densely over the center and in undulating concentric rings	Conidia subglobose to ovoidal	Globose, intercalary hyphae and Terminal phialides	Trichoderma harzianum	
FSU/AW2	Dark green, mottled with white flecks	Chlamydospores terminal, globose to subglobose. Smooth green conidia	Phialides mainly arising singly, in divergent whorls and typically cylindrical	Trichoderma Iongibrachiatum	
FSU/AW4	Dark grown colonies	Conidia ellipsoidal, thick- walled, smooth and grayish green	Phialides flask shaped, widest below	Hypocrea neorufa	
FISO3	White dense colony	White, smooth and oblong conidial chlamydospores not formed.	Phialides in whorls at the tip of fertile branches	Trichoderma polysporum	
FISO14	Deep green with appressed mycelium with conspicuous radial lines	Conidia green, smooth and oblong or ellipsoidal	Long straight phialides, typically flask-shaped and enlarged in the middle	Trichoderma ressei	
FSU/AW1	Dense mycelium, appressed off-white	White conidia, smooth, oblong chlamydospores forming in abundance	Phialides typically terminating cells of branches in pairs	Trichoderma stromaticum	
FSU/AW3	Diffusing yellow pigment conidiation	Conidia broadly ellipsoidal to ovoid	Phialides mainly arising in closely appressed whorls. Less frequently in pairs	Trichoderma virens	
FISO10	Conidia typically forming moderately well in concentric rings	Smooth and ellipsoidal conidia	Phialides produced singly	Hypocrea stilbohypoxyli	
FISO12	Dark green, dense wooly colony	Green conidia, smooth and sub-globose	Phialides conspicuously swollen in the middle and with a sharply constricted, straight long neck	Trichoderma pleuroticola	
FAD1	Yellowish green, uniformly dispersed colonies	Thin-walled, smooth, green, ellipsoidal conidia hlamydospore not formed	Straight phialides widest at the middle	Hypocrea patella	
FOG1	Conidia formed densely in a central disk and concentric rings of conidial production. No pigment in the agar	Smooth green conidia and ellipsoidal in shape	Basal phialides tending to be held in more or less divergent whorl while terminal phialides slightly hooked	Trichoderma fertile	
FISO11	Deep brown powdery colony with evanescent greenish tone in very old cultures	Conidia globose more or less pear shaped and coarsely roughened	Non-septate hyphae vessels thin-walled. Metullae and phiallides present	Aspergillus sp.	

Table 1. Cultural, morphological and microscopic characteristics of fungal isolates.

AU J.T. 15(3): 179-186 (Jan. 2012)

		Lipolytic Activity Diameter (mm) Incubation Time				
Isolate Code	Bacterial Isolates					
		24	48	72		
ISO1	Artrobacter sp.	0.00	0.00	0.00		
ISO2A	Artrobacter sp.	5.0 ¹	8.0 ^h	9 ^t		
ISO2B	Bifidobacterium sp.	7.0 ^j	8.0 ^h	8 ^h		
ISO3	Acinetobacter calcoaceticus	0.00	8.5 ⁹	8.5 ⁹		
ISO4	Arthrobacter sp.	0.00	6.0 ^j	6.0 ¹		
ISO5	Yersinia sp.	0.00	0.00	0.00		
ISO7	Acinetobacter sp.	5.0 ¹	5.0 ^l	5.0 ¹		
ISO8	Brevibacterium sp.	11.0 [°]	11.0 ^c	11.0 ^c		
ISO9	Acetobacterium sp.	8.0 ^h	8.0 ^h	8.0 ^h		
ISO10	Bifidobacterium sp.	0.00	0.00	0.00		
ISO11	Aeromonas hydrophilla	4.0 ^m	7.0'	7.5 ^h		
ISOI2	Acinetobacter sp.	7.5'	8.0 ⁿ	8.0 ^h		
ISO13	Acinetobacter sp.	9.0 ^t	9.0 ^t	9.0 ^t		
ISO14	Brevibacterium sp.	4.0 ^m	4.0 ^m	4.0 ^m		
ISO15	Yersinia sp.	8.0 ^h	8 ^h	8.0 ^h		
ISO16	Acinetobacter sp.	0.00	0.00	3.0 ⁿ		
ISO17	Serratia marcescens	0.00	0.00	0.00		
ISO18	Acidomonas sp.	7.0 ^j	7.0 ⁱ	7.0 ⁱ		
SU/AW1	Lactobacillus sp.	0.00	0.00	0.00		
SU/AW2	Bifidobacterium sp.	4.0 ^m	4.0 ^m	4 ^m		
SU/AW3	Streptococcus sp.	0.00	0.00	0.00		
SU/AW4	Acinetobacter sp.	5.0'	5.0 ^l	5'		
SU/AW5	Acinetobacter sp.	5.0	5.5 ^k	5.5 ^k		
SU/AW6	Yersinia sp.	0.00	0.00	0.00		
ID1	Acinetobacter sp.	10.5 ^d	10.5 ^d	10.5 ^d		
AP11	Bacillus sp.	0.00	0.00	0.00		
AP12	Aeromonas sp.	0.00	0.00	4.0 ^m		
AP21	Acinetobacter sp.	8 ⁿ	8.0 ⁿ	8.5 ⁹		
AP22	Yersinia sp.	7.5'	8.0 ⁿ	8.0 ^h		
AP23	Acinetobacter sp.	7.5'	8.0 ^h	8.0 ^h		
OG1	Staphylococcus sp.	0.00	0.00	0.00		
OG2	Acinetobacter sp.	11.5 [⊳]	11.5 ^b	12.5 ^b		
OG3	Citrobacter sp.	15.5ª	15.5ª	16.0 ^a		
AD1	Acinetobacter sp.	3.0 ⁿ	3.0 ⁿ	3.0 ⁿ		
AD2	Acinetobacter sp.	9.5 ^e	10.0 ^e	10 ^e		
AD3	Staphylococcus sp.	8.5 ^g	9.0 ^t	9 [†]		
AD4	Acinetobacter sp.	5.5 ^k	5.5 ^k	5.5 ^k		

