

**Original Research Article**

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PHYLOGENETIC UTILITY OF GENE ORDER AND SYNTENY AMONG THE CHLOROPLAST GENOMES OF MICROALGAE**Suneetha Saragadam^{1*}, Uma Devi Koduru¹, Prajna Muthabathula^{1,2}**

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ABSTRACT: Chloroplast plays a major role in photosynthesis due to small size genome and it houses a small number of genes compared to the nuclear genome. The present study compares the gene order and synteny among the microalgae. A phylogenetic tree is inferred from gene order data. The synteny analysis specifies that microalgae undergo many genome rearrangements and high variability in gene order between and within phyla. Phylogenetic tree from gene order data is applicable to class level.

KEYWORDS: chloroplast genome, gene order, conserved, synteny, phylogeny.

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1. INTRODUCTION

Genome data is accumulating with the available genome sequencing strategies which are aiding the comparative genomics. Phylogenetic relationships are studied based on two types of data i.e., gene order data and sequence data. The first kind of data relates to the order of genes on the chromosomes whereas the second kind relates to the gene (DNA) sequence. All these categories were analysed for their conservatism at different levels in the genome of related species or organisms. Synteny blocks is another kind which contains the genes that share similar functions and are mostly co-regulated [1], which are much more complex in eukaryotes than the prokaryotes. Poor conservation of gene order in prokaryotes provides better for analysis of the species at strain level evolution [2]. As the prokaryotic genes are regulated by a single regulatory element called operons which are absent in the higher plant and animal genomes with some exceptions. The accumulating sequenced data