CHAPTER VII

SUMMARY

With the alarming growth of global population proportionate growth of food and nutrition is always a prime concern. The issue becomes even grim with depletion of potent agricultural land and other resources. The issue that started finding importance is management of solid waste which also includes agricultural waste. All of the above apprehension can be entertained to considerable extent partly through mushrooms. Mushrooms are rich in nutrition with many therapeutic virtues. The current study involves detail taxonomic and biochemical evaluation of some wild mushrooms that are mostly consumed in this region. The area is inhibited by many different group of population. Mycophagy has been observed to be a common practice. Peoples practice mushroom hunting and collects different group of mushroom species with their traditional knowledge with regard to its edibility. Many instances due to misidentification resulted in poisoning and even death.

In the present study five commonly found edible mushrooms were taken which includes *Volvariella volvacea, Termitomyces heimii, Lentinus sajor-caju, Chlorophyllum hortense and Cantharellus subamethysteus.* They were collected from different locations of kokrajhar. The mushrooms were studied in details for their macro-morphological and microscopical parameters for their identification with classical and molecular taxonomy. Since classical taxonomy is sometimes insufficient to delimit some species so molecular taxonomy was used as a further confirmatory tool.

The macroscopical characters like colour, shape, diameter of pileus and stipe was recorded. The spore print colour, its habitat, substrate, temperature, collection numbers were recorded. The length of stipe, diameter and other characters like smell, taste, consistency, lamellae etc were studied. In microscopical characters the basidia, basidiospores, cystidia, hyphal types, clamp connection etc were also studied.

In molecular identification the ITS and LSU region were taken as marker, ITS regions are the flanking region of conserved rDNA region. The rDNA regions do not evolve but the ITS regions are rapidly evolving region. The ITS 1 and ITS 2 regions were amplified using primers ITS 1 and ITS 4B for all other species except in *Cantharellus subamethysteus* where LR05 and ITS 4R primers were used. The amplified fragments were subjected to sequencing and the sequence obtained were analysed in NCBI BLAST and deposited to NCBI GenBank

with accession numbers (MK681889, MK724034, MK660091, MK660092, and MK660093). The confirmations of species level identity were done by classical and molecular taxonomic results.

Mushrooms are also good source of various nutrients and the studied species were evaluated for their nutritional properties. The results suggested that wild species were rich in protein and carbohydrate. They were also found to have low quantity of fats with most of the fat content being dominated by unsaturated fatty acids. They were rich in different minerals. The protein content ranged from 29.7-52% across the species. The carbohydrate content varied from 20.4-46.65%. The fat content was in a range of 1.02-3.21%. The studied mushrooms were also a good source of amino acid with almost all of the essential amino acids. The fatty acid profiling revealed the presence of different fatty acids with higher content of unsaturated fatty acids, dominated by fatty acids like linoleic acid, oleic acid, stearic acid and palmitic acid. The different extracts of mushrooms were studied for their phenolic contents and it is found to be rich in phenolic content. It was found that phenolic contents were higher in aqueous extract than other extracts like ethanolic and methanolic extracts. *Lentinus sajor-caju* had higher content of phenols and flavonoid among the samples. The flavonoid content was higher in ethanolic extract. Mushrooms are found to have good antioxidant potentials. The samples were studied for Ferric reducing antioxidant potentials, ABTS radical scavenging activity, DPPH radical scavenging activity, Superoxide scavenging activity and Nitric oxide scavenging activity. The studied samples showed good antioxidant activity by scavenging free radicals to different extent.

The samples were also tested against five different pathogenic microbes and the mushroom samples inhibited the microbes to different extent with different zone of inhibitions. The mushrooms samples were also found to possess many bioactive compounds of different groups. The bioactive molecules identified from different mushrooms were employed for *in silico* studies on antimicrobial proteins and found to be interacting with the antimicrobial proteins to different extent with good docking scores.