ANNEXURE I:

LIST OF PUBLISHED PAPER

1. **A Study on Biochemical Properties of Mushroom (*Pleurotus florida*),** ECOBIOS, Vol. 5. (1&2), ISSN: 0972-6446 (International Journal for Biology, Ecology and Allied Sciences)
   R. Ali., M. Rava, H. Boro., S. Das*
   Department of Biotechnology, Bodoland University, Kokrajhar, India

2. **Studies on Growth, Anti-oxidant properties, Minerals, Macro and Micro morphological characters of *Volvariella volvacea* collected from Kokrajhar, (ASSAM) INDIA. Mushroom Research Vol 2 2017**. ISSN: 0972-4885
   Raju Ali, Mamoni Rava, Hankhray Boro, Sandeep Das*
   Department of Biotechnology, Bodoland University,
   Kokrajhar, 783370, BTAD (ASSAM), INDIA

3. **Fatty acid, Amino acid, Bioactive compounds and Anti-microbial properties of wild *Volvariella volvacea* from Kokrajhar, Assam, INDIA. Mushroom Research Vol 2 2018** ISSN 0972-4885**.**
   Raju Ali, Mamoni Rava, Sandeep Das*
   Department of Biotechnology, Bodoland University
   Kokrajhar, Assam, India.

ANNEXURE II:

LIST OF CONFERENCE ATTENDED

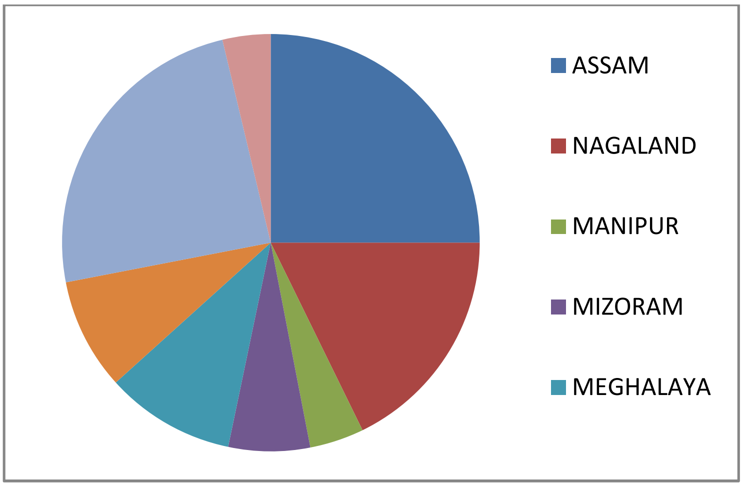
Presented a joint paper entitled **“Mushroom as ethno medicine and Traditional Food”** in National seminar organized by Centre for Bodo Studies, Bodoland University.

Presented a Paper in International Conference on Contemporary Antimicrobial Research (**ICCAR**) 2016, Assam University, Silchar, India. Nov 14-17 2016, entitled “**Study on antimicrobial properties of some wild edible mushrooms of Kokrajhar, BTAD, Assam**”.

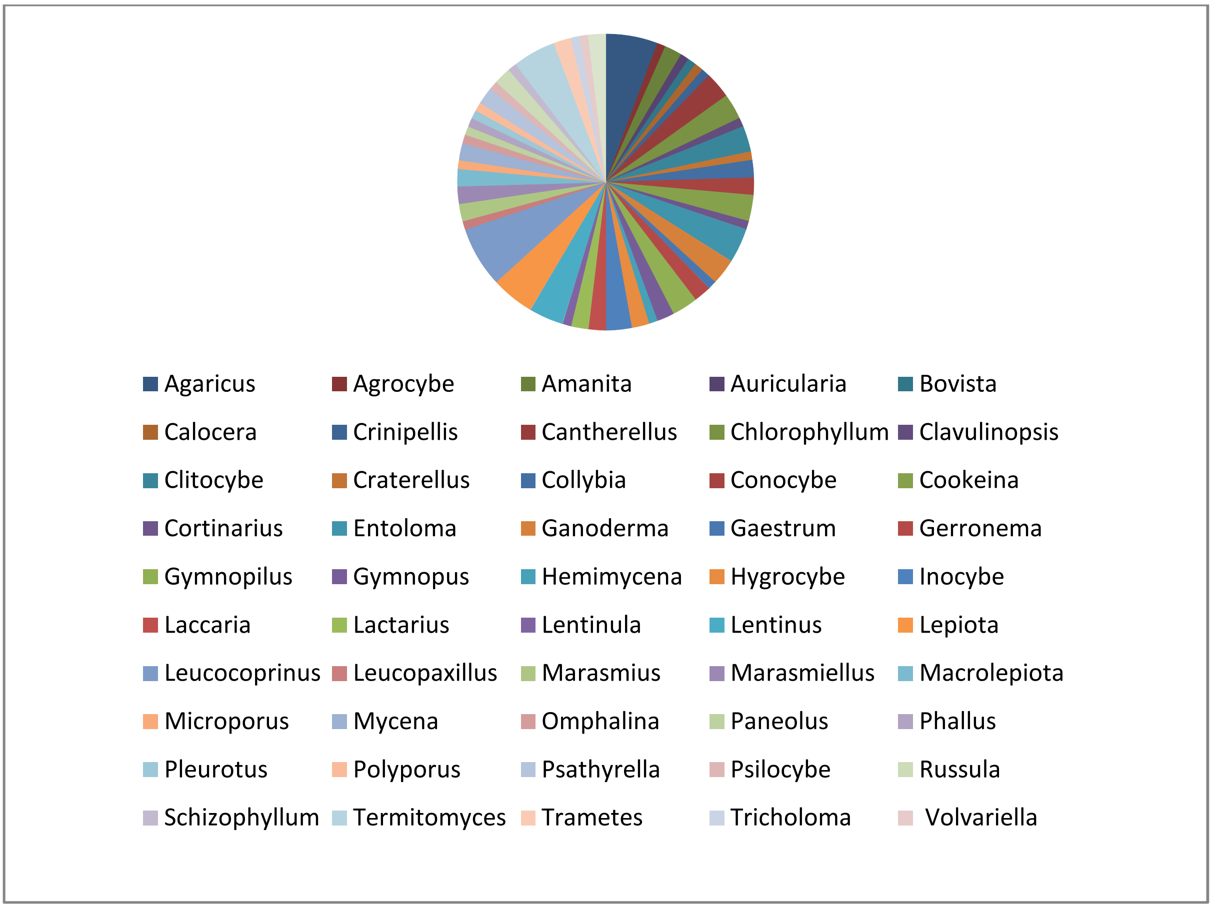
Presented a paper entitled **“ANTIOXIDANT AND NUTRITIONAL PROFILE OF SOME WILD EDIBLE MUSHROOMS SPECIES FROM KOKRAJHAR, BTAD,ASSAM, INDIA”** in National seminar on Applied science, Sustainable and Evolving Technologies held at C.I.T on 9th – 11th March 2018.

ANNEXURE III:

Diversity in Noth-East India; State wise.



