

LACCASE FASTA SEQUENCE:

>Bsp. TH007_Lac

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>Bsp.Y3_Lac

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AWVRQEGADADHIQVVIGPSIGSCCYIVDDVVIDQVKQLPFTTEDVYSEMSQGQYKIDLKTLNKNVLLHAGLKEENIHVSSMCTSCNEQ
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>Bpu_Lac

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DAWVRQEGADADHIQVVIGPSIGSCCYIVDDVVIDQVKQLPFTTEDVYSEMSQGQYKIDLKTLNKNVLLHAGLKEENIHVSSMCTSCNE
QHFFSHRRDQGKTGRMMSFVGFKEA

>Pae_Lac

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AEARSAFVPSANPGRFMADIYRLARIRLGAHGVTAVHGGGLCTFSDTARFYSYRRSSRTGRFASLVWLQD

>Sma_Lac

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>Ctr_Lac

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SIHWHGIRQKDTMHMDGVNGITQCPAIPLDHFVYSWNATQYGSSWYHSHYSVQYADGLQAPITIHGPTSAQYDESIDPIIVTDW
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CELLULASE FASTA SEQUENCE:

>Rde_Cel

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YAQAVINAIRAVDPDNLIIVGTPNWSQDVDAASRDPI SGANIAYTLHFYAGSHGQWLRDKAQTALNNGIALFVTEWGSV GASDGGVA
TSETWAWVDFMKAKGISNANWALNDKSEGASALVPGAS SQGWSAGQLTASGALTKQIIGGWPAGPAPTGC TRVSIPAQIQAEAYC
QMSGVQVEATTDVNGGSNVGYIDTGDWLT YD VNVPAAGSYVVKYRVASASGGGTIQMEKGGGGAVYGT VNL PSTGGWQNWTTVT
QTVSLPAGQQT LGIVAKSGGFNLNWVDISRSGDPVDSGITIQAENFDAMSGVQTEATTD SGGGLNVGYLDAGDWLSYPTVNIATAGTY
TIEYRVASLNGGGNLQLEEAGGSVYVYGSVNIPSTGGWQNWVTVKHTVQLPAGQRKFGIAVRNGGYNLWFRITKS

>Rte_Cel

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MGVDEGGGYLQDPAGNKARVKAVVDAAIANDMYVIIDWHS HAEDYRSQAVAFFEEMARTYGKNNHVIYEVYNEPLNISWSGTIKP
YAQAVIGAIRAIDPDNLIIVGTPNWSQDVDAASRDPI SGANIAYTLHFYAGSHGQWLRDKAQTALNNGIALFVTEWGSV GASDGGVA
TSETWAWVDFMKAKGISNANWALNDKSEGASALVPGAS SQGWSAGQLTRSGALAKQIISGWSGTPPPAGCSRVS VPAQIQAEAYC
QMSGVQVEATSDANGGSNVGYIDSGDWMTYD VNVPAAGNYVVKYRVASASGGGVIQMEKGGGGAVYGT VNV PSTGGWQSWTTVS
QTVSLPAGQQMLGLVAKSGGFNLNWVDISR VGDVDSGITIQAENFDAMNGVQTEATTD SGGGLNVGYLDAGDWLSYPTVNIASAGT
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>Rsp. BIM B-1768_Cel

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SAIRAIIDPDNLIIVGTPNWSQDVDAASRDPI SGANIAYTLHFYAGSHGQWLRDKAQTALNNGIALFVTEWGSV GASDGGVAEGETQA
WVDFMKAKGISNANWALNDKSEGASALVPGAS SQGWSAGQLTRSGALAKQIISGWSGTPPPAGCSRVS VPAQIQAEAYC
QVETTTDTDGGSNVGYIETGDWMTYD VNVPTAGTYVVKYRVASASGGGVVQLERGGGGATYGT VNVGATGGWQNWTTVSHNVTL
PAGQQT LAILAKSGGFNINWLDISRPGEPATGTTIQAENFDAMYGVQTEATTD SGGGLNVGYLDAGDWLSYPTINVPTAGSYTVEYRV
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>Psp. P8_Cel

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KPYAQAVINAIRAIDPDNLIIVGTPNWSQDVDAASRDPI SGANIAYTLHFYAGSHGQWLRDKAQTALNNGIALFVTEWGSV NASGDG
GVNESETWAWVDFMKAKGISNANWALNDKAE GASALVAGASAQGGWSAGQLTRSGALARQIIGGWPAGPTNSGCTRMAVPAQLQA
EAYCNSMGVQVEGTTDTDGGSNVGYIDTGDWMTYD VNVPAAGSYLVK YRVASQS GGGVIQLERGGGGATYGTINVPSTGGWQNW
TVSHTVTLAAGQQT LAILAKSGGFNINWLDISRPTDPVSGGITIQAENFDSQSGVQTEATTD SGGGLNVGYLDAGDWLSYPSVNLATAG
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>Bba_Cel

