

Prologue

Photosynthesis has provided life-energy for the biosphere during most of earth's history. It provides us with all our food and fuel for our vehicles, and much of our building materials and other commodities. When our society now faces the big energy crisis, this ancient process may come to our rescue, both in the form of biofuel produced by plants and in novel, technologically modified versions. Current Science has begun the publication of a series of articles on the theme of 'Photosynthesis and the Global Issues'. Those who would solve the energy crisis would need information on all aspects of the process of photosynthesis. In this first review article, Lars Olof Björn (Sweden) and Govindjee (USA) discuss the very first theme: the evolution of photosynthesis and the chloroplasts.

The evolution of photosynthesis and chloroplasts^{†,§}

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This review focuses on what has been learned about the evolution of photosynthesis in the past five years, and omits evolution of CO₂ assimilation. Oxygenic photosynthesis (using both photosystems I and II) has evolved from anoxygenic photosynthesis. The latter occurs in different variants, using either a type 1 photosystem resembling photosystem I, or a type 2 photosystem resembling photosystem II. Opinions differ as to how two types of photosystem came to be combined in the same organism, whether by gene transfer between bacteria, by fusion of bacteria, or as a result of gene duplication and evolution within one kind of bacterium. There are also different opinions about when oxygenic photosynthesis arose, in conjunction with the Great Oxygenation Event, 2.3 billion years before the present, or more than a billion years before that.

Cyanobacteria were the first organisms to carry out oxygenic photosynthesis. Some of them gave rise to chloroplasts, while others continued to evolve as independent organisms, and the review outlines both lines of evolution. At the end we consider the evolution of photosynthesis in relation to the evolution of our planet.

Keywords: Bacteria, bacteriochlorophyll, chloroplast, cyanobacteria, horizontal gene transfer, red algae.

THERE are three forms of life: Archaea, Bacteria and Eukarya¹. The first common ancestor of these three forms is

[†]We dedicate this review to Professor Achim Trebst on his 80th birthday on 9 June 2009.

[§]This is the first of six papers on the theme 'Photosynthesis and the Global Issues' being guest-edited by Govindjee, George C. Papageorgiou and Baishab C. Tripathy.

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thought to have possessed membrane-bounded cells, a translation machinery for synthesis of proteins, an energy transducing system involving electron transport and high-energy phosphate, but no photosynthesis. Photosynthesis has arisen in the Bacteria, but when we encounter the word 'photosynthesis', we are likely to first think of land plants with green leaves. Plants are eukaryotes, just as we are, composed of cells with a nucleus and organelles separated from other cell constituents by membranes. There are many other kinds of photosynthetic organisms, many of which are lumped together under 'algae'². Some live in water. Many are also living in symbiosis, either with terrestrial organisms such as fungi (forming lichens), or with aquatic organisms such as corals or molluscs. A common trait for the photosynthesis carried out by eukaryotes^{3,4} is that it involves oxidation of water and evolution of molecular oxygen, O₂.

In addition to eukaryotic photosynthesizers, there are bacteria carrying out photosynthesis. Among bacteria, only the cyanobacteria are able to oxidize water and evolve oxygen⁵. Another type of photosynthesis is carried out by several other coloured (e.g. green, purple) bacteria; it is anoxygenic and does not evolve oxygen^{6,7}. Chen and Zhang⁸ have discussed an interesting relationship between the oxygen content of the peptides and the proteins of the oxygenic and anoxygenic organisms; in particular that the D1 and D2 polypeptides of oxygenic photosystem II contain more oxygen than the corresponding polypeptides in anoxygenic bacteria.

Olson and Blankenship⁹ have pioneered many thoughts about the evolution of photosynthesis; most importantly that different parts of the photosynthetic apparatus of green plants have different evolutionary histories. Much

has been published since then. In this review we shall focus on some of the current thinking about the evolution of photosynthesis and of chloroplasts. We shall restrict our discussion to organisms containing chlorophyll or chlorophyll-like pigments. However, it is also known that some bacteria (and some archaea) harvest light energy by means of a rhodopsin-like pigment.

Phylogeny of photosynthetic bacteria

Photosynthetic bacteria that lack the ability to evolve oxygen, possess one of the two different types of photosynthetically active pigment protein complexes, called type 1 and type 2 photosystems. Both have various forms of bacterial chlorophyll (called bacteriochlorophyll) in

the 'reaction centers' (RC-1 and RC-2), where light-requiring primary charge separation takes place: electrons are transferred to an acceptor molecule, leaving a hole (or a positive charge) on the bacteriochlorophyll molecules. The principal difference between type 1 and type 2 photosystems lies in the kinds of acceptor molecules or groups of atoms that take up the electron from bacteriochlorophyll. In the case of type 1 reaction centres, these are nonheme iron-sulphur proteins, but in the case of type 2 reaction centres, they are quinone molecules.