Genus wise Diversity in Assam.



ANNEXURE IV

BLAST RESULTS

Sequences producing significant alignments:

Select: All None Selected:0

☐	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☐	Volvariella volvacea voucher BU 01 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	1490	1490	100%	0.0	100.00%	MK681889.1
☐	Volvariella volvacea strain OSM-6 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2	338	338	64%	2e-88	76.42%	KC142117.1
☐	Volvariella volvacea strain OSM-8 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and	338	338	64%	2e-88	76.42%	KC142114.1
☐	Volvariella volvacea strain OE-305 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and	338	338	64%	2e-88	76.42%	JN086665.1
☐	Volvariella volvacea strain ATCC MYA-4696 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribe	338	338	64%	2e-88	76.42%	HQ999973.1
☐	Volvariella volvacea strain NIH1001 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	338	338	64%	2e-88	76.42%	HM367073.1
☐	Volvariella diplasia strain CBS 355.64 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcri	336	336	64%	7e-88	76.29%	MH858454.1

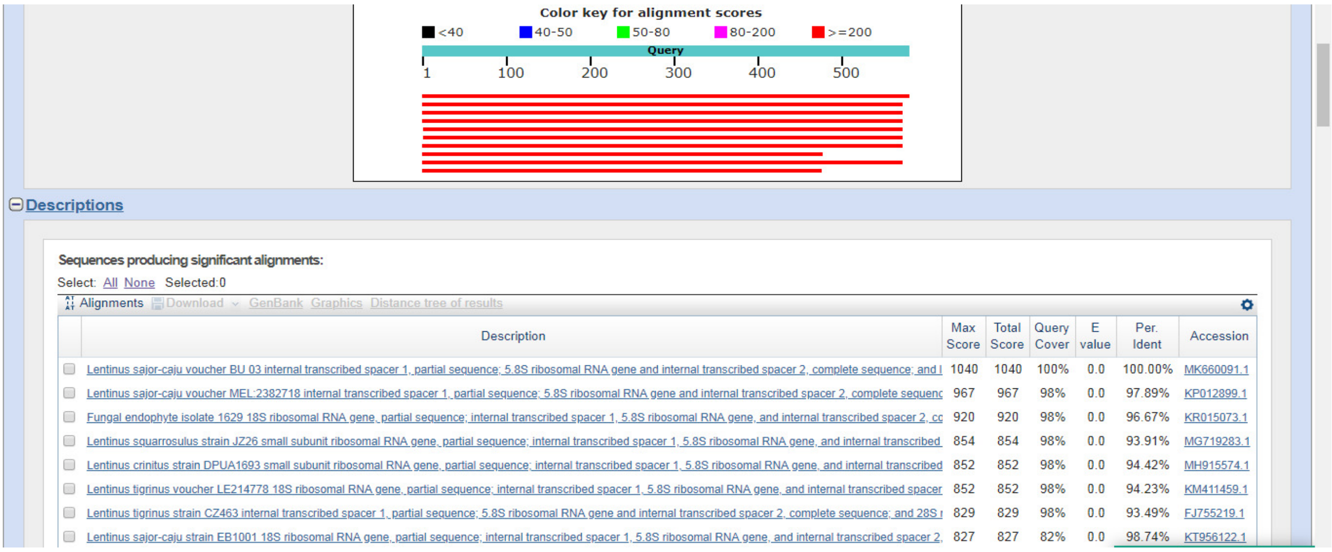
A. *Volvariella volvacea.*

Sequences producing significant alignments:

Select: All None Selected:0

☐	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☐	Termitomyces sp. TB 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete seq	1222	1222	98%	0.0	99.14%	GU001667.1
☐	Uncultured Sinotermitomyces clone JZ-SJ04 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	1217	1217	98%	0.0	98.99%	KY679676.1
☐	Termitomyces sp. 1021 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete se	1217	1217	98%	0.0	98.99%	GU001671.1
☐	Termitomyces sp. CE 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete seq	1217	1217	98%	0.0	98.99%	GU001669.1
☐	Termitomyces sp. OI genes for 18S rRNA, ITS1, 5.8S rRNA, ITS2, 26S rRNA, partial and complete sequences, from Ulu Gombak	1217	1217	98%	0.0	98.99%	AB051888.1
☐	Termitomyces sp. JK 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete seq	1213	1213	98%	0.0	98.85%	GU001668.1
☐	Termitomyces sp. 414 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, complete se	1211	1211	98%	0.0	98.85%	GU001672.1

B. *Termitomyces heimii.*



Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☐	Lentinus sajor-caju voucher BU 03 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and l	1040	1040	100%	0.0	100.00%	MK660091.1
☐	Lentinus sajor-caju voucher MEL:2382718 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequenc	967	967	98%	0.0	97.89%	KP012899.1
☐	Fungal endophyte isolate 1629 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, cc	920	920	98%	0.0	96.67%	KR015073.1
☐	Lentinus squarrosulus strain JZ26 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	854	854	98%	0.0	93.91%	MG719283.1
☐	Lentinus crinitus strain DPUA1693 small subunit ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed	852	852	98%	0.0	94.42%	MH915574.1
☐	Lentinus tigrinus voucher LE214778 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer	852	852	98%	0.0	94.23%	KM411459.1
☐	Lentinus tigrinus strain CZ463 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S r	829	829	98%	0.0	93.49%	FJ755219.1
☐	Lentinus sajor-caju strain EB1001 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2,	827	827	82%	0.0	98.74%	KT956122.1

