**Supplementary**

**Table 1**: BLAST analysis of mushroom ITS sequence for query-63801 showing that the sample is *C.* *scabella* strain and its classification is as follows:

Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; *Agaricomycotina*; Agaricomycetes; Agaricomycetidae; Agaricales; Marasmiaceae; *Crinipellis*

(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=230788)

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| Scientific Name | Max Score | Total Score | Query Cover | E value | Percent identity | Accession Length | Accession |
| *C. scabella* | 1229 | 1229 | 100% | 0 | 99.56 | 711 | [MH857178.1](https://www.ncbi.nlm.nih.gov/nucleotide/MH857178.1?report=genbank&log$=nucltop&blast_rank=1&RID=JZF94HJK016) |
| *C. scabella* | 1225 | 1225 | 100% | 0 | 99.41 | 716 | [JF907969.1](https://www.ncbi.nlm.nih.gov/nucleotide/JF907969.1?report=genbank&log$=nucltop&blast_rank=2&RID=JZF94HJK016) |
| *C. scabella* | 1212 | 1212 | 100% | 0 | 99.11 | 711 | [MH857177.1](https://www.ncbi.nlm.nih.gov/nucleotide/MH857177.1?report=genbank&log$=nucltop&blast_rank=3&RID=JZF94HJK016) |

**Table 2:** BLAST analysis of mushroom ITS sequence for query-35787 showing that the sample is *P.* *conopilea* strain and its classification is as follows:

Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; *Agaricomycotina*; Agaricomycetes; Agaricomycetidae; Agaricales; Psathyrellaceae; *Parasola*

(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=230816)

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| Scientific Name | Max Score | Total Score | Query Cover | E value | Percent identity | Accession Length | Accession |
| *P. conopilea* | 1212 | 1212 | 99% | 0 | 99.85 | 659 | [MK966573.1](https://www.ncbi.nlm.nih.gov/nucleotide/MK966573.1?report=genbank&log$=nucltop&blast_rank=1&RID=JZJPH59G013) |
| *P. conopilea* | 1206 | 1206 | 99% | 0 | 99.7 | 659 | [MK966574.1](https://www.ncbi.nlm.nih.gov/nucleotide/MK966574.1?report=genbank&log$=nucltop&blast_rank=2&RID=JZJPH59G013) |
| *P. conopilea* | 1201 | 1201 | 100% | 0 | 99.25 | 703 | [MH856033.1](https://www.ncbi.nlm.nih.gov/nucleotide/MH856033.1?report=genbank&log$=nucltop&blast_rank=3&RID=JZJPH59G013) |
| *G. aporos* | 750 | 750 | 99% | 0 | 87.5 | 774 | [MK397584.1](https://www.ncbi.nlm.nih.gov/nucleotide/MK397584.1?report=genbank&log$=nucltop&blast_rank=4&RID=JZJPH59G013) |
| *P. lilatincta* | 656 | 656 | 100% | 0 | 84.82 | 687 | [KY928615.1](https://www.ncbi.nlm.nih.gov/nucleotide/KY928615.1?report=genbank&log$=nucltop&blast_rank=5&RID=JZJPH59G013) |

**Table 3:** BLAST analysis of mushroom ITS sequence for query-45217 showing that the sample is *A.* *pediades* strain and its classification is as follows:

Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; *Agaricomycotina*; Agaricomycetes; Agaricomycetidae; Agaricales; Bolbitiaceae; *Agrocybe*

(https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=84607)

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| Scientific Name | Max Score | Total Score | Query Cover | E value | Percent identity | Accession Length | Accession |
| *A. pediades* | 1206 | 1206 | 100% | 0 | 99.7 | 711 | [KM375928.1](https://www.ncbi.nlm.nih.gov/nucleotide/KM375928.1?report=genbank&log$=nucltop&blast_rank=1&RID=JZKX6HKJ013) |
| *A. pediades* | 1206 | 1206 | 100% | 0 | 99.7 | 669 | [MZ067555.1](https://www.ncbi.nlm.nih.gov/nucleotide/MZ067555.1?report=genbank&log$=nucltop&blast_rank=2&RID=JZKX6HKJ013) |
| *A. pediades* | 1206 | 1206 | 100% | 0 | 99.7 | 659 | [AY168829.1](https://www.ncbi.nlm.nih.gov/nucleotide/AY168829.1?report=genbank&log$=nucltop&blast_rank=3&RID=JZKX6HKJ013) |
| *A. praecox* | 1000 | 1000 | 96% | 0 | 95.17 | 676 | [MN294860.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN294860.1?report=genbank&log$=nucltop&blast_rank=4&RID=JZKX6HKJ013) |
| *A. putaminum* | 998 | 998 | 94% | 0 | 95.43 | 661 | [KM975434.1](https://www.ncbi.nlm.nih.gov/nucleotide/KM975434.1?report=genbank&log$=nucltop&blast_rank=5&RID=JZKX6HKJ013) |

