

Studying the evolution of photosynthesis using phylogenetic trees

Term paper 498Bio; Peter Fleck; 12/5/2001

Phylogenetic trees are supposed to group species according to common ancestors [2]. Mapping the evolutionary relationships of all living beings have been undertaken by comparing highly conserved gene sequences present in all of the above [1] and considerable intellectual effort has been invested to reduce the systematic errors of sequence alignment [1] and tree construction [3]. Even when limiting oneself to important subgroups of species, discussion is vivid as to which methods represent the underlying evolutionary families and relationships best [6, 7].

These tree maps can however be used as well to map the evolution of subsystems of living beings, the example of photosynthesis being discussed in the following [5]. The authors constructed phylogenetic trees for representatives of all photosynthetic living organisms by neighbor-joining, maximum parsimony, and maximum-likelihood methods respectively, independently applied to both the DNA sequences and primary protein structure of (bacterio)chlorophyll genes. To double-check the trees' statistical significance, genes of evolutionarily close, but non-photosynthetic bacteria, forming the so-called outgroup, were included into the study. In distinction to previous publications, this paper investigates directly the evolution of the system of photosynthesis itself instead of the photosynthetic organisms: the authors were able to determine for the first time the bacteriochlorophyll genes in green sulfur and green non-sulfur bacteria, whereas their analogues in all other photosynthetic organisms, namely purple bacteria, helio bacteria, cyano bacteria, and photosynthetic eukaryotes had been known already. All the trees generated by the above-mentioned six different methods show a close relationship of photosynthetic eukaryotes (plants etc.) to helio and in particular cyano bacteria, while all the green and purple bacteria form one further evolutionary related group each. Members of the outgroup consistently exhibit larger evolutionary distances to any of the photosynthetic organisms, yielding statistical credibility to the aforementioned results.

The authors detail explicitly the number of genes found to be associated with each part of the entire photosynthetic apparatus, fail however unfortunately to mention, which genes were precisely used to construct the phylo-

genetic trees. Assuming this to be rather a flaw of presentation rather than methodology, it is astonishing, to which degree the various trees, generated by different methods on either DNA or protein data, agree: they coincide entirely within the ingroup except for a minor difference in distance between the main groups of purple bacteria, green bacteria and all other photosynthetic organisms. This tree topology supports the known hypothesis that eukaryotes "learned" photosynthesis from cyanobacteria by a gene or a complete system transfer at an early evolutionary stage¹. It hints furthermore that chlorophyll proteins found in photosynthetic eukaryotes developed later than bacteriochlorophyll ones in bacteria contrary to a previous suggestion[4]. Combining this fact with the knowledge of chlorophyll absorbing light from a larger frequency window than bacteriochlorophyll, the authors suggest that there had been an evolutionary pressure to absorb photons at shorter wavelength during some geological aera.

Phylogenetic trees therefore not only classify living organisms, but more importantly can provide indications to the mechanisms of evolution when being combined with further biological information such as the functionalities of the encoded proteins alike in the above example.

References

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¹Unless a coincidental parallel evolution of photosynthesis in both species is assumed

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