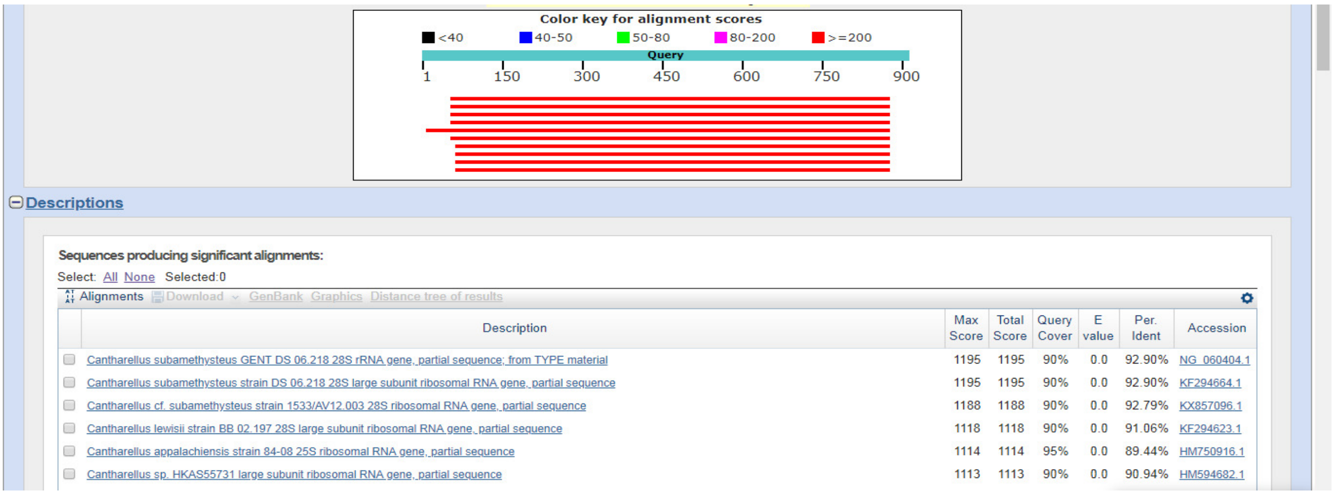
C. *Lentinus sajor-caju.*

Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☐	Chlorophyllum hortense voucher BU 04 5.8S ribosomal RNA gene, partial sequence; internal transcribed spacer 2, complete sequence; and large subunit ribosomal RNA	881	881	100%	0.0	100.00%	MK660092.1
☐	Chlorophyllum hortense isolate S19 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and	849	849	99%	0.0	98.98%	MK554576.1
☐	Chlorophyllum hortense isolate S15 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and	845	845	99%	0.0	98.78%	MK554575.1
☐	Chlorophyllum hortense isolate S14 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and	841	841	99%	0.0	98.78%	MK554574.1
☐	Chlorophyllum hortense isolate S13 internal transcribed spacer 1, partial sequence; 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and	802	802	98%	0.0	97.56%	MK554573.1
☐	Chlorophyllum sp. BAB-4973 18S ribosomal RNA gene, partial sequence; internal transcribed spacer 1, 5.8S ribosomal RNA gene, and internal transcribed spacer 2, com	683	683	81%	0.0	98.02%	KR155063.1

D. *Chlorophyllum hortense.*



Sequences producing significant alignments:

Select: All None Selected:0

	Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
☐	Cantharellus subamethysteus GENT DS 06.218 28S rRNA gene, partial sequence; from TYPE material	1195	1195	90%	0.0	92.90%	NG_060404.1
☐	Cantharellus subamethysteus strain DS 06.218 28S large subunit ribosomal RNA gene, partial sequence	1195	1195	90%	0.0	92.90%	KF294664.1
☐	Cantharellus cf. subamethysteus strain 1533/AV12.003 28S ribosomal RNA gene, partial sequence	1188	1188	90%	0.0	92.79%	KX857096.1
☐	Cantharellus lewisii strain BB 02.197 28S large subunit ribosomal RNA gene, partial sequence	1118	1118	90%	0.0	91.06%	KF294623.1
☐	Cantharellus appalachiensis strain 84-08 25S ribosomal RNA gene, partial sequence	1114	1114	95%	0.0	89.44%	HM750916.1
☐	Cantharellus sp. HKAS55731 large subunit ribosomal RNA gene, partial sequence	1113	1113	90%	0.0	90.94%	HM594682.1

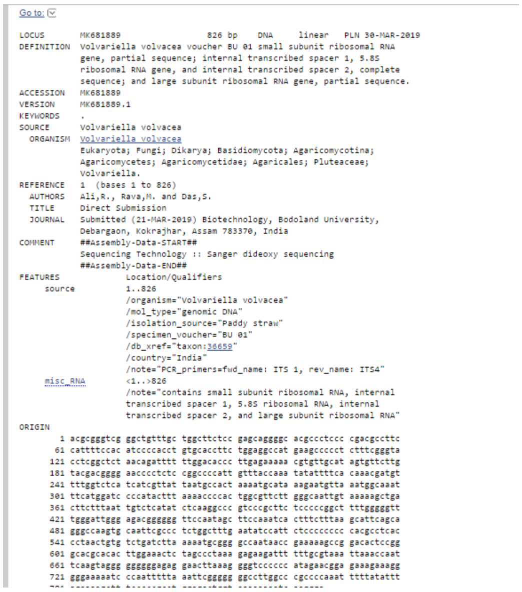
E. *Cantharellus subamethysteus.*

ANNEXURE V

Accession report

```
LOCUS       MK724034                 703 bp    DNA     linear   PLN 07-APR-2019
DEFINITION  Termitomyces heimii voucher BU 141 small subunit ribosomal RNA
            gene, partial sequence; internal transcribed spacer 1, 5.8S
            ribosomal RNA gene, and internal transcribed spacer 2, complete
            sequence; and large subunit ribosomal RNA gene, partial sequence.
ACCESSION   MK724034
VERSION     MK724034.1
KEYWORDS    .
SOURCE      Termitomyces heimii
  ORGANISM  Termitomyces heimii
            Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
            Agaricomycetes; Agaricomycetidae; Agaricales; Lyophyllaceae;
            Termitomyces.
REFERENCE   1  (bases 1 to 703)
  AUTHORS   Ali,R., Rava,M. and Das,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-APR-2019) Biotechnology, Bodoland University,
            Debargaon, Kokrajhar, Assam 783370, India
COMMENT     ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..703
                     /organism="Termitomyces heimii"
                     /mol_type="genomic DNA"
                     /specimen_voucher="BU 141"
                     /db_xref="taxon:71929"
                     /country="India"
     misc_RNA        <1..>703
                     /note="contains small subunit ribosomal RNA, internal
                     transcribed spacer 1, 5.8S ribosomal RNA, internal
                     transcribed spacer 2, and large subunit ribosomal RNA"
ORIGIN
        1 ttccgtaggt gaacctgcgg aaggatcatt aaagaattta aaccctggtt gggttgttgg
       61 tggcctttag gggcatgtgc acgcctgcca ccgttttcaa ccacctgtgc accttttgta
      121 gactttggat atataccgtt cgagggtcaa accccctcct cggttttgag ggcttgctgt
      181 gctgcaaagt tcggcttccc ttgcattccc agtctatgca tcttcttata ccccgtaatg
      241 aatgtattag aatgtttttt tattggcctt tttagtgcct ttaatcaaat acaactttca
      301 gcaacggatc tcttggctct cgcatcgatg aagaacgcag cgaaatgcga taagtaatgt
      361 gaattgcaga attcagtgaa tcatcgaatc tttgaacgca ccttgcgctc cttggtatta
      421 cgaggagcat gcctgtttga gtgtcattaa attctcaacc ttaaccagct tttgcgagtt
      481 ggtttaggct tggatgtggg ggtttttgca ggcttcttaa gaagtcagct tcccttaaat
      541 gcattagtgg aaccctttgt tggcctgttc ctggtgtgat aattatctac atcgtgcgca
      601 gtcaacttta ttctaatggg cttttctgct tctaactcgt acttcctctt tgttgaggaa
      661 gacgcttttg accattgacc tcaaatcagg aggattccca tcc
//
```