We can imagine that both type 1 and type 2 reaction centres were first together in an ancient anoxygenic cyanobacterium, and by a loss of type 1 or type 2 different branches of anoxygenic photosynthetic bacteria evolved (the loss hypothesis); however, addition of the oxygen evolving complex (OEC) lead to the oxygenic

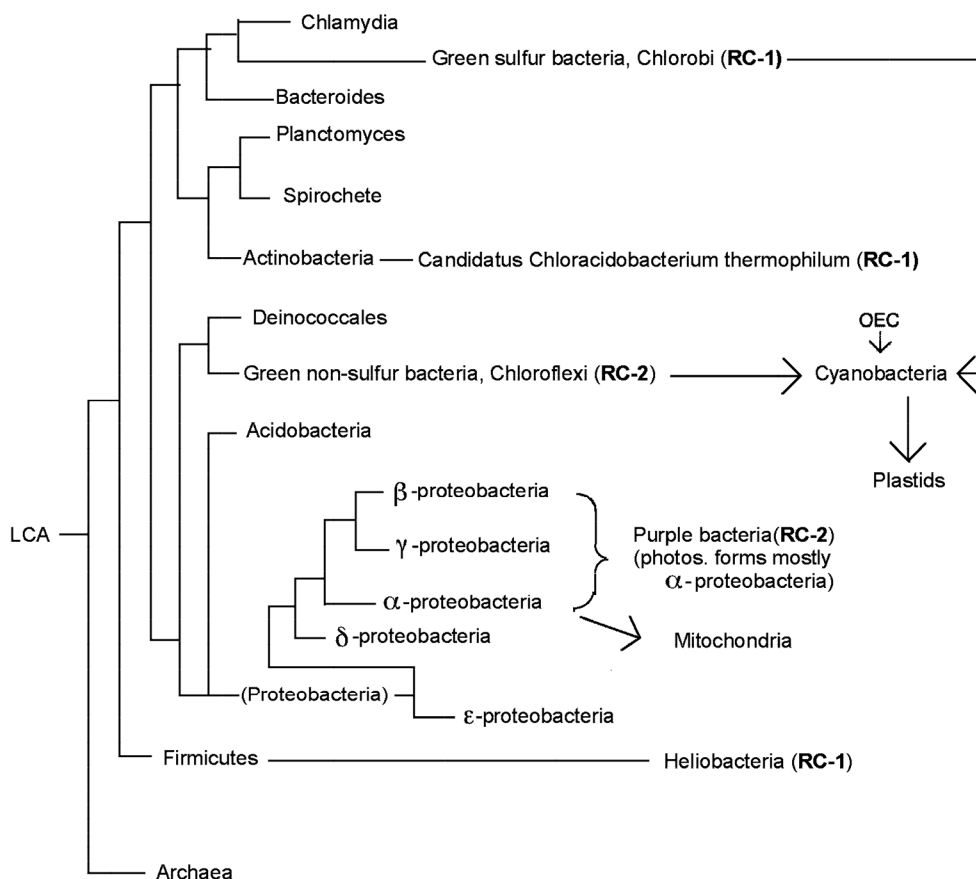


Figure 1. A scheme for a bacterial tree of relationships (LCA, last common ancestor). In those groups where photosynthetic forms occur, the type of photosystem is indicated in bold letters. The α -, β - and γ -proteobacteria are collectively referred to as purple bacteria. Most of the photosynthetic purple bacteria are α -proteobacteria, but there are also some among the β - and γ -proteobacteria. Mitochondria of eukaryotic organisms are derived from α -proteobacteria. As can be seen from this diagram, the various types of bacteria having RC-1 are not closely related, neither are those having RC-2. The oxygenic cyanobacteria harbour both photosystems I and II, clearly derived from RC-1 and RC-2 respectively, but from where they have acquired these is uncertain. A major difference is that RC-2 has now evolved to be able to split water to oxygen using the oxygen evolving complex (OEC). We have added OEC at the same point as where the two kinds of photosystems join in the evolution of cyanobacteria, but it is unlikely that these events took place simultaneously. One possibility is that cyanobacteria are derived from green sulphur bacteria, and have taken up RC-2 from green sulphur bacteria by horizontal gene transfer. The green non-sulphur bacteria are also called 'filamentous anoxygenic phototrophs', since several members of the group do indeed obtain electrons from sulphur or sulphide compounds. The above diagram is speculative, because of the high frequency of horizontal gene transfer taking place among prokaryotes.

cyanobacteria¹⁰. An alternate hypothesis is the fusion hypothesis, where type 1 and type 2 reaction centres came together later¹⁰. There is great uncertainty concerning the path of organismal evolution among Archaea and Bacteria^{11,12}. A possible scheme is shown in Figure 1. Because horizontal gene transfer occurs frequently, it is more appropriate to consider the evolution of genes, or groups of genes. That horizontal gene transfer still takes place among genes for proteins involved in photosynthesis is well known. The marine environment is full of viruses harbouring such genes¹³⁻¹⁵; cf^{16,17}. Because of this high frequency of horizontal gene transfer, it is more appropriate for us, at least for Archaea and Bacteria, to speak of a 'web of life' rather than a 'tree of life' (Figure 2)¹⁸.

