



PROCESO SELECTIVO POR EL SISTEMA DE ACCESO LIBRE PARA INGRESO EN LA ESCALA DE TÉCNICOS SUPERIORES ESPECIALIZADOS DE LOS ORGANISMOS PÚBLICOS DE INVESTIGACIÓN, CONVOCADO POR RESOLUCION DE 21 DE FEBRERO DE 2023 (BOE N° 48 DE 25 DE FEBRERO) – OEP 2020-2021-2022

TERCER EJERCICIO, ESPECIALIDAD VI-TÉCNICAS INSTRUMENTALES TRANSVERSALES EN CIENCIAS DE LA VIDA.

TEXTO (PARA TRADUCIR AL CASTELLANO)

THE ORIGIN AND PHYLOGENY OF PHOTOAUTOTROPHS

The determination of evolutionary relationships has been greatly aided by molecular biological methods. Molecular techniques permit quantitative measurement of the genetic diversity of organisms. One of the most common approaches to deducing diversity compares nucleic acid sequences, especially those obtained from ribosomal RNA. The two rRNA molecules that are commonly used in constructing phylogenetic trees are the 16S and 18S rRNAs. Analysis of these sequences is particularly useful because of the large databases for these molecules from a wide variety of organisms. The 16S rRNA molecule, together with about 21 proteins, constitutes the small subunit of the 70S ribosome that is responsible for translating organellar and prokaryote messenger RNA. The 18S rRNA molecule, together with about 30 proteins, constitutes the small subunit of the 80S ribosome that translates nuclear-encoded mRNA of eukaryotic cells. Both the 16S and 18S rRNA molecules contain both conserved and variable sequence regions. The distinction between conserved and variable regions is related to the frequency with which base substitutions are made at specific positions relative to the entire molecule. These sequences are compared using a variety of mathematical criteria to obtain a measure of the evolutionary distance or divergence between organisms.

This analysis provided a basis for distinguishing between two major groupings of bacteria: the eubacteria and the archaebacteria. The latter are believed to have been among the first life-forms to evolve on the Earth.

Eukaryotic photoautotrophs contain, in addition to the nucleus, two membrane-bound organelles, namely chloroplasts (often called plastids) and mitochondria. The prevailing theory for the origin of these organelles is the so-called “endosymbiotic hypothesis”. This hypothesis suggests that progenitor eukaryotes originated as prokaryotic cells, which phagotrophically engulfed and incorporated other prokaryotes to form intracellular symbionts. The engulfed, ancestral prokaryotes formed organelles. Thus, according to the hypothesis, chloroplasts arose from oxygenic cyanobacteria. The template for mitochondria appears to have been a branch of eubacteria, the alpha-proteobacteria. Such a proposal seems plausible because

symbiotic associations of protists with eukaryotic and prokaryotic algae have been well documented, especially for the dinoflagellates.

A key aspect of the endosymbiont hypothesis is that the incorporated organelle has become an obligate symbiont – chloroplasts cannot reproduce without their host cell. The obligate nature of the organelle is assured by the transfer of many of the genes necessary for its independent function to the nucleus of the host cell, as well as the loss of genes that would permit the endosymbiont to revert to a free-living existence.

Historically, the systematics and classification of aquatic photosynthetic organisms have been based largely on the characteristics of organelles, especially chloroplasts and their pigments. Because of the ease with which they can be assayed, photosynthetic pigments have been used to distinguish among algal classes.

P. G. Falkowski, J.A. Raven. Aquatic photosynthesis (1997)