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| **Table 4:** BLAST analysis of mushroom ITS sequence for query-46765 showing that the sample is *C.* *macrospora* strain and its classification is as follows:  Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; *Agaricomycotina*; Agaricomycetes; Agaricomycetidae; Agaricales; Bolbitiaceae; *Conocybe*  (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1276686)   |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | | Scientific Name | Max Score | Total Score | Query Cover | E value | Percent identity | Accession Length | Accession | | *C. macrospora* | 1166 | 1166 | 100% | 0 | 98.93 | 1573 | [MK859902.1](https://www.ncbi.nlm.nih.gov/nucleotide/MK859902.1?report=genbank&log$=nucltop&blast_rank=1&RID=JZMR6JAS016) | | *C. macrospora* | 1155 | 1155 | 99% | 0 | 98.92 | 652 | [JX968175.1](https://www.ncbi.nlm.nih.gov/nucleotide/JX968175.1?report=genbank&log$=nucltop&blast_rank=2&RID=JZMR6JAS016) | | *C. semiglobata* | 649 | 649 | 100% | 0 | 84.78 | 694 | [MK412366.1](https://www.ncbi.nlm.nih.gov/nucleotide/MK412366.1?report=genbank&log$=nucltop&blast_rank=3&RID=JZMR6JAS016) | | *C. spicula* | 647 | 647 | 100% | 0 | 84.82 | 697 | [MH856186.1](https://www.ncbi.nlm.nih.gov/nucleotide/MH856186.1?report=genbank&log$=nucltop&blast_rank=4&RID=JZMR6JAS016) | | *C. alkovii* | 621 | 621 | 96% | 2.00E-173 | 84.18 | 649 | [JQ247196.1](https://www.ncbi.nlm.nih.gov/nucleotide/JQ247196.1?report=genbank&log$=nucltop&blast_rank=5&RID=JZMR6JAS016) | |
| **Table 5:** Blast analysis of mushroom ITS sequence for query-63801 showing that the sample is *A.* *pusiola* strain and its classification is as follows:  Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; *Agaricomycotina*; Agaricomycetes; Agaricomycetidae; Agaricales; Bolbitiaceae; *Agrocybe*  (<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=373327>)   |  |  |  |  |  |  |  |  | | --- | --- | --- | --- | --- | --- | --- | --- | | Scientific Name | Max Score | Total Score | Query Cover | E value | Percent identity | Accession Length | Accession | | *A. pusiola* | 1182 | 1182 | 99% | 0 | 100 | 1615 | [DQ389732.1](https://www.ncbi.nlm.nih.gov/nucleotide/DQ389732.1?report=genbank&log$=nucltop&blast_rank=1&RID=JZP0S7UH01R) | | *Agrocybe* sp. | 756 | 756 | 100% | 0 | 87.99 | 663 | [MW485541.1](https://www.ncbi.nlm.nih.gov/nucleotide/MW485541.1?report=genbank&log$=nucltop&blast_rank=2&RID=JZP0S7UH01R) | | *A. smithii* | 747 | 747 | 100% | 0 | 87.65 | 1640 | [KC176296.1](https://www.ncbi.nlm.nih.gov/nucleotide/KC176296.1?report=genbank&log$=nucltop&blast_rank=3&RID=JZP0S7UH01R) | | *Galerina* sp. | 686 | 686 | 100% | 0 | 86.15 | 674 | [MK131663.1](https://www.ncbi.nlm.nih.gov/nucleotide/MK131663.1?report=genbank&log$=nucltop&blast_rank=4&RID=JZP0S7UH01R) | | *H. alpinum* | 640 | 640 | 100% | 7.00E-179 | 84.83 | 656 | [MW445560.1](https://www.ncbi.nlm.nih.gov/nucleotide/MW445560.1?report=genbank&log$=nucltop&blast_rank=5&RID=JZP0S7UH01R) | |

