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Chloroplast Genome as a New Source of Information in the Study of Taxonomy, Phylogeny, and Evolution of Green Plants

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At least 500 million years ago, green plants containing chlorophyll a and b had emerged on the earth. Currently, the term "green plants" include chlorophytes (green algae) and streptophytes (charophytes and embryophytes). Embryophytes (land plants) include non-vascular plants (bryophytes) and vascular plants (pteridophytes and seed plants). Algal greens include charophytes and chlorophytes. Even though many phylogenetic questions on vascular plants have been answered, the questions on the phylogenetic relationships on basal green plants including bryophytes have poorly been answered. One of the reason is limited number of comparable phenotypic characters among basal green plants. Others are long branch attraction and limited outgroup information on green plants, both of which are critical in molecular systematic study. Last a few years, a few complete chloroplast genomic sequences have been available in basal green plants, which have given us better understanding of streptophyte evolution. Here, the author addresses the use of chloroplast genomic phenotypic characters, which are rarely changed during this long evolutionary history. These include the evolutionary information on group I intron, group II intron, genes, and operons. Through the character analyses, 1) some groups of green plants are defined by chloroplast genomic phenotypic characters, 2) the limitation of phylogenetic usages on some characters is addressed, and 3) the possible use of some characters in population study. This talk includes partial chloroplast genomic information on several unknown chloroplast genomes, and covers from non-green algae to angiosperms.