The step from anoxygenic to oxygenic photosynthesis required a number of innovations, of which we mention

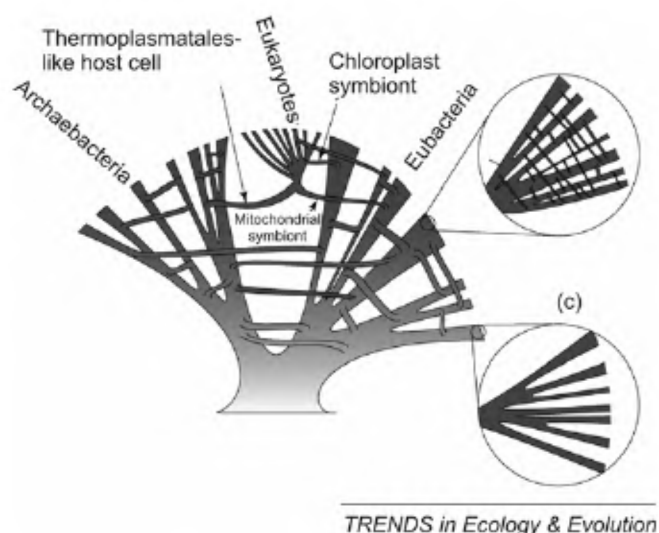


Figure 2. The 'web of life' according to McInerney *et al.*¹⁸, slightly modified. Lateral gene transfer, here indicated as connections between the 'branches' is common in some groups, and almost absent in others.

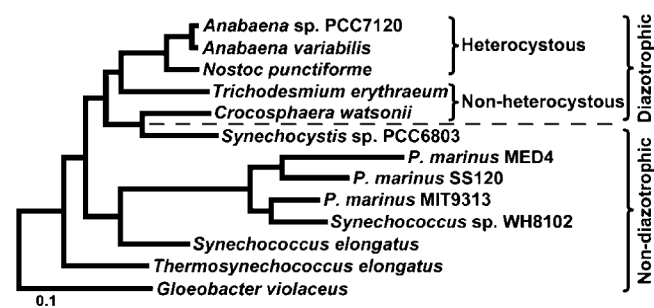


Figure 3. The 'tree of evolution' for cyanobacteria according to Shi and Falkowski²⁶, slightly simplified. The tree is reconstructed based on the concatenation of 323 core proteins. *Gloebacter* is a primitive organism differing from other cyanobacteria in lacking thylakoids. The scale bar refers to the number of amino acid substitutions per site. Copyright (2008) National Academy of Sciences, USA.

here only the most important. This type of photosynthesis uses two photosystems: photosystem II (PSII; light-induced water plastoquinone oxidoreductase³) and photosystem I (PSI)¹⁹. There must be an OEC attached to the type 2 photosystem to make it a true PS II. The two photosystems must be connected in series to generate sufficient difference in redox potential between the oxidizing and reducing ends of the process, water on one side and CO₂ on the other. In between the series-connected photosystems there is an 'electron buffer' in the form of a plastoquinone pool. The oxidation state of this pool controls the channelling of energy from light-harvesting complexes for short-term adjustment of energy allocation. But it also controls, via gene regulation, the synthesis of new reaction centres according to long-term needs²⁰. For this series connection to have any effect, the redox potential spans of the two photosystems must also be adjusted to be sufficiently different. This has been achieved using chlorophyll *a* (in some cases also chlorophyll *d*) instead of bacteriochlorophyll in the reaction centers, and by modifications of the bonding to protein and other effects on pigment environments²¹⁻²³. For a description of chlorophylls and bacteriochlorophylls, see Grimm *et al.*²⁴.

Finally, a mechanism must be provided to make the two photosystems work 'in step'. This last feature was achieved by a newly discovered redox regulator, sensing the redox potential between the photosystems¹⁹.

The most primitive cyanobacteria, of the genus *Gloebacter*, lack thylakoids and harbour the photosynthetic apparatus in the cell membrane. They may provide a link to anoxygenic photosynthetic bacteria, and may be close to the last common ancestor of oxygenic organisms²⁵. (For a 'tree of evolution' of cyanobacteria, see Figure 3.)

Although horizontal gene transfer among and to cyanobacteria is frequent, it is possible to define a 'core' of genes and to construct from this a more tree-like evolution²⁶ (Figure 3). According to Nelissen *et al.*²⁷, the evolutionary path to plastids of eukaryotic organisms diverges (based on 16 S rRNA) from extant cyanobacteria before the branching-off of *Gloebacter*, while Deusch *et al.*²⁸, based on other genes, regard an origin within the heterocystous clade as probable. Further, Gross *et al.*²⁹ show that not all photosynthetic genes in plastids are derived from cyanobacteria closely related to any extant ones, and this brings us to the phylogeny of genes important for photosynthesis.