**Table 6:** BLAST analysis of mushroom ITS sequence for query-53867 showing that the sample is *P.* *demidoffii* strain and its classification is as follows:

Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; *Agaricomycotina*; Agaricomycetes; Agaricomycetes incertae sedis; Polyporales; Polyporaceae; *Pyrofomes*

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=574370>)

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| Scientific Name | Max Score | Total Score | Query Cover | E value | Percent identity | Accession Length | Accession |
| *P. demidoffii* | 1131 | 1131 | 100% | 0 | 99.84 | 679 | [JF895469.1](https://www.ncbi.nlm.nih.gov/nucleotide/JF895469.1?report=genbank&log$=nucltop&blast_rank=1&RID=K4JGJ40D016) |
| *P. demidoffii* | 1125 | 1125 | 100% | 0 | 99.67 | 659 | [JX968553.1](https://www.ncbi.nlm.nih.gov/nucleotide/JX968553.1?report=genbank&log$=nucltop&blast_rank=2&RID=K4JGJ40D016) |
| fungal sp. | 754 | 754 | 96% | 0 | 90.07 | 586 | [KY322586.1](https://www.ncbi.nlm.nih.gov/nucleotide/KY322586.1?report=genbank&log$=nucltop&blast_rank=3&RID=K4JGJ40D016) |
| *Pe. amazonica* | 739 | 739 | 100% | 0 | 88.73 | 660 | [JQ861754.1](https://www.ncbi.nlm.nih.gov/nucleotide/JQ861754.1?report=genbank&log$=nucltop&blast_rank=4&RID=K4JGJ40D016) |
| *D. expansa* | 734 | 734 | 100% | 0 | 88.69 | 658 | [KX449510.1](https://www.ncbi.nlm.nih.gov/nucleotide/KX449510.1?report=genbank&log$=nucltop&blast_rank=5&RID=K4JGJ40D016) |
| *G. parvulum* | 713 | 713 | 100% | 0 | 88.05 | 760 | [KU569555.1](https://www.ncbi.nlm.nih.gov/nucleotide/KU569555.1?report=genbank&log$=nucltop&blast_rank=6&RID=K4JGJ40D016) |

**Table 7:** BLAST analysis of mushroom ITS sequence for query-53867 showing that the sample is *C.* *palaeotropicum* strain and its classification is as follows:

Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; *Agaricomycotina*; Agaricomycetes; Agaricomycetidae; Agaricales; Agaricaceae; *Chlorophyllum* (<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=2172833>)