A. *Termitomyces heimii.*

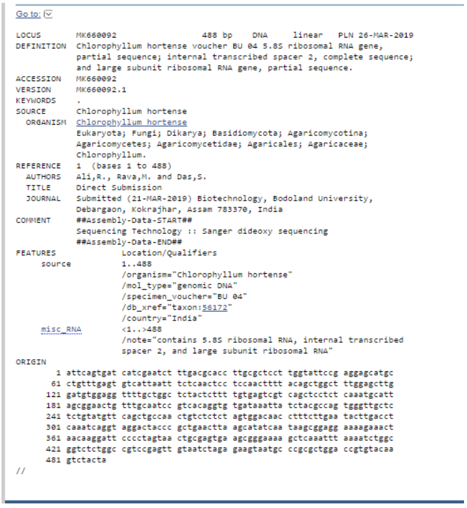


```
LOCUS       MK681889                 826 bp    DNA     linear   PLN 30-MAR-2019
DEFINITION  Volvariella volvacea voucher BU 01 small subunit ribosomal RNA
            gene, partial sequence; internal transcribed spacer 1, 5.8S
            ribosomal RNA gene, and internal transcribed spacer 2, complete
            sequence; and large subunit ribosomal RNA gene, partial sequence.
ACCESSION   MK681889
VERSION     MK681889.1
KEYWORDS    .
SOURCE      Volvariella volvacea
  ORGANISM  Volvariella volvacea
            Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
            Agaricomycetes; Agaricomycetidae; Agaricales; Pluteaceae;
            Volvariella.
REFERENCE   1  (bases 1 to 826)
  AUTHORS   Ali,R., Rava,M. and Das,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-2019) Biotechnology, Bodoland University,
            Debargaon, Kokrajhar, Assam 783370, India
COMMENT     ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..826
                     /organism="Volvariella volvacea"
                     /mol_type="genomic DNA"
                     /isolation_source="Paddy straw"
                     /specimen_voucher="BU 01"
                     /db_xref="taxon:36659"
                     /country="India"
                     /note="PCR_primers=fwd_name: ITS 1, rev_name: ITS4"
     misc_RNA        <1..>826
                     /note="contains small subunit ribosomal RNA, internal
                     transcribed spacer 1, 5.8S ribosomal RNA, internal
                     transcribed spacer 2, and large subunit ribosomal RNA"
ORIGIN
        1 acgcgggtcg ggctgtttgc tggcttctcc gagcaggggc acgccctccc cgacgccttc
       61 cattttccac atccccacct gtgcaccttc tggaggccat gaagccccct ctttcgggta
      121 cctcggctct aacagatttt ttggacaccc ttgagaaaaa cgtgttgcat agtgttcttg
      181 tacgacgggg aacccctctc cggccccatt gtttaccaaa tatattttca caaacgatgt
      241 tttggtctca tcatcgttat taatgccact aaaatgcata aagaatgtta aatggcaaat
      301 ttcatggatc cccatacttt aaaaccccac tggcgttctt gggcaattgt aaaaagctga
      361 cttctttaat tgtctcatat ctcaaggccc gtcccgcttc tcccccggct tttgggggtt
      421 tgggattggg agacgggggg ttccaatagc ttccaaatca ctttctttaa gcattcagca
      481 gggccaagtg caattcgccc tctggctttg aatatccatt ctcccccccc cacgcctcac
      541 cctaactgtg tctgatctta aaaatgcggg gccaataacc gaaaaagccg gacactccgg
      601 gcacgcacac ttggaaactc tagccctaaa gagaagattt tttgcgtaaa ttaaaccaat
      661 tcaagtaggg ggggggagag gaacttaaag gggtccccccc atagaacgga gaaagaaagg
      721 gggaaaaatc ccaattttta aattcggggg ggccttggcc cgccccaaat ttttatattt
```

B. *Volvariella volvaceae.*

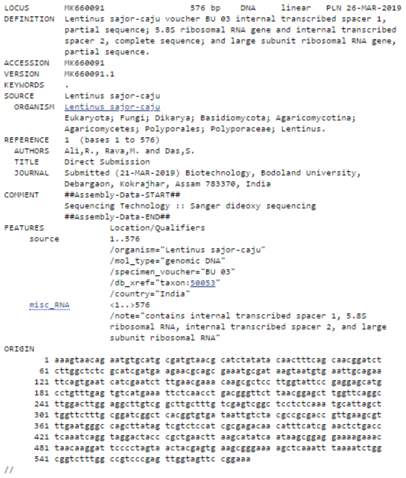
```
LOCUS       MK660093                 906 bp    DNA     linear   PLN 02-MAY-2019
DEFINITION  Cantharellus subamethysteus voucher BU 05 large subunit ribosomal
            RNA gene, partial sequence.
ACCESSION   MK660093
VERSION     MK660093.1
KEYWORDS    .
SOURCE      Cantharellus subamethysteus
  ORGANISM  Cantharellus subamethysteus
            Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
            Agaricomycetes; Cantharellales; Cantharellaceae; Cantharellus.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Ali,R., Rava,M. and Das,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-2019) Biotechnology, Bodoland University,
            Debargaon, Kokrajhar, Assam 783370, India
COMMENT     ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..906
                     /organism="Cantharellus subamethysteus"
                     /mol_type="genomic DNA"
                     /specimen_voucher="BU 05"
                     /db_xref="taxon:1495858"
                     /country="India"
     rRNA            <1..>906
                     /product="large subunit ribosomal RNA"
ORIGIN
        1 ttcttaaaca ataggccgag gtcaacgaaa ttaaataggc ctctccctac atttgcgcgt
       61 gaagagagaa gagctcatca ttagaatctg gtagtgtcgc tccgtccgtc tcgtagatgt
      121 ggactagttt ctcttgggcc ccatggcgta caagcacaat agggcgtcag tgcgacatta
      181 tagagggtga caattccgtc gttgaaccca atgagcaagt ccgttacgat ggctatgtca
      241 gagagtcgag cagtttggga tctgccgttt cacatgggag gtagattcct cctaaagcta
      301 aatacagggg agagaccgat agagaacaag taccgcaagg gaaagatgaa atagaactct
      361 gtgaagggag tcaaaaggcg tgaaattgtt gcgagagaag cgattcaagt cagcgtagct
      421 aggcccatca agcgttcttc gctttggact agctttgcca gcggtcttgt cctttagagg
      481 cttgactttt gttatacgtg tccagcctgg tatgtacagg tagcccctct tgggggcca
      541 gtggcatggc tggtggaatg gcttgcaatc gacccgtctt gaaacacgga ccaaggagtc
      601 taacatgtat gcgagtataa gggtggcaaa cccgtatgcg caatgaaagt gattttcgtc
      661 gattgagaat ggcctgacga ccagacaagc aatacatgtc cctcggacgg ccattgccca
      721 agttccgtgg tagatcccac gaacaaggag ttggagccta catgctagga cccgacagat
      781 ggtgaactaa gcctgtacat cgtgaagcca atcgaaactg tcgtagacgc tcgtagcgat
      841 tctgatcgtg cgatatctct cgtcttatcc gatgatacaa gtgacgcgga gaattttccc
      901 tccccc
//
```