Phylogeny of genes important for photosynthesis

As already pointed out, phylogenetic relationships among bacteria are blurred by horizontal gene transfer. However, more certain conclusions can be drawn regarding individual genes or groups of genes. An example is provided by the enzymes catalysing some of the final steps in the synthesis of chlorophyll *a* and of bacteriochlorophyll. All photosynthetic prokaryotes (and many eukaryotes) having

chlorin-type chlorophylls (like chlorophyll *a* and bacteriochlorophyll *a*) possess a light-independent (dark) protochlorophyllide-oxidoreductase (DPOR) by which they can carry out the reduction of the D-ring (Figure 4) in the absence of light. This enzyme is derived from nitrogenase³⁰⁻³³. In the synthesis of bacteriochlorophyll *a*, the same enzyme catalyses two different reduction steps³⁴. Also, the light-dependent NADPH-protochlorophyllide oxidoreductase, typical of angiosperms, traces its origins back to cyanobacteria³⁵, as do genes for the synthesis of cellulose³⁶ and starch³⁷, and for the photorespiratory glycolate metabolism³⁸.

The most important difference between the type 2 photosystem of non-oxygenic photosynthetic bacteria and PSII of cyanobacteria and eukaryotes is the presence of an OEC in the latter; its origin has been reviewed by Raymond and Blankenship³⁹. The OEC is a metallo-enzyme that has a redox-active core with four manganese atoms and one calcium atom. These authors speculate that a precursor of the OEC might first have associated with a manganese catalase (having two manganese atoms; however, no calcium atom). The precursor might then have developed its own suitably positioned binding site for two manganese atoms and taken these over from the catalase. Association with another molecule of catalase would then result in a four-manganese core. Further studies on how the OEC is assembled during development might show whether this scenario is plausible.

Ribulose-*bis*-phosphate carboxylase-oxygenase (RuBisCO), the enzyme binding carbon dioxide in many photosynthetic organisms, is derived from a similar enzyme in bacteria carrying out carbon dioxide assimilation chemosynthetically before the origin of the extant forms of photosynthesis^{40,41}.

When did oxygenic photosynthesis arise: 3.7 Ga versus 2.3 Ga ago?

The timing of the origin of oxygenic photosynthesis is controversial. Buick⁴², based on hydrocarbon biomarkers in sandstone, suggests that oxygenic organisms existed 2.45 Ga (2,450,000 years) ago, and that a transient pulse of oxygen took place 2.5 Ga ago. He also considers it as likely that stromatolites and biomarkers as old as 2.7 Ga indicate oxygenic organisms; however, it is possible that 3.2-Ga-old kerogenic shales indicate the presence at that time of oxygenic photoautotrophs, and that oxygenic photosynthesis could have evolved as early as 3.7 Ga ago. Hoashi *et al.*⁴³ have come to a similar conclusion from the study of hematite formation. However, Kirschvink and Kopp⁴⁴ suggest a different scenario. They depart from the notion that (1) systems to detoxify molecular oxygen or superoxide anion must precede the origin of oxygenic photosynthesis, (2) there would be no evolutionary pressure for the evolution of such biochemical systems in the absence of oxygen, and (3) there must have been another source of

sufficient molecular oxygen before the origin of oxygenic photosynthesis. Such a source could have been hydrogen peroxide, and it is likely that catalase, the enzyme decomposing hydrogen peroxide to water and molecular oxygen, is older than the oxygen evolving enzyme in PSII. In fact, this enzyme could have evolved from the manganese-containing form of catalase (see above). A possible source of hydrogen peroxide could be the glaciers. Hydrogen peroxide is formed by the action of solar ultraviolet radiation on cloud droplets, brought to the earth's surface with snow, and embedded in the glacier ice. When the ice melts the hydrogen peroxide, and oxygen formed from it, become available to the biosphere.

According to Kirschvink and Kopp⁴⁴, oxygenic photosynthesis could have commenced as late as 2.3 Ga ago, triggering global glaciation (by lowering the amount of the greenhouse gases methane and carbon dioxide).

Phylogeny of eukaryotic photosynthesizers

Eukaryotic organisms carry out photosynthesis in organelles called chloroplasts, which we now know for certain are derived from cyanobacteria, which more than 1.2 billion years ago entered into intimate symbiosis with a non-photosynthetic host organism (also see Wise and Hooper⁴⁵). Because of this composite nature of eukaryotes, their phylogeny is somewhat complicated. We must distinguish between the phylogeny of the host organisms (Figure 5) and of the chloroplasts (Figure 6), and start with the former.

According to Burki *et al.*⁴⁶, the 'host' of most photosynthetic organisms is a member of the same 'megagroup', which is a sister group to another 'megagroup' containing animals, fungi and Amoebozoa.

A third, less well-supported 'megagroup' contains, among the investigated organisms, a single photosynthetic member, the genus *Euglena*. This latter 'megagroup'

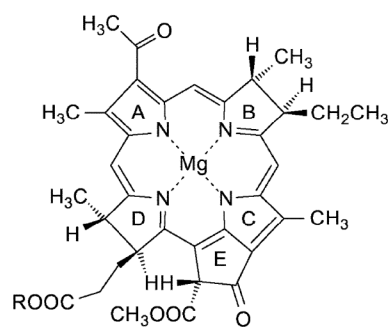


Figure 4. The structure of bacteriochlorophyll *a*. R is a hydrocarbon group. Chlorophyll *a* differs by having two double bonds in the B ring, and a vinyl ($-\text{CH}=\text{CH}_2$) instead of a formyl ($-\text{CO}-\text{CH}_3$) side group in ring A.