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Lipase production ranged within 0.70^{n} - 12.35^{a} U/ml, 1.8^{k} - 19.15^{a} U/ml and 2.50^{n} -19.8^a U/ml in which Hypocrea patella FAD1, T. stromaticum FSUAW1 and T. virens FSU/AW3 had the highest at day 3, 7 and 14, respectively. Trichoderma viriens FSU/AW3 had the highest production at day 14 followed order by Trichoderma stromaticum in FSUAW1 (19.15 U/ml) while Trichoderma minutisporum FAP2S had the least production at day 7, respectively. Lipases are ubiquitous in nature and can be derived from various sources such as plants, animals and microorganisms. Microbial lipases represent the most widely used class of enzymes in biotechnological applications and organic chemistry (Saxena et al. 1999; Jaeger et al. 1994). It could thus be inferred that there was an increase in lipase production by some of the isolates (T. *Polysporum, T. harzianum and T. pleuroticola*) as the incubation period increases. However, in most of the isolates the lipase production decreased with the increase of the incubation period. This is in agreement with work of Rajesh et al. (2010) who stated that the lipase production increases as the incubation time increases but later falls with the increase in incubation time. Reduction in lipase production could be due to proteolytic degradation of the enzyme system. Pera et al. (2006) have reported 51% increase in extracellular lipase production by Aspergillus niger after 4 days of incubation.

AU J.T. 15(3): 179-186 (Jan. 2012)

Isolate Code	Bacterial Isolates	Lipase Production (U/ml)	Growth (Absorbance@600nm)	Growth (Dry Weight (g))	
ISO1	Artrobacter sp.	2.9	0.568	0.188	
ISO2A	Artrobacter sp.	2.7	0.278	0.137	
ISO2B	Bifidobacterium sp.	7.2	0.093	0.122	
ISO3	Acinetobacter calcoaceticus	4.7	0.462	0.166	
ISO4	Arthrobacter sp.	3.15	0.129	0.033	
ISO5	Yersinia sp.	5.7	0.744	0.204	
ISO7	Acinetobacter sp.	1.8	0.376	0.212	
ISO8	Brevibacterium sp.	1.95	0.493	0.054	
ISO9	Acetobacterium sp.	1.9	0.825	0.074	
ISO10	Bifidobacterium sp.	2.9	0.295	0.063	
ISO11	Aeromonas hydrophilla	5.6	0.365	0.069	
ISOI2	Acinetobacter sp.	5.8	0.535	0.052	
ISO13	Acinetobacter sp.	5.7	0.347	0.065	
ISO14	Brevibacterium sp.	3.3	0.435	0.233	
ISO15	Yersinia sp.	1.25	0.527	0.245	
ISO16	Acinetobacter sp.	4.2	0.119	0.222	
ISO17	Serratia marcescens	8.0	0.397	0.091	
ISO18	Acidomonas sp.	1.95	0.852	0.062	
SU/AW1	Lactobacillus sp.	3.0	0.792	0.000	
SU/AW2	Bifidobacterium sp.	3.9	0.914	0.000	
SU/AW3	Streptococcus sp.	3.4	0.543	0.000	
SU/AW4	Acinetobacter sp.	1.5	0.441	0.000	
SU/AW5	Acinetobacter sp.	8.65	0.527	0.000	
SU/AW6	Yersinia sp.	3.3	0.691	0.006	
ID1	Acinetobacter sp.	4.2	1.003	0.006	
AP11	Bacillus sp.	3.8	0.415	0.000	
AP12	Aeromonas sp.	4.5	0.277	0.000	
AP21	Acinetobacter sp.	7.65	0.6	0.000	
AP22	Yersinia sp.	7.05	0.7	0.000	
AP23	Acinetobacter sp.	3.6	0.412	0.000	
0G1	Staphylococcus sp.	3.2	0.839	0.021	
OG2	Acinetobacter sp.	1.8	0.65	0.000	
OG3	Citrobacter sp.	7.25	0.633	0.012	
AD1	Acinetobacter sp.	1.75	0.801	0.216	
AD2	Acinetobacter sp.	6.45	0.626	0.014	
AD3	Staphylococcus sp.	2.3	0.645	0.005	
AD4	Acinetobacter sp.	2.0	1.003	0.106	

Table 3. Screening of bacterial isolates for lipase production and growth determination using submerged fermentation.