C. *Cantharellus subamethysteus.*



```
LOCUS       MK660092                 488 bp    DNA     linear   PLN 26-MAR-2019
DEFINITION  Chlorophyllum hortense voucher BU 04 5.8S ribosomal RNA gene,
            partial sequence; internal transcribed spacer 2, complete sequence;
            and large subunit ribosomal RNA gene, partial sequence.
ACCESSION   MK660092
VERSION     MK660092.1
KEYWORDS    .
SOURCE      Chlorophyllum hortense
  ORGANISM  Chlorophyllum hortense
            Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
            Agaricomycetes; Agaricomycetidae; Agaricales; Agaricaceae;
            Chlorophyllum.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Ali,R., Rava,M. and Das,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-2019) Biotechnology, Bodoland University,
            Debargaon, Kokrajhar, Assam 783370, India
COMMENT     ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..488
                     /organism="Chlorophyllum hortense"
                     /mol_type="genomic DNA"
                     /specimen_voucher="BU 04"
                     /db_xref="taxon:56172"
                     /country="India"
     misc_RNA        <1..>488
                     /note="contains 5.8S ribosomal RNA, internal transcribed
                     spacer 2, and large subunit ribosomal RNA"
ORIGIN
        1 attcagtgat catcgaatct ttgacgcacc ttgcgctcct tggtattccg aggagcatgc
       61 ctgtttgagt gtcattaatt tctcaactcc tccaactttt acagctggct ttggagcttg
      121 gatgtggagg ttttgctggc tctactcttt tgtgagtcgt cagctcctct caaatgcatt
      181 agcggaactg tttgcaatcc gtcacaggtg tgataaatta tctacgccag tgggttgctc
      241 tctgtatgtt cagctgccaa ctgtctctct agtggacaac ctttcttgaa tacttgacct
      301 caaatcaggt aggactaccc gctgaactta agcatatcaa taagcggagg aaaagaaact
      361 aacaaggatt cccctagtaa ctgcgagtga agcgggaaaa gctcaaattt aaaatctggc
      421 ggtctctggc cgtccgagtt gtaatctaga gaagtaatgc ccgcgctgga ccgtgtacaa
      481 gtctacta
//
```