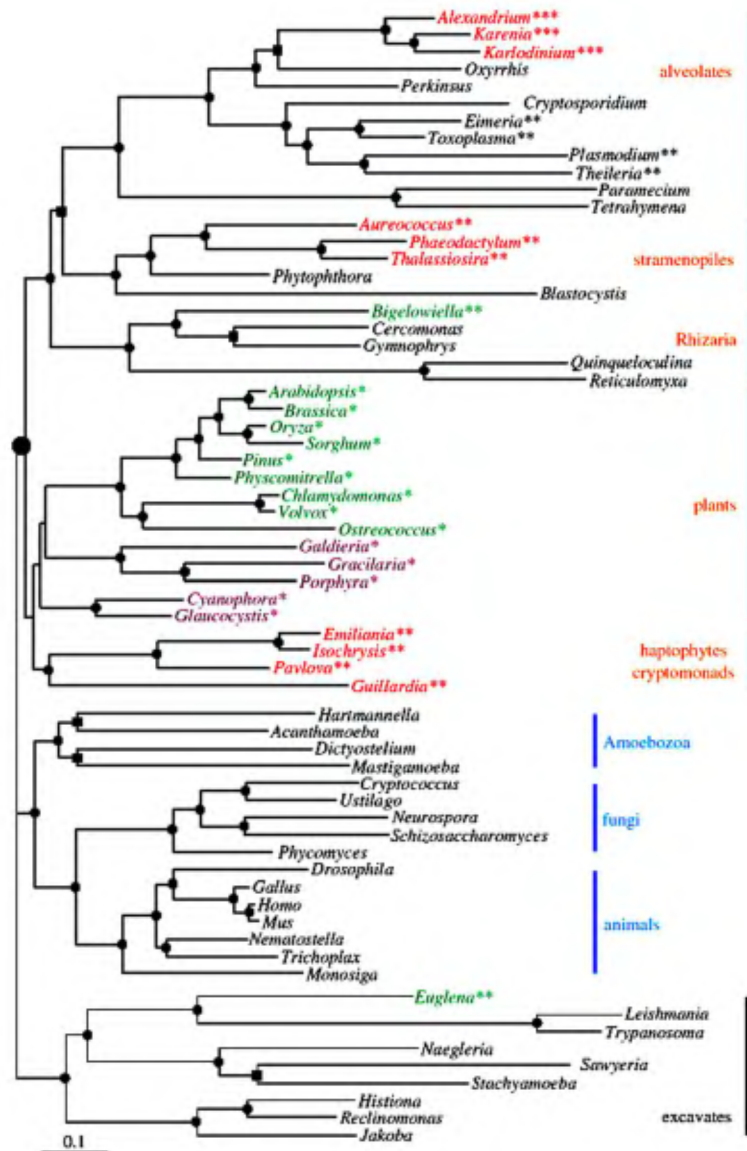


Figure 5. The ‘host’ phylogenetic tree according to Burki *et al.*⁴⁶, slightly simplified. There exists no consensus on what the real relationships are; so this figure represents one opinion. The same DNA sequences can give rise to different trees depending on the statistical method used. The tree is ‘unrooted’, i.e. does not show the position of the LCA. It shows three main groups, of which the top one is deeply split into two groups. The asterisks show organisms with plastids acquired by primary (*), secondary (**), or tertiary (***) symbiosis. The scale bar represents the estimated number of amino acid substitutions per site.

also contains the genera *Leishmania* and *Trypanosoma*, which are parasitic organisms descended from photosynthetic ancestors.

There are strong indications that the primary endosymbiotic event giving rise to plastids took place very early, before the divergence of the ‘green’ and ‘red’ evolutionary lines described below. This does not preclude that many extant organisms harbour symbiotic photosynthesizers, and occasionally they almost appear on the way to become chloroplasts. But there is a big difference between

an endosymbiotic cyanobacterium and a chloroplast. A chloroplast has lost many genes (mostly transferred to nucleus) that are essential for a free-living organism, and it must have acquired new import mechanisms for proteins as well as export mechanisms for metabolites. The endosymbiont of *Paulinella chromatophora*⁴⁷ has been described as a plastid in the making⁴⁸.

Whatever we call it, it is different from the plastids of the ‘red’ and ‘green’ evolutionary lines⁴⁹ described below. One of its characteristics is that it retains the cyanobacte-

rial phycobiliproteins. Another similar case is the endosymbiont of the diatom, *Rhopalodia gibba*⁵⁰. The *Rhopalodia* endosymbiont, contrary to real plastids, has retained the ability to fix molecular nitrogen.

Arguments for assigning the origin of all true plastids to a common endosymbiotic event are reviewed by McFadden and Van Dooren⁵¹, and Nozaki⁵². They include similar import mechanisms into the plastids for nuclear-encoded proteins, and similarity in a chlorophyll-binding protein, which differs from the corresponding one in cyanobacteria.