Table 4. Screening of fungal isolates for growth and lipase production using submerged fermentation.

Isolate Code	Fungal Isolates		Growth			Lipase Production (U/ml)		
		Incuba	Incubation Time (Days)			Incubation Time (Days)		
		3	7	14	3	7	14	
FAP25	Trichoderma minutisporum	0.0130 ^g	0.028 ^h	0.1490 [†]	4.90 ⁿ	1.00	2.60 ^m	
FISO12	Trichoderma pleuroticola	0.1500 [⊳]	0.064 ^g	0.2690 ^b	1.50 [']	5.45 ^e	9.55 [°]	
FISO1	Trichoderma	0.2000 ^a	0.2440 ^a	0.2590 ^c	2.80 ^k	4.80 ^g	6.50 ^e	
FISO7	Trichoderma	0.0000 ⁱ	0.1970 ^d	0.0490 ^k	3.2 ⁱ	2.40 ⁱ	2.40°	
FISO3	Trichoderma polysporum	0.0000 ^j	0.2170 ^c	0.0890 ^h	2.95 ^j	2.00 ^j	3.40 ^k	
FISO15	Trichoderma	0.1200 ^c	0.0400 ^h	0.1990 [†]	6.50 ^f	3.50 ^h	2.50 ⁿ	
FSU/AW3	Trichoderma virens	0.0070 ^{ih}	0.2500 ^a	0.3190 ^a	8.31 ^d	2.35 ⁱ	19.8 ^ª	
FSUAW2	Trichoderma longibrachiatum	0.0000 ⁱ	0.0760 ^t	0.0720 ⁱ	4.90 ^h	17.10 ^b	2.05 ^p	
FISO6	Trichoderma harzianum	0.0000 ⁱ	0.0000 ^m	0.0050 ⁿ	1.20 ^m	4.60 ^g	4.47 ⁱ	
FISO11	Aspergillus sp.	0.055 ^e	0.0280 ^h	0.2090 ^e	7.99 ^e	1.80 ^ĸ	16.75 [⊳]	
FAD1	Hypocrea patella	0.136 [°]	0.1010 ^e	0.1190 ^g	12.35 ^a	7.60 ^d	7.65 ^d	
FISO9	Trichoderma	0.119 ^d	0.2240 ^b	0.0590 ^J	10.00 ^c	1.00	2.80 ¹	
FISO14	Trichoderma ressei	0.012 ^{gh}	0.2150 ^c	0.2190 ^d	10.60 ^b	4.90 ^t	3.65 ^j	
FSUAW1	Trichoderma stromaticum	0.023 ^f	0.0250 ^{ih}	0.0000 ⁿ	5.70 ⁹	19.15 ^a	5.60 ^f	
FOGI	Trichoderma fertile	0.0120 ^{gh}	0.0220 ^j	0.015l ^m	2.95 ^j	4.60 ^g	2.58 ^{mn}	
FISO10	Hypocrea stilbohypoxyli	0.0000 ⁱ	.00000 ¹	0.0000 ⁿ	0.70 ⁿ	11.05 [°]	5.35 ^h	
FSU/AW4	Hypocrea neorufa	0.0060'	0.004 ^ĸ	0.0000 ⁿ	10.00 ^c	5.35 ^t	5.45 ⁹	

Means with different superscripts within the column are significantly different. $P \ge 0.005$.

Conclusion

The present study revealed that Acinetobacter sp. And Trichoderma virens gave the best lipase production (8.65 U/ml and 19.80 U/ml) amongst the 37 and 17 bacterial and fungal isolates screened for lipase production using submerged fermentation. Other isolates such as: T. stromaticum, T. longibrachiatum, Aspergillus sp., Hypocrea patella, H. stilbohypoxyli, T. ressei, and H. neorufa with 19.15 U/ml, 17.10 U/ml, 16.75 U/ml, 12.35 U/ml, 11.05 U/ml, 10.60 U/ml, and 10.00 U/ml enzyme activity, respectively, are also high potential lipase producers. Research on production, characterization and their purification of enzyme through optimization of process parameters such as pH, temperature and various substrate utilizations would reveal those strains with higher lipase production potential.

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