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Evolution without divergence
Nobuo Tamiya and Tatsuhiko Yagi

Dayhoff edited a series books entitled “Atlas of Protein Sequence and Structure” (1). She wrote that [1] all cells utilize ATP, [2] synthesize, store and break down fats, carbohydrates and proteins by similar reactions, [3] live on proteins made of same 20 amino acids, [4] synthesize proteins by the same coding system, and [5] utilize similar ubiquitous compounds, i.e. vitamins and others. She concluded that all the living things evolved from a single common ancestor, which emerged only once. If it is not only once, the other type creatures died out very soon or were eaten up by the common ancestor. According to her, if a certain type of proteins is found in two species, the original type must have been present in their common ancestor, from which they diverged. This is the assumption to deduce the dendritic divergence map of living creatures.

The idea is widely accepted and quoted in recent textbooks of biochemistry e.g. by Voet et al. (2) and of biology e.g. by Cain et al. (3). Voet et al. say, however, also that the existence of hemoglobin-like proteins in some species of bacteria is evidence of gene transfer from animals to bacteria at one or more points during evolution (2). We cannot agree with Dayhoff’s idea to expand the conclusion to all the living things. If the conclusion is the case, the ancestor should have carried an enormously large information, i.e. not only on 20 amino acids, 8 nucleotides and their codons, but also on homeodomain proteins, which are found commonly in insects and mammals. As for chaperon proteins, which are large hetero-oligomers found in bacteria and mammals, was their information present in the ancestor before divergence? Rather, the information to build these proteins must have been collected from various sources of the living world.

It is well established that viruses squeeze into genomes, and virus infection is suggested to be significant for evolution (4).

There is a textbook of bacteriology, which recognizes wide gene exchange among bacteria (5). There is an idea that viruses are the fragments of DNA (6, 7).

The ways living things exchange genes are open vertically and horizontally, namely through cell fusion, sex, hybridization, symbiosis and infection. Gene exchange through sex is efficient even among human beings. Only in 33 generations, namely in 1000 years, the theoretical number of ancestors can exceed $8 \times 10^9$, which is larger than the world human population. Symbiosis and infection are often difficult to distinguish. Amoeba, infected with an
endosymbiont came to require it as cytoplasmic component (8, 9). Margulis’ idea that our cytoplasmic component mitochondrion is originally a symbiotic bacterium is now widely accepted (10). The gene exchange between hosts and symbionts is an efficient way for evolution because it can happen between remotely related organisms. It is an efficient way for evolution to transfer related genes together at the same time.

The fact that all the known living creatures are composed mostly of one group of the optical isomers, e.g. L-amino acids, is often considered as the evidence for the single ancestor. The authors believe that it is not necessary to think the ancestor or its descendants destroyed the others, but can consider that the continued communication unified the creatures to the present form.

The similarity of cell components, metabolites, and the pathways to produce and break down them is often quoted as the evidence for the single ancestor theory. There are, however, many cases against it. In archaea, plasma membrane components are synthesized from sn-1-phosphatidate instead of ordinary sn-3-phosphatidate from which bacterial and eucaryal membrane phospholipids are synthesized (11, 12). If archaea and bacteria diverged from a common ancestral cell, it must have occurred that one of domain precursor cells began to synthesize its membrane phospholipids from enantiomeric ones. It is difficult to imagine a transient cell having membrane composed of racemic mixture of sn-1- and sn-3-glycerophospholipids. Rather, primitive cells of archaea and bacteria emerged separately at some time in early days of earth’s history, and evolved independently. Since DNA can be transferred from a cell of one domain to a cell of another domain without membrane fusion, genetic coding system could coevolve to use the same code system.

There are more examples of metabolic diversity among three domains of living matters, eucarya, bacteria, and procarya. [1] In procarya, isoprenoid biosynthesis proceeds not through ordinary pathway via mevalonate, but via a sugar derivative, 2-C’-methyl-D-erythritol (13, 14). [2] Some bacteria use polyphosphate instead of ATP (NTP) for their energy metabolism (15, 16, 17), and some