Phylogeny of plastids

An overview of plastid phylogeny is shown in Figure 6.

Only in three organismal groups, the Chlorophyta (green algae, and plants that have evolved from them), the Rhodophyta (red algae) and Glaucophyta (Glaucocystophyta), the chloroplasts are direct descendents of the cyanobacterium engulfed in the primary endosymbiosis. Among these, the evolutionary path to the Glaucophyta is the first one to branch-off⁵³. Stiller and Harrell⁵⁴ point out the great uncertainties and show how different methods can result in different patterns of deep eukaryotic phylogeny. The Glaucophyta is a small group without great ecological importance, consisting of the genera *Glaucocystis*, *Cyanophora* and *Gloeochaete*.

The Embryophyta (which we usually understand to be plants) have evolved from the Chlorophyta, specifically

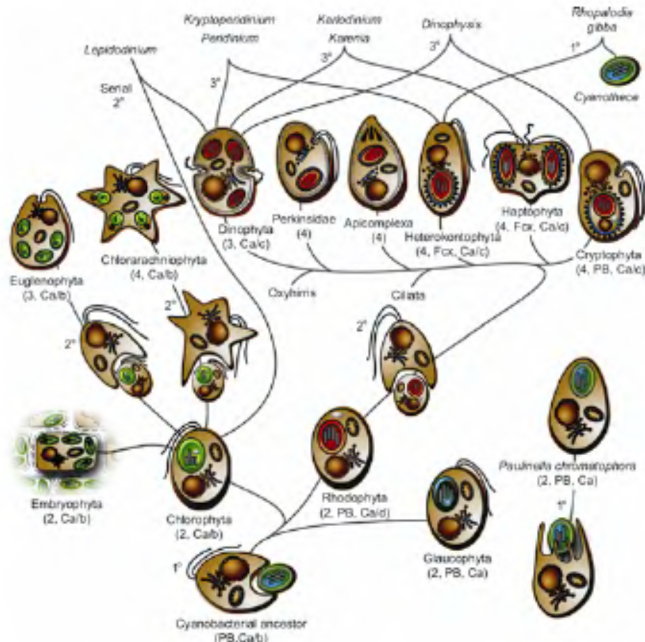


Figure 6. Evolutionary relations of plastids. The main branches diverging from the primary endosymbiotic event are those going to Chlorophyta (the ‘green line’) and Rhodophyta (the ‘red line’), but even before their divergence the Glaucophyta plastids branch-off. For an explanation of other relationships, see text. From Gould *et al.*⁵⁹. Reprinted, with permission, from the *Annual Review of Plant Biology*, vol. 59. © 2008 by Annual Reviews <http://www.annualreviews.org/>.

from the group within them, the Charophyta. The Chlorophyta have also contributed to Euglenophyta and Chlorarachniophyta, not by straightforward evolution, but by being engulfed into other organisms by a secondary endosymbiotic event.

Similarly, the Rhodophyta have contributed to a range of other algae by secondary endosymbiosis. When there has been a secondary endosymbiosis, the chloroplast is shown to have four membranes surrounding it. An example is a haptophyte, *Emiliania huxleyi*. There are also indications that there has been only one event of endosymbiosis, with later divergence into several evolutionary lines⁵⁵.

There are also examples of tertiary endosymbiosis, in which case the plastids obtained by secondary endosymbiosis have been replaced with others. The dinoflagellates (Dinophyta) constitute an organismal group excelling in experimentation with plastids. Normally their chloroplasts are derived from endosymbiotic red algae. In Figure 6, three cases are shown where these chloroplasts have been replaced by respectively, a heterokontophyte, an haptophyte and a cryptophyte. Each one of those latter organisms contains a plastid evolved from a rhodophyte.

We have used the word ‘chloroplast’ frequently above. However, not all the plastids are chloroplasts. In all higher plants we also have other types of plastids, which lack chlorophyll, at least (in most cases) in the roots. In most higher plants also the colourless, endosymbiotic, red alga plastids retain the ability to develop, under appropriate environmental conditions, into chloroplasts⁵⁶, and whole green plants can be regenerated even from roots that have been grown isolated in culture for a long time⁵⁷. In some parasitic seed plants, this ability has been lost, but the plastids are retained. Even if they cannot carry out photosynthesis they have a range of other important functions. There are also a number of non-photosynthetic protists evolved from photosynthetic forms that maintain plastids, which in some cases are so reduced that it took a long time to recognize them, e.g. the malaria parasite⁵⁸.

Detailed reviews of the evolution of plastids have been published^{59–62}. For the evolution of photosynthetic carbon dioxide assimilation, we refer to Björn and Govindjee⁴⁰ and Mueller-Cajar and Badger⁶³. Estimated divergence times during evolution⁶⁴ are shown in Figure 7.