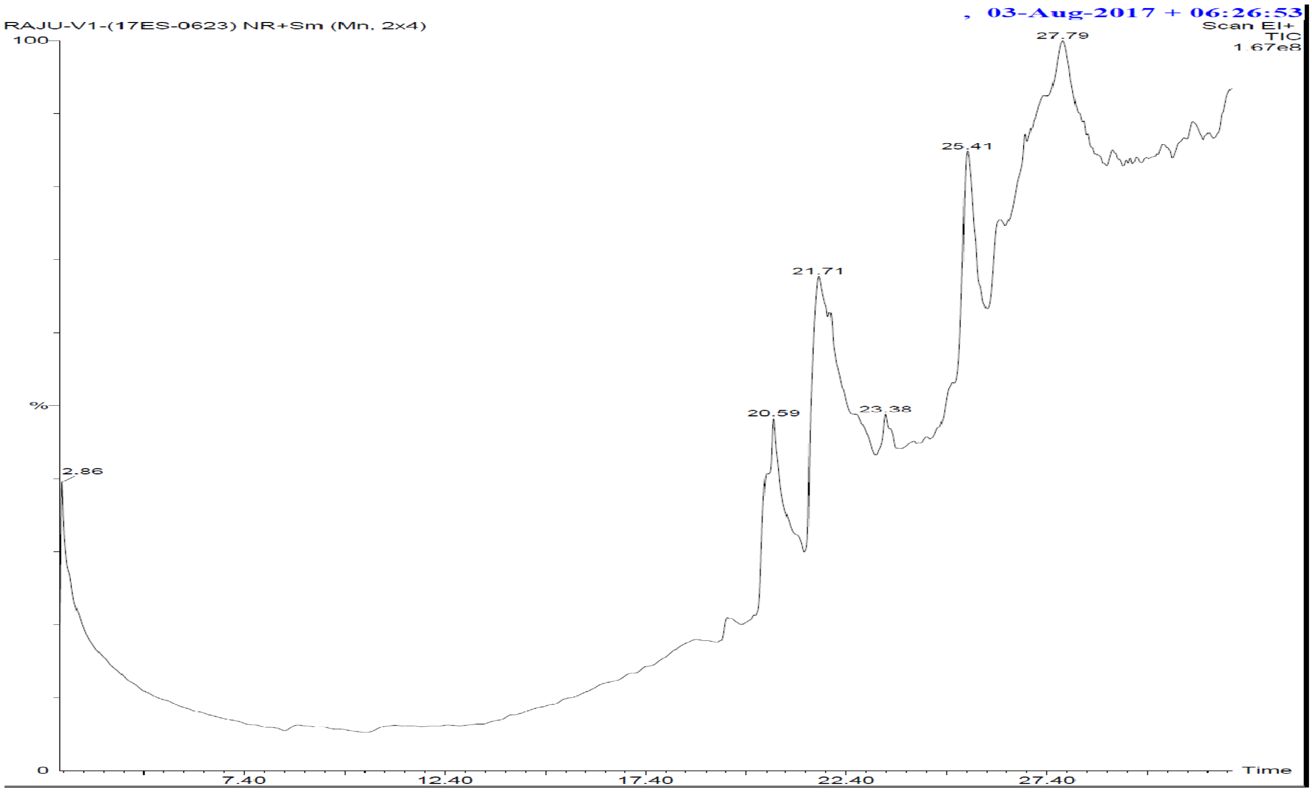
D. *Chlorophyllum hortense.*



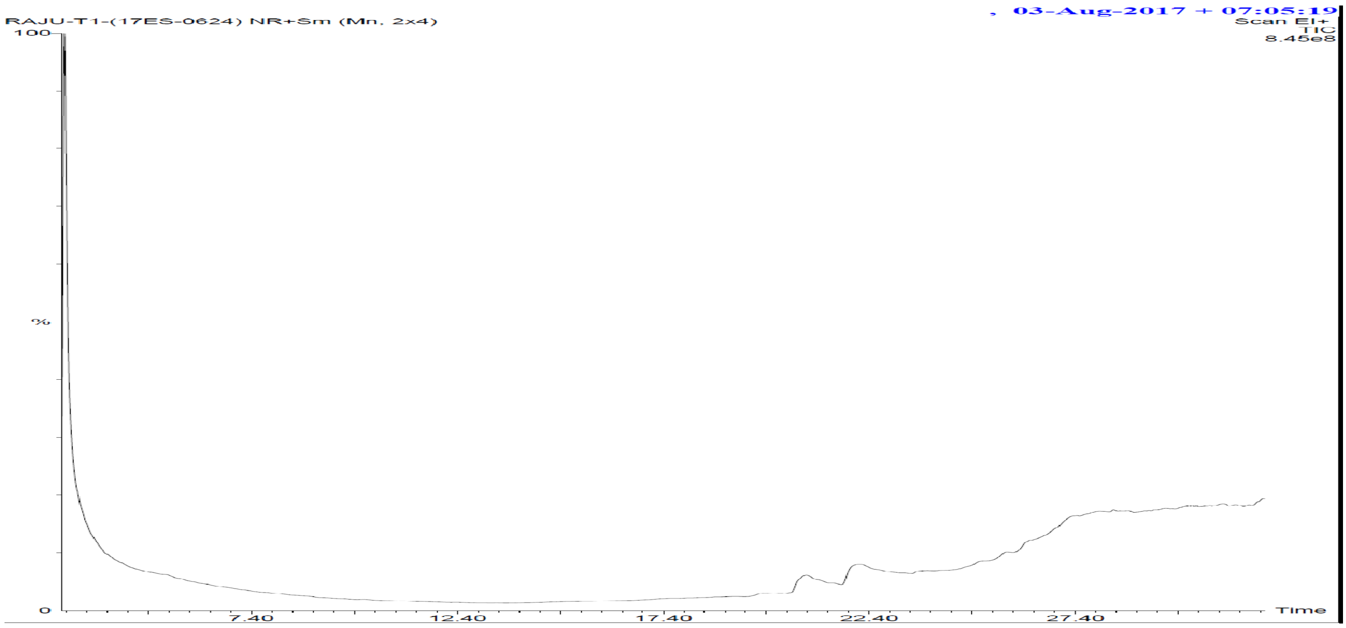
```
LOCUS       MK660091                 576 bp    DNA     linear   PLN 26-MAR-2019
DEFINITION  Lentinus sajor-caju voucher BU 03 internal transcribed spacer 1,
            partial sequence; 5.8S ribosomal RNA gene and internal transcribed
            spacer 2, complete sequence; and large subunit ribosomal RNA gene,
            partial sequence.
ACCESSION   MK660091
VERSION     MK660091.1
KEYWORDS    .
SOURCE      Lentinus sajor-caju
  ORGANISM  Lentinus sajor-caju
            Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
            Agaricomycetes; Polyporales; Polyporaceae; Lentinus.
REFERENCE   1  (bases 1 to 576)
  AUTHORS   Ali,R., Rava,M. and Das,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-2019) Biotechnology, Bodoland University,
            Debargaon, Kokrajhar, Assam 783370, India
COMMENT     ##Assembly-Data-START##
            Sequencing Technology :: Sanger dideoxy sequencing
            ##Assembly-Data-END##
FEATURES             Location/Qualifiers
     source          1..576
                     /organism="Lentinus sajor-caju"
                     /mol_type="genomic DNA"
                     /specimen_voucher="BU 03"
                     /db_xref="taxon:50053"
                     /country="India"
     misc_RNA        <1..>576
                     /note="contains internal transcribed spacer 1, 5.8S
                     ribosomal RNA, internal transcribed spacer 2, and large
                     subunit ribosomal RNA"
ORIGIN
        1 aaagtaacag aatgtgcatg cgatgtaacg catctatata caactttcag caacggatct
       61 cttggctctc gcatcgatga agaacgcagc gaaatgcgat aagtaatgtg aattgcagaa
      121 ttcagtgaat catcgaatct ttgaacgaaa caagcgctcc ttggtattcc gaggagcatg
      181 cctgtttgag tgtcatgaaa ttctcaacct gacgggttct taacggagct tggttcaggc
      241 ttggacttgg aggcttgtcg gcttgctttg tcgagtcggc tcctctcaaa tgcattagct
      301 tggttctttg cggatcggct cacggtgtga taattgtcta cgccgcgacc gttgaagcgt
      361 ttgaatgggc cagcttatag tcgtctccat cgcgagacaa catttcatcg aactctgacc
      421 tcaaatcagg taggactacc cgctgaactt aagcatatca ataagcggag gaaaagaaac
      481 taacaaggat tcccctagta actacgagtg aagcgggaaa agctcaaatt taaaatctgg
      541 cggtctttgg ccgtcccgag ttggtagttc cggaaa
//
```

