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Phylogenetic based studies on medicinal mushrooms found in Nagaland, India reveal closely related species

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Abstract

Nagaland is a state of India which lies in the northeast part of the Indian continent. The majority of the forest area of the state is still unexplored. Nagaland has rich biodiversity including wild mushrooms. There are many medicinal mushrooms available in Nagaland like *Auricularia auricula-judae*, *A. polytricha*, *Lentinula edodes*, *Schizophyllum commune*, *Trametes gibbosa*, *T. versicolor*, *Pycnoporus cinnabarinus*, *Microporus xanthopus*, *Coprinus disseminatus*, *Daldinia concentrica*, *Ganoderma lucidum*, *Aleuria aurantia* etc. Mushrooms are one of the most sought after food in Nagaland because of their nutritional and medicinal properties. This investigation is an attempt to study the phylogenetic relationship of the medicinal mushrooms using bioinformatics approaches. This study was based on the multiple sequence alignment of the nucleotide sequence of the mushrooms and generation of their phylogenetic tree to infer their evolutionary history.

Keywords: Nagaland, medicinal mushrooms, phylogenetic relationship

Introduction

The state of Nagaland lies in the Indo-Myanmar biodiversity hotspot zone, and is very rich in mushroom biodiversity. Mushrooms are popular because of their nutritional and medicinal properties. They have wide pharmaceutical applications. In this investigation, 10 species of medicinal mushrooms used by the ethnic tribes of Nagaland are taken for phylogenetic analysis based on the field survey report by Ao *et al.* (2016) [1]. Initially, the 18S *rRNA*, ITS region and the 28S *rRNA* gene of 10 species were retrieved from the NCBI database (National Centre for Biotechnology Information, USA). Then, the sequences were imported in the CLC Sequence Viewer 8.0 and aligned using Clustal W [2]. The multiple sequence alignment (MSA) thus obtained was used to construct the phylogenetic tree based on the Neighbor Joining algorithm using Kimura 80 parameter with a bootstrap replication of 100 to test the validity of the tree obtained. The dendrogram obtained was used to analyze the evolutionary relationship among these medicinal mushroom species. Based on the field survey conducted by Ao *et al.* (2016) [1], 21species of medicinal mushrooms were reported from Nagaland, out of which some are edible as well. Ten globally popular medicinal mushrooms available in Nagaland were selected for the present study. A data mining experiment was carried out to retrieve the nucleotide sequences (*Mutarase K* gene) of these ten species from NCBI GenBank Database, USA [3]. The retrieved sequences were imported in CLC Sequence Viewer 8.0. A multiple sequence alignment (MSA) was generated having an open gap cost of 10.0 and extension of 1.0. The MSA generated was used to construct the phylogenetic tree implementing Neighbor Joining algorithm and Kimura 80 as the nucleotide distance measure with bootstrapping of 100.

The multiple sequence alignment depicting the conserved sequences among the 10 medicinal mushrooms is shown in Fig. 1. The phylogenetic tree along with their tree distances generated using the Neighbor Joining algorithm is shown in Fig. 2 as a linear phylogram and in Fig. 3 as a circular phylogram. It is unveiled from Fig. 2 phylogenetic tree that *Auricularia auricula-judae, A. polytricha, Lentinula edodes, Schizophyllum commune* and *Daldinia concentrica* share common ancestry as they formed a clade together with a bootstrap value of 100. It is seen that *Auricularia auricula-judae*, *A. polytricha* and *Daldinia concentrica* clustered together with a bootstrap value of 56 inferring that these mushrooms share common ancestor and *Lentinula edodes* and *Schizophyllum commune* clustered together with a bootstrap value of 73 sharing common ancestor. On the other hand, *Ganoderma lucidum, Trametes gibbosa, T. versicolor*, *Pycnoporus cinnabarinus* and *Microporus xanthopus* formed separate small clusters of their own showing their common evolution from one common ancestor. *Ganoderma lucidum* mushroom shows common ancestry with the clade formed by *A. auricula-judae*, *A. polytricha*, *Lentinula edodes*, *Schizophyllum commune* and *Daldinia concentrica* species. Even though *Daldinia concentrica* is an Ascomycetes mushroom, interestingly it shows common ancestry with the remaining mushrooms. The remaining mushrooms belong to Basidiomycetes class of Fungi. Further analysis can be taken up to study their evolutionary relationship. In addition, the frequency of the nucleotide distribution reveals the variation in the A, T, G, C, A+T and G+C distribution (Fig. 4). Also, the heatmap analysis showed the distribution of nucleotide distribution and frequency is correlated (Fig. 5).