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VEAAIANDLYVIIDWHS HAEDYRTQAVAFFEEMARTYGRSNHVIYEVYNEPLNVSWSGTIKPYAQAVINAIRAIDPDNLIIVGTPNWSQ
DVDAASRDPIRGTNIA YTLHFYAGTHGQLRDKAQTALNNGIPLFVTEWGSVNASGDGAVAEAEATAAWMDFLKTRGISHANWALND
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WMTYDINVP TAGSYVVKYRVASVPGGGVIQLERAGGGAVFGTVNVPATGGWQSWTTVQHTVNL PAGAQTVAIVAQAGGFNVNWLDF
SPAGNPAPSGIT IQAENFDAQSGVQTEPTTDTGGGLNVGYLDAGDWLSFPAINLPAGGTYLIEYRVASLNGGGNLQLEEAGGSVYVYGAL
NVPSTGGWQNWTTISHTVTL PAGSRKFGIAVRNGGWNLWFRVTKT

>Psp._Cel

ASFAGNSLFWSTGWGGEKYNNASAVGWLKSDWKS RVV RVVAMGVDEGGGYLQDPAGNKARVKAVVDAAIANDMYVIIDWHS HA
EDYRTQAVAFFEEMARTYGRSNHVIYEVYNEPLNVSWSGTIKPYAQAVINAIRAIDPDNLIIVGTPNWSQDVDAASRDPIRGTNIA YTLH
FYAGTHGQGLRDKAQTALNNGIPLFVTEWGSVNASGDGAVAEAEATAAWMDFLKTRGISHANWALNDKSEGASALVPGTSAQGGWT
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ASAPGGGVIQLERAGGGTVFGTVNVPATGGWQNWTTVQHTVNL PAGAQTVAIVA KTGGFNVNWL DLSPAGSPTPSGVTVQAESFDA
QSGVLT EATTD TGGGLNVGYLDAGDWLSYPAINLPAGGTYLIEYRVASLNGGGNLQLEEAGGSVYVYGALNVPSTGGWQNWTTLSHTV
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>Bli_Cel

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YALSKGAPIFVTEWGTSDASNGGVYLDQSREWLKYLDSKKISVWNWNLSDKQESSAALNPGASKNGGWSQSDLSPSGKFVRDNIRS

GSNGSSGDSGNSKGSQKDKKQDKPGQDSGAAANTIAVQYRAGDNNVNGNQIRPQLNIKNSKKTVSLNRITVRYWYKTRKGG
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GKLIWGTEPNWCPFSYIL

>Dro_Cel

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AYKNYASAVINRCKNSSAIFAWELANEPNCAADKTKGLPRSANCTYETTSAWYQEMGAFVKSIDPHHMVTWGGEGEFYEEGATDGFY
AGSEGGHFYHELALPEMDFGTFHLYPDWWVRSVEWSNQWVVDHGVAAQTLKPKVLFEEYGWLSPARRLEYLNREAPANETRVSVLG
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PECTINASE FASTA SEQUENCE:

>Bzh_Pes

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YIEGTVDFFIGSATAVFKRAEIKSLGNGYITAASTTEAQKYGYVFIESTLNKGTAAAQSVYLGRPWRPYSAVTFLHTKMEDHIKTEGWH
NWDNRDNERTARYKEFGSTGAGSNVTHR.VKWSTILTKNEASQITVQSVLGGTDGWNPEKR

>Bpu_Pes

MKYGKVVWLVFVLSLLIDSASLQAAGHQNTNRVLVVDHKNGTFRFTVQSAIDAIPANNQQRVTIYKNGVYKEKILLPQNKPVSFIGE
ENQHKILTLYDDTNARTGSTTSSSTMIRSNDFYAENITFQNTAGRHAGQAVALYVSGDRAAFKQIRVLGYQDTLYATGSGRQYYENC
YIEGTVDFFIGSATAVFKRAEIKSLGNGYITAASTTEAQRYGYVFDSTLKKGTAAAQSVYLGRPWRPHSAVTFLYTKMDEHIKAEQWH
NWDNRDNERTARYKEYGSTGTGSNVANRVKWSNLTKEASQITVQAVLGGTDGWNPEKR

>Pla_Ply

MTKPSFTTACKLASAVFGALLFSSVPAHAADIWLDVATTGWATQNGGTKGGSRAAANDIYTVKNAEELKALSASAGSNGRIIKITGII
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NVWVDHVTFTDGRRTDDQNGTEHERPKQHHDGALDVKNGANFVTISYSVFKSHEKNLIGSSDSRTTDDGKLVKVTIHNITLFENISARA
PRVRYGQVHLYNNYHVGSTSHKVPFSYAHGVGKNSKIFSERNVFEIAGISGCDKIAGDYGGSVYRDTGSTLNLSALSCSWSSSIGWTP
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>Psa_Ply