E. *Lentinus sajor-caju*.

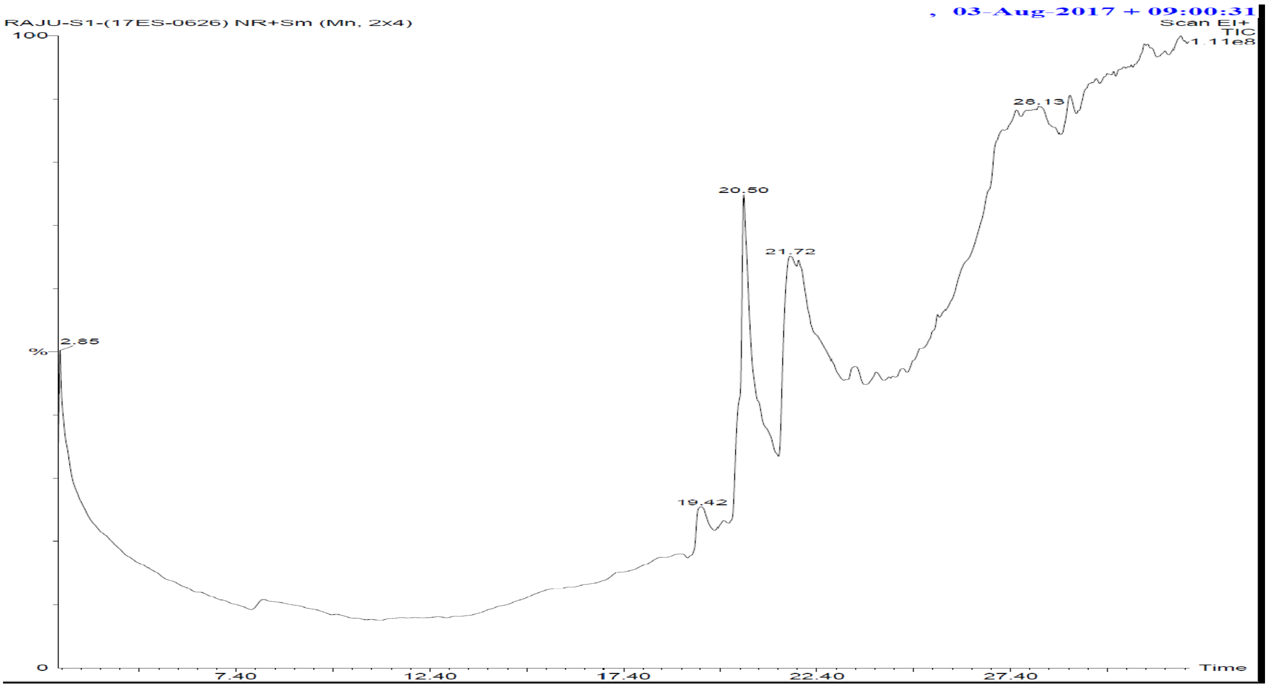
ANNEXURE VI
GC-MS Chromatogram



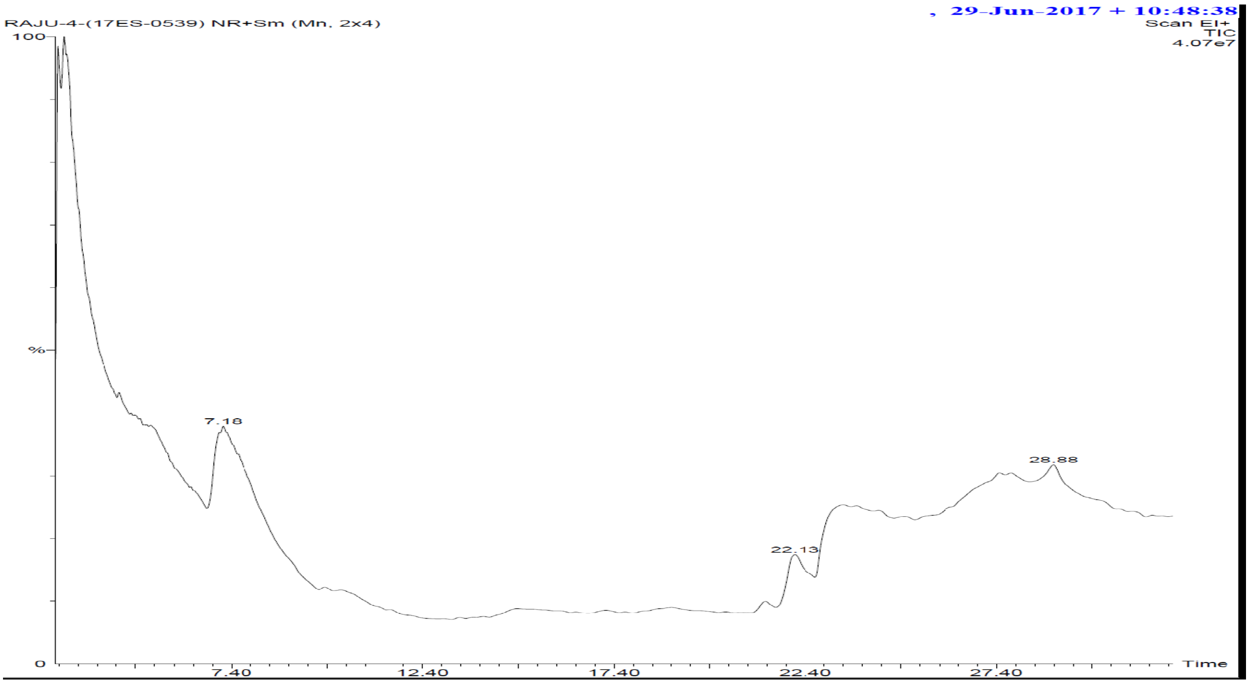
Volvariella volvacea



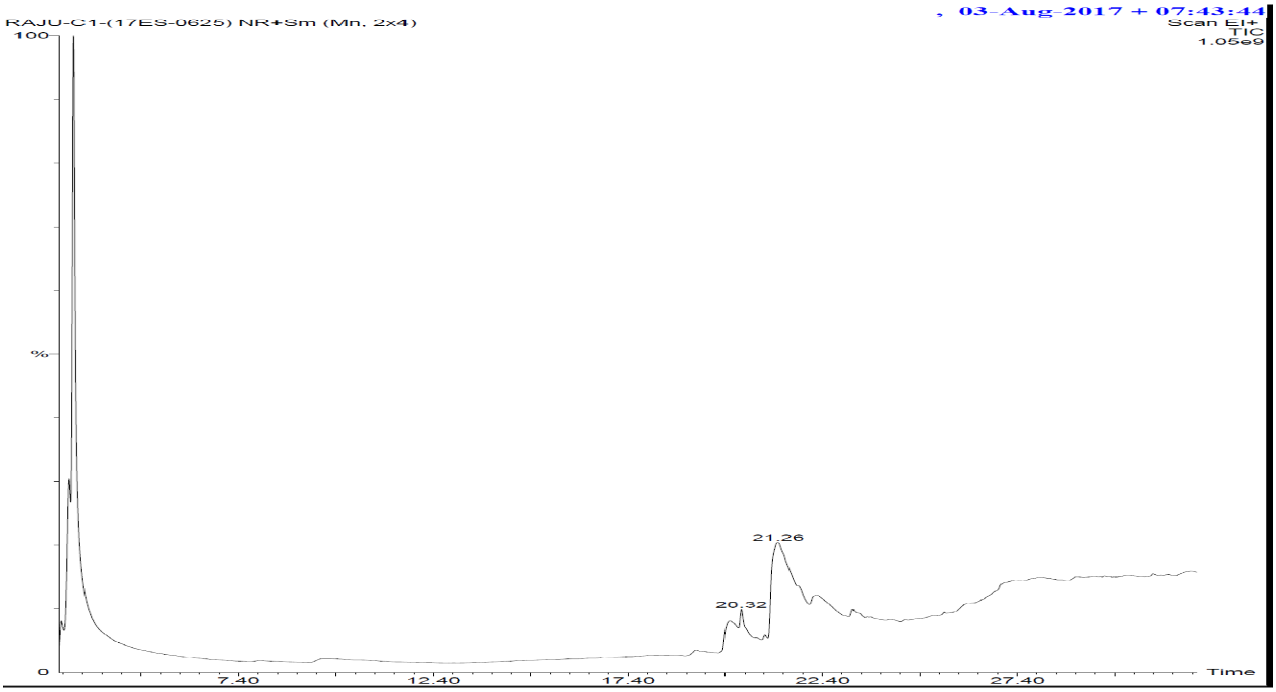
Termitomyces heimii



Lentinus sajor-caju

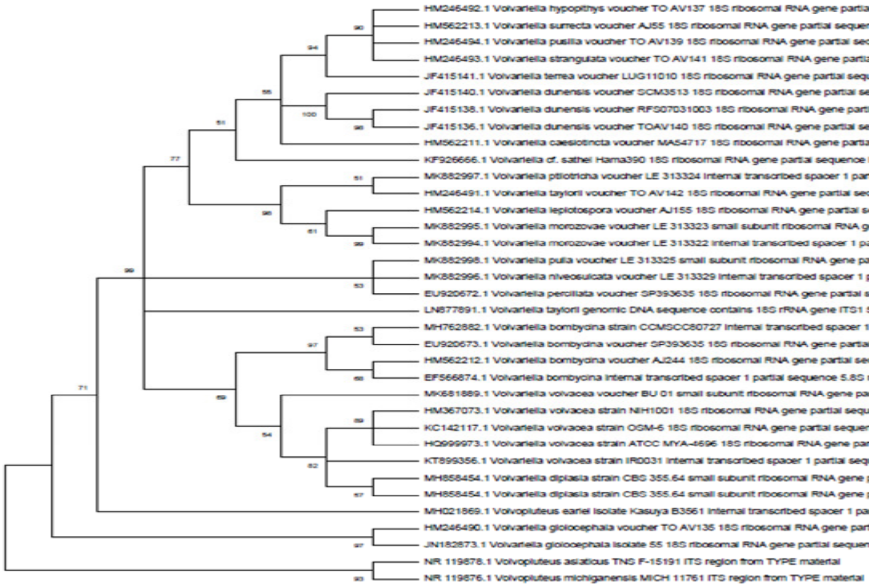


Chlorophyllum hortense



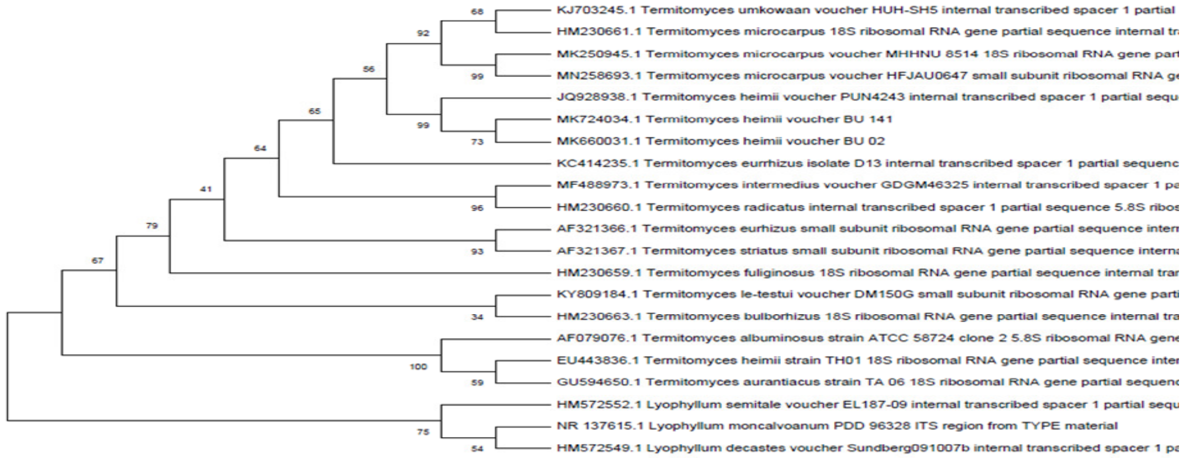
Cantharellus subamethysteus

ANNEXURE VII



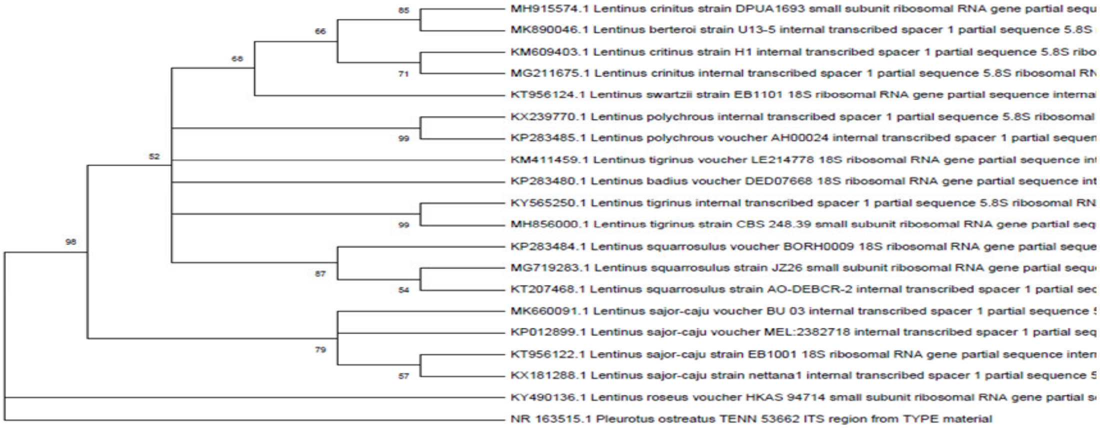
The evolutionary history was inferred by using the Maximum Likelihood method and Kimura 2-parameter model [1]. The bootstrap consensus tree inferred from 1000 replicates [3] is taken to represent the evolutionary history of the taxa analyzed [3]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 0.7939)). This analysis involved 35 nucleotide sequences. There were a total of 1298 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [2].

ML tree *Volvariella volvacea*



The evolutionary history was inferred by using the Maximum Likelihood method and Hasegawa-Kishino-Yano model [1]. The bootstrap consensus tree inferred from 1000 replicates [3] is taken to represent the evolutionary history of the taxa analyzed [3]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 1.1986)). This analysis involved 50 nucleotide sequences. There were a total of 2251 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [2].

ML tree *Termitomyces heimii*

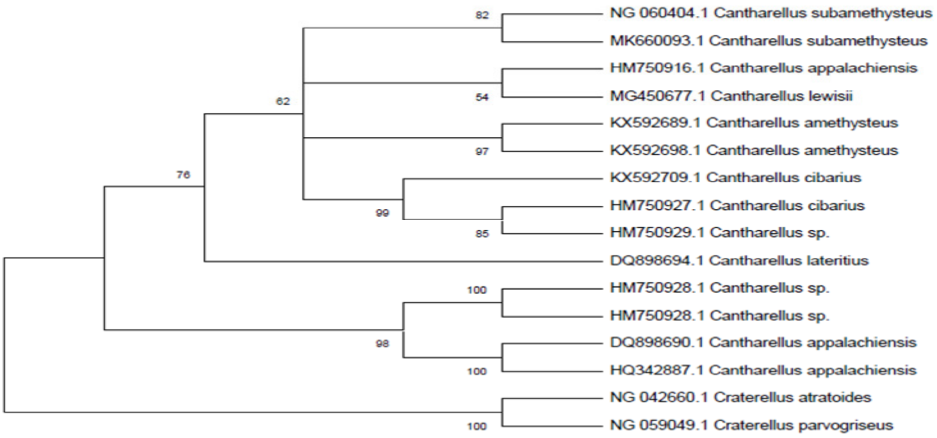


