

**Original Research Article****DOI:10.26479/2019.0501.50****COMPARATIVE MITOCHONDRIAL GENOME ANALYSIS OF
HYPOCREALEAN FUNGI WITH DIFFERENT LIFESTYLES****Prajna Muthabathula^{1, 2*}, Uma Devi Koduru¹, Suneetha Saragadam¹**

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ABSTRACT: Mitochondria play a key role in energy production in all eukaryotic systems and these are autonomous organelles containing their own genetic material in the form of mt genome. With the advent of DNA sequencing, mt genomes were sequenced and with the help of computational biology tools sequenced genomes can be annotated and analyzed in various ways to bring out the aspects like genetic structure, gene compositions, rearrangements, codon usage bias (CUB), intron analysis, synteny, phylogeny etc. The present study compares Hypocrealean fungal mt genomes. A variety of comparative analyses were performed using various bioinformatics tools to explore the details of mt genomes. Mt genomes being smaller with a limited number of key genes, the comparative analysis showed highly conserved nature among the organisms with similar lifestyle and they were grouped together when a phylogenetic tree is constructed. All the mt genomes encoded 14 conserved core protein coding genes with a slight varying number of tRNA genes.

KEYWORDS: mt genome, Hypocreale, bioinformatics, synteny, phylogeny.

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1. INTRODUCTION

In eukaryotic cells, mitochondria play essential roles, primary function in respiration and energy production using electron transport coupled with oxidative phosphorylation to generate ATP [1]. The