The continued evolution of free-living cyanobacteria

As shown in Figure 7, plastids arose from cyanobacteria well over one and a half billion years ago; most cyanobacteria remained not only free-living, but also continued to evolve. The most remarkable innovations among the free-living cyanobacteria are mechanisms for the concentration of CO₂. Such mechanisms probably mostly evolved when the availability of CO₂ started to fall and the O₂ concentration started to rise around 400 million years

ago⁶⁵. By this change in ratio between CO₂ and O₂, the ability of CO₂ to compete with O₂, at the surface of rubisco decreased. Carbon dioxide concentrating mechanisms evolved along several paths, and they consist of membrane pumps for both CO₂ and the bicarbonate ions, the key enzyme being carbonic anhydrase. This enzyme catalyses the interconversion between CO₂ and bicarbonate. Many cyanobacteria possess a complex structure, the carboxysome, that is situated in the lumen; it has a protein shell that is permeable to bicarbonate and other ions, but not to carbon dioxide. However, most other cyanobacteria accumulate bicarbonate in the cytosol using pumps in the cell membrane. The cytosol does not contain carbonic anhydrase, so the bicarbonate is maintained as such as it diffuses into the thylakoid lumen. In carboxysome containing cyanobacteria, carbonic anhydrase and rubisco are located inside that shell⁶⁶. When bicarbonate diffuses in, it is converted to CO₂ that cannot escape, and reaches a high concentration at the surface of the rubisco, which therefore can work efficiently despite its low affinity for this substrate.

Since the evolution of carboxysomes started after the origin of plastids, algae and plants do not have this method of concentrating CO₂, but many other concentration mechanisms have evolved on this line^{40,67-69}. Some plants have evolved CAM (crassulacean acid metabolism) and C₄ metabolism, which allow them to use CO₂ efficiently⁴⁰.

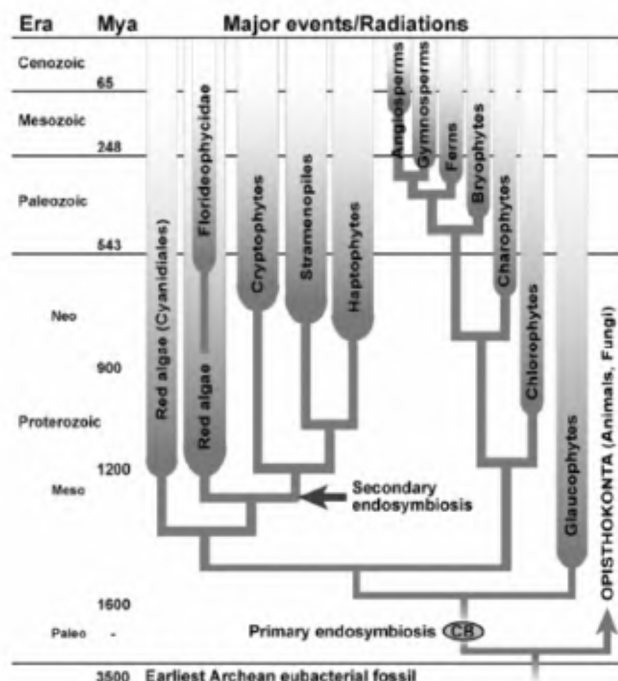


Figure 7. Schematic representation of the evolutionary relationships and divergence times for the red, green, glaucophyte and chromist algae, according to Yoon *et al.*⁶⁴. The branches on which the cyanobacterial (CB) primary and red algal chromist secondary endosymbioses occurred are shown. Divergence times in the evolution of eukaryotic phototrophs; Mya, million years; CB, Paleo, Paleozoic.

The evolution of photosynthesis in relation to the evolution of the earth

The evolution of photosynthesis has affected the planet as a whole, and not only its atmosphere. For instance, the evolution of a terrestrial biosphere, made possible by photosynthesis, has greatly increased weathering of rocks, and indirectly erosion of the continents.

On the other hand, processes such as plate tectonics have also had an effect on photosynthesis. The increase over the ages in atmospheric oxygen and the decrease in atmospheric carbon dioxide is a result of photosynthesis, but it is a mistake to think that other processes have not been necessary to make this evolution possible. It is not only the gradual increase in the efficiency of photosynthesis by evolution, and the creation of terrestrial flora that has caused the atmospheric change. Continents collide periodically to form supercontinents with a life-time of ca 340 million years⁷⁰, which then break up again into smaller continents. When continents collide, mountain ranges result (such as the Himalayas, resulting from a collision between India and the rest of Asia). Mountain formation results in increased erosion, which makes more mineral nutrition available to photosynthetic organisms, and also increased sedimentation and burial of organic carbon, resulting in a net increase in molecular oxygen⁷¹. Rey and Coltice⁷² have calculated that the early earth was 'flat', without mountains. Because of insufficient supporting strength of the mantle, the highest mountains could not have reached a height of 1749 m until 2.7 Ga ago. Thus, even if oxygenic organisms would have existed much earlier, sedimentation would not have been sufficient to bury the organic carbon and prevent its reoxidation. In other words, lack of oxygen in the atmosphere at earlier epochs is no proof that oxygenic photosynthesis did not take place.