The evolutionary history was inferred by using the Maximum Likelihood method and Kimura 2-parameter model [1]. The bootstrap consensus tree inferred from 1000 replicates [3] is taken to represent the evolutionary history of the taxa analyzed [3]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 0.7916)). This analysis involved 20 nucleotide sequences. There were a total of 3147 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [2].

ML tree *Lentinus sajor-caju*

The evolutionary history was inferred by using the Maximum Likelihood method and Tamura 3-parameter model [1]. The tree with the highest log likelihood (-4476.95) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 0.3399)). The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. This analysis involved 19 nucleotide sequences. There were a total of 1383 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [2].

ML tree *Chlorophyllum hortense*



The evolutionary history was inferred by using the Maximum Likelihood method and Kimura 2-parameter model [1]. The bootstrap consensus tree inferred from 1000 replicates [3] is taken to represent the evolutionary history of the taxa analyzed [3]. Branches corresponding to partitions reproduced in less than 50% bootstrap replicates are collapsed. The percentage of replicate trees in which the associated taxa clustered together in the bootstrap test (1000 replicates) are shown next to the branches [3]. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. A discrete Gamma distribution was used to model evolutionary rate differences among sites (5 categories (+*G*, parameter = 1.2368)). This analysis involved 15 nucleotide sequences. There were a total of 1506 positions in the final dataset. Evolutionary analyses were conducted in MEGA X [2].

ML tree *Cantharellus subamethysteus*