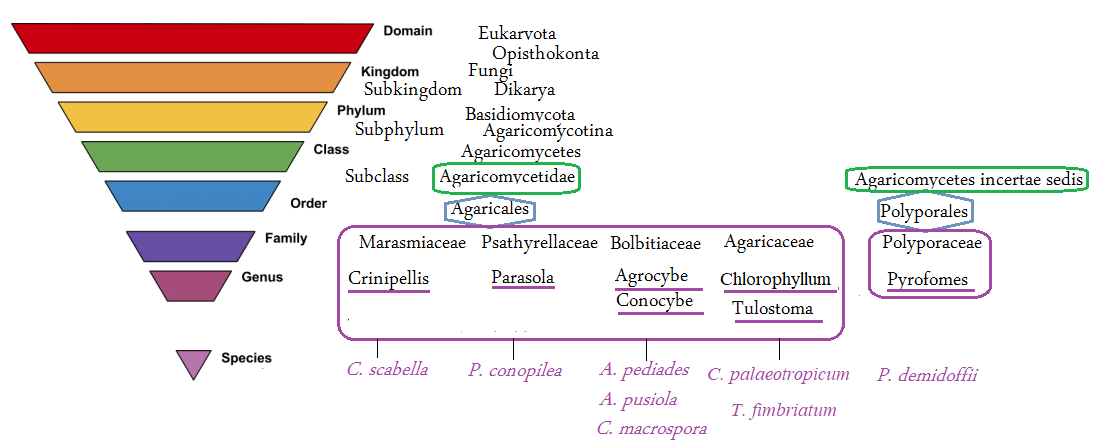
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| Scientific Name | Max Score | Total Score | Query Cover | E value | Percent identity | Accession Length | Accession |
| *C. palaeotropicum* | 1297 | 1297 | 100% | 0 | 99.3 | 776 | [MN318425.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN318425.1?report=genbank&log$=nucltop&blast_rank=1&RID=K4KTXE3N01R) |
| *C .palaeotropicum* | 1297 | 1297 | 100% | 0 | 99.3 | 776 | [MN099357.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN099357.1?report=genbank&log$=nucltop&blast_rank=2&RID=K4KTXE3N01R) |
| *Leucoagricus* sp. | 1262 | 1262 | 98% | 0 | 98.45 | 741 | [KY026054.1](https://www.ncbi.nlm.nih.gov/nucleotide/KY026054.1?report=genbank&log$=nucltop&blast_rank=3&RID=K4KTXE3N01R) |
| *C. molybdites* | 1107 | 1107 | 98% | 0 | 94.96 | 720 | [KP229777.1](https://www.ncbi.nlm.nih.gov/nucleotide/KP229777.1?report=genbank&log$=nucltop&blast_rank=4&RID=K4KTXE3N01R) |
| *C. globosum* | 1048 | 1048 | 97% | 0 | 93.44 | 727 | [AF482842.1](https://www.ncbi.nlm.nih.gov/nucleotide/AF482842.1?report=genbank&log$=nucltop&blast_rank=5&RID=K4KTXE3N01R) |
| *S. gueinzii* | 977 | 977 | 90% | 0 | 93.56 | 665 | [MN161877.1](https://www.ncbi.nlm.nih.gov/nucleotide/MN161877.1?report=genbank&log$=nucltop&blast_rank=6&RID=K4KTXE3N01R) |
| *S. gueinzii* | 977 | 977 | 90% | 0 | 93.56 | 665 | [NR\_169695.1](https://www.ncbi.nlm.nih.gov/nucleotide/NR_169695.1?report=genbank&log$=nucltop&blast_rank=7&RID=K4KTXE3N01R) |

**Table 8:** BLAST analysis of mushroom ITS sequence for query-53867 showing that the sample is *T.* *fimbriatum* strain and its classification is as follows:

Eukaryota; Opisthokonta; Fungi; Dikarya; Basidiomycota; *Agaricomycotina*; Agaricomycetes; Agaricomycetidae; Agaricales; Agaricaceae; *Tulostoma*

(<https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1305709>)

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| Scientific Name | Max Score | Total Score | Query Cover | E value | Percent identity | Accession Length | Accession |
| *T. fimbriatum* | 1275 | 1275 | 100% | 0 | 100 | 2131 | [KU518965.1](https://www.ncbi.nlm.nih.gov/nucleotide/KU518965.1?report=genbank&log$=nucltop&blast_rank=1&RID=K4R1EAM8013) |
| *T. fimbriatum* | 1275 | 1275 | 100% | 0 | 100 | 2131 | [KU518964.1](https://www.ncbi.nlm.nih.gov/nucleotide/KU518964.1?report=genbank&log$=nucltop&blast_rank=2&RID=K4R1EAM8013) |
| *T. berkeleyi* | 1190 | 1190 | 98% | 0 | 98.24 | 1258 | [MK578704.1](https://www.ncbi.nlm.nih.gov/nucleotide/MK578704.1?report=genbank&log$=nucltop&blast_rank=3&RID=K4R1EAM8013) |
| *T. submembranaceum* | 854 | 854 | 100% | 0 | 88.97 | 792 | [NR\_154521.1](https://www.ncbi.nlm.nih.gov/nucleotide/NR_154521.1?report=genbank&log$=nucltop&blast_rank=4&RID=K4R1EAM8013) |
| Uncultured Agaricales | 761 | 761 | 95% | 0 | 87.74 | 678 | [KP995464.1](https://www.ncbi.nlm.nih.gov/nucleotide/KP995464.1?report=genbank&log$=nucltop&blast_rank=5&RID=K4R1EAM8013) |
| T. cf. cretaceum MJ6103 | 732 | 732 | 97% | 0 | 86.54 | 2089 | [KU518995.1](https://www.ncbi.nlm.nih.gov/nucleotide/KU518995.1?report=genbank&log$=nucltop&blast_rank=6&RID=K4R1EAM8013) |

**Figure 1:** Taxonomy of identified samples collected from Saudi Arabia.