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NVWVDHVTFTDGRRTDDQNGTANNRPKQHHDGALDVKNGANFVTISYSVFKSHEKNLIGSSDSRTTDDGKLVKVTIHNITLFEDISARA
PRVRYGQVHLYNNYHVGSTSHKVPFSYAHGVGKNSKIFSERNAFEIAGISGCDKIAGDYGGSVYRDTGSTLNLSALSCSWSSSIGWTP
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>Lmu_Pes

MITVDINNGDFTSIQEAISLKNKTSKGVTFIKNGVYKERVEILKDNVSLIGESRDGVIIITESYYANEILEDGKIGRTFRSYTFMVNANF
HATNITFKNEAGFGKMGQAVAVY.AEGDKITFKNCAMYGHQDTLFTGPLPKAEREVGGFTGPTMDAERRIVHQLYDDCYIEGEVDFIF
GSAVCYFNRECTLYALDRNEKINSYTTAPSTYEESKYGYVFNKCLTGNCPKHTVLSLRPWRIYAKAVFIDCEYSQVIEEGFCDWNKPE
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>Pae_Paces

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AMCMDGSPYKIFVNRVPSSNFLIYFEPGGMCTDYESTGQKKGLSAINYDGISDDYLT.KLAPSTLARRYITPLVVRTHPRRIEATKKWN
IYAPYCSGDMHAGDAVKLFESETGEKVIQFRGLKNARSVVS.WLKENLERPAQLLVGTASAGGYGAQLNYAHLRHDLAPERSYLLND
SGPFFQITDSTTPGYQAYRQLIEFTGIDNGYSKFISL.VPNVDVHN.PISYAAYSVAYPEDRMGMAYFWHDKTIPRYFYQLEPDIVNAVA
DADRERIREGWSKQATQKI.WENLNSLPNVGAYFPQYRGILD.SHTLTS.LDFRHS.DIQEENLELED.FIENLMNRKTVPMVDVSETS.DAEDL
ERKFLN.WDLSSALFLARL.VMMV.GIDIVRKLISDPLGAMKDLVDIVF

>Eco_Pes

MSAQEKVGLNPGWQCYTSFFMRVCQGKPGTRPIVNEDYVSESGFFGSMMHVGIHELRRQCSENCQQLKAINTH

>Ani_PecA

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MSGTDITVKQASGAKINCDGAR.WWDG.KGSNGGKTKPKFFKAHKL.DESTITGLKIYNTPVQGFSILADHLTITDVTIDNSAGTSKGHN
TIDAFD.IGQSTYITIDGATVYNQDDCLAINSGEHITFTNGYCDGGHLSIGSIGGRSDNTVSDVTISNSKVLNSQNGVRIKTIYGKTGTVENVK
FEDITLSDISKYGIVVEQDYENGSPTGKPTNGVKVEDITFKKVTG.SVKSSGTDIYILCGSGSCSNWTWSGVDVTGGK.KSSCKKNVPSGAS
CSD

Table S1: Microbial strains showing similar enzymatic activity, ABTS-oxidizing capacity, and released reducing sugar activity (DNS assay) like newly isolated strains from the mangrove ecosystem

Serial number	Microorganism name	Laccase activity	Cellulase activity	Pectinase activity	ABTS assay	DNS assay	Reference
1	<i>Bacillus sp. TH007</i>	+	+	+	+	+	58
2	<i>Bacillus sp. Y3</i>	+	+	+	+	+	59
3	<i>Bacillus pumilus</i>	+	+	+	+	+	60
4	<i>Pseudomonas aeruginosa</i>	+	+	+	+	+	61
5	<i>Stenotrophomonas maltophilia</i>	+	+	+	+	+	62
6	<i>Colletotrichum trifolii</i>	+	+	+	+	+	63
7	<i>Roseateles depolymerans</i>	+	+	+	+	+	64
8	<i>Roseateles terrae</i>	+	+	+	+	+	65
9	<i>Roseateles sp. BIM B-1768</i>	-	+	-	-	+	66
10	<i>Pelomonas sp. P8</i>	-	+	-	-	+	67
11	<i>Burkholderiales bacterium</i>	+	+	+	+	+	68
12	<i>Pelomonas sp.</i>	+	+	+	+	+	69
13	<i>Bacillus licheniformis</i>	+	+	+	+	+	70
14	<i>Diplocarpon rosae</i>	+	+	+	+	+	71
15	<i>Bacillus zhangzhouensis</i>	+	+	+	+	+	72
16	<i>Bacillus pumilus</i>	+	+	+	+	+	73
17	<i>Pseudomonas lactucae</i>	+	-	+	+	+	74
18	<i>Pseudomonas salomonii</i>	+	+	+	+	+	75
19	<i>Lachnospira multipara</i>	+	+	+	+	+	76
20	<i>Escherichia coli</i>	+	+	+	+	+	77
21	<i>Aspergillus niger</i>	+	+	+	+	+	78
22	GD1	+	+	+	+	+	This study
23	GD2	+	+	+	+	+	This study
24	GD3	+	+	+	+	+	This study