Glaciations offer another case of interaction between geological processes and photosynthesis. Increase in photosynthesis removes the greenhouse gas carbon dioxide from the atmosphere, and may favour the initiation of glaciation. The immediate effect of the initiation of a glaciation is decreased photosynthesis, but in the longer perspective glaciation increases erosion and nutrient supply. And these processes interact with the supercontinent cycles just described.

Conclusion

The origin of photosynthesis is almost as ancient as life itself. A turning point for the biosphere was the Great Oxidation Event, around 2.3 billion years ago, caused by the appearance of oxygen evolving photosynthesis at least several hundred million years earlier. Another important step was the evolution of eukaryotic organisms containing chloroplasts, which were derived from endosymbiotically

acquired cyanobacteria. The relation between photosynthesis and the rest of the planet and the biosphere has been two-sided. The evolution of photosynthesis could not have taken the course it did without the special circumstances on our planet, with plate tectonics and gradually growing continents, and the atmosphere and the surface of earth have been drastically affected by photosynthesis. Thus the chance of finding spectroscopic signature of oxygenic photosynthesis on an exoplanet is very small⁷³.

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Antibiotic resistance: an overview of mechanisms and a paradigm shift

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Antibiotic resistance is the biggest challenge to the medical profession in the treatment of infectious diseases. Resistance has been documented not only against antibiotics of natural and semi-synthetic origin, but also against purely synthetic compounds (such as the fluoroquinolones) or those which do not even enter the cells (such as vancomycin). The wide range of occurrence of antibiotic resistance suggests that, in principle, any organism could develop resistance to any antibiotic. The phenomenon of horizontal gene transfer compounds the problem by facilitating rapid spread of antibiotic resistance. Unfortunately, the discovery and development of newer antibiotics have not kept pace with the emergence of antibiotic resistance. In this article a broad overview of the various mechanisms of antibiotic resistance will be presented mainly to illustrate their variety, rather than to catalogue everything that is known. Of late, a paradigm shift in the traditional perception of antibiotics and antibiotic resistance is emerging. Antibiotics are beginning to be viewed as intermicrobial signalling agents and even as sources of nutrition to microorganisms, rather than as weapons in the hands of antibiotic producer organisms to fight against competitors which might cohabit with them. Likewise, mechanisms of antibiotic resistance are being believed to have evolved not as defence strategies which microbes use to thwart the action of antibiotics, but as integral components of processes involved in basic bacterial physiology. However, when these mechanisms get placed out of their natural context their resistance property alone gets highlighted. Many leading workers in the field call this emerging trend of thought as a Copernican turning point. Some of these trends will be discussed towards the end.

Keywords: Antibiotics, inactivation, influx–efflux, resistance, resistome.

THE quest for antibacterial agents for the treatment of infectious diseases began towards the end of the 19th century and early 20th century. One of the early successes was the discovery of Salvarsan (an arsenical, arsphenamine, discovered by Paul Ehrlich in 1910). Salvarsan was used as an anti-syphilitic drug during the World War I. Another remarkable early antibacterial drug was Prontosil (a

conjugate of sulphanilamide with an aromatic dye), discovered by Gerhard Domagk. Prontosil is the progenitor of the family of sulpha drugs which are in use even today, either alone or in combination with other antibacterials. It is documented that one of the early patients to be treated with Prontosil was Domagk's own daughter, who was critically ill with a streptococcal infection and made a miraculous recovery after receiving the drug. While Ehrlich was already a Nobel laureate when he discovered Salvarsan, Domagk was awarded the Nobel Prize in 1939 for the discovery of Prontosil. (However, he could not receive the Prize because of the political climate of Nazi Germany at that time.) The discoveries of Salvarsan and Prontosil mark the beginnings of the age of chemotherapy of bacterial infectious diseases. The real breakthrough occurred in the late 1930s and early 1940s when penicillin and streptomycin were discovered by Alexander Fleming and Selman Waksman respectively.

The discovery of the two progenitor antibiotics is an event of greatest significance in the history of medicine and a blessing to humanity. The clinical use of antibiotics has mitigated lot of suffering and has saved (and continues to do so) millions of lives from certain death. There was also an unprecedented development of the pharmaceutical and health-care industries. However, there was also an unanticipated and undesirable consequence, namely the emergence and spread of antimicrobial resistance which impedes the efficacy of treatment, escalates the costs and often results in treatment failure. As more and more antibiotics were discovered, the emergence of drug resistance also kept mounting. Another confounding problem was/is the phenomenon of multidrug resistance (MDR). When a pathogen acquires resistance to a given antibiotic and gets selected after prolonged use of that antibiotic, it becomes a favoured host to acquire resistance to several others. Pulmonary tuberculosis which was once considered to have been vanquished by the use of streptomycin, rifampin, isoniazid, etc. emerged in the MDR form in the 1980s. When synthetic antimicrobials such as the fluoroquinolones were introduced, it was hoped that the bacteria would not develop resistance to synthetic compounds; however, such hopes were short-lived since bacteria did develop resistance soon. Another unexpected case is the development of resistance to vancomycin (a glycopeptide) which binds noncovalently to the cell walls of

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