In this short communication, the phylogenetic relationship of the ten medicinal mushrooms of Nagaland is reported for the first time. It is observed that all the mushroom species share common ancestry at some point of evolution.

Conflict of interest

The author's declare no conflict of interest.

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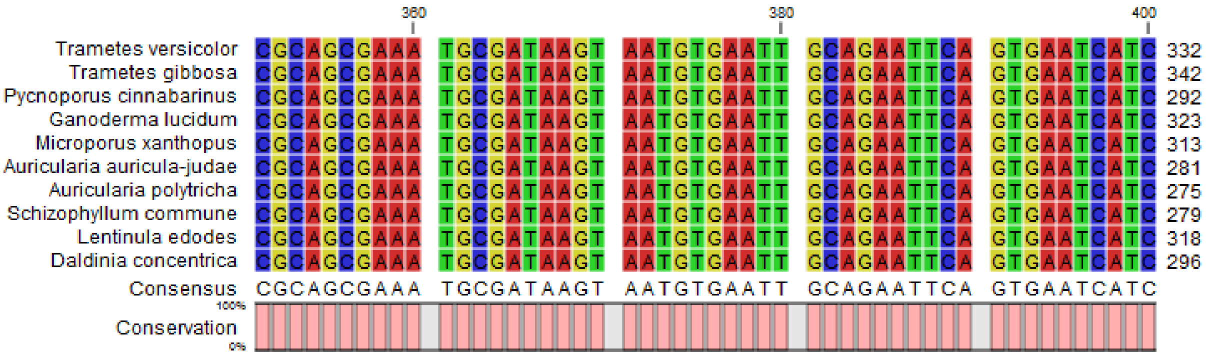
List of figures



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                                      360                  380                  400
Trametes versicolor      CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC 332
Trametes gibbosa         CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC 342
Pycnoporus cinnabarinus  CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC 292
Ganoderma lucidum        CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC 323
Microporus xanthopus     CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC 313
Auricularia auricula-judae CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC 281
Auricularia polytricha   CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC 275
Schizophyllum commune    CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC 279
Lentinula edodes         CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC 318
Daldinia concentrica     CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC 296
Consensus                CGCAGCGAAA TGCGATAAGT AATGTGAATT GCAGAATTCA GTGAATCATC
                     100%
Conservation
                       0%
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Fig 1: Multiple sequence alignment (MSA) of the studied mushroom species

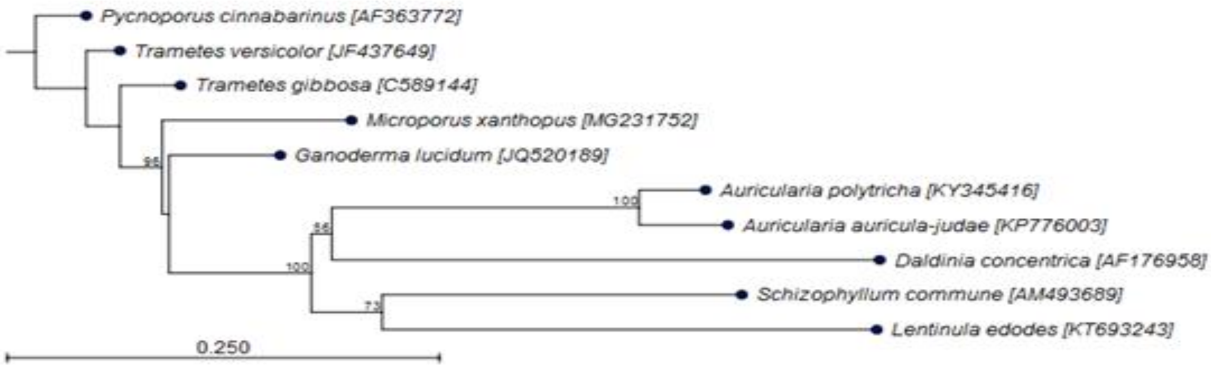

Fig 2: Phylogenetic generated using CLC Sequence Viewer for MSA

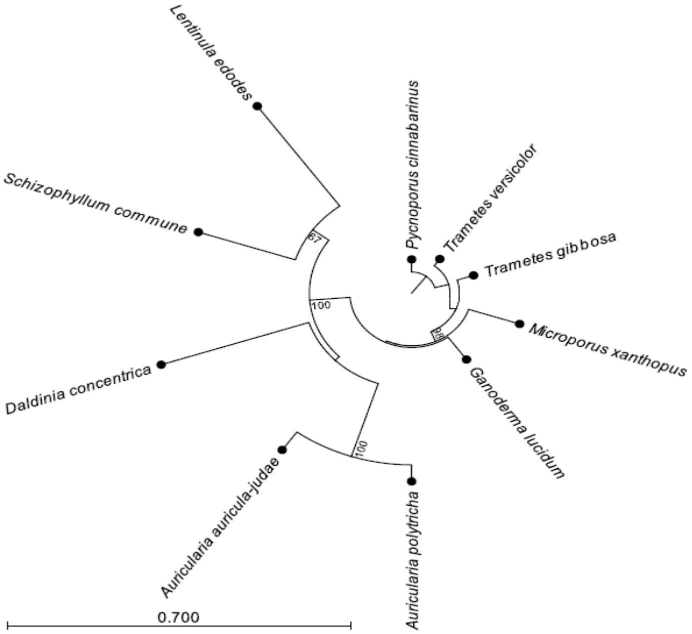

Fig 3: Circular Phylogram of the studied mushroom species

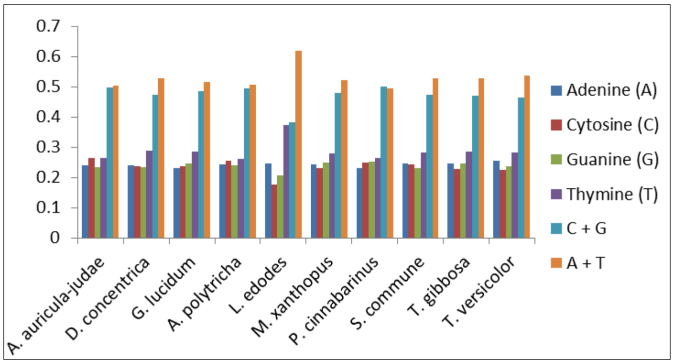

Fig 4: Nucleotide compositional analysis of the mushroom species

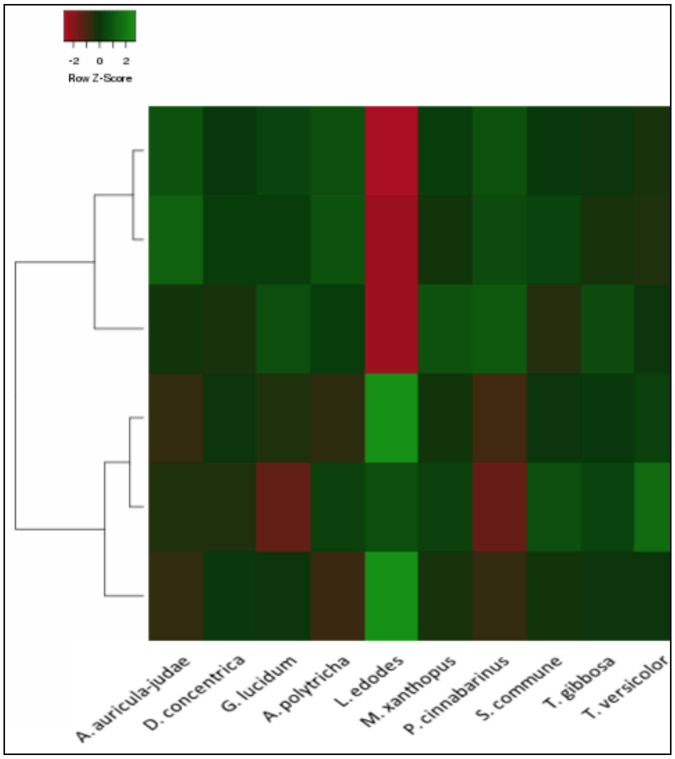

Fig 5: Heat map generated from the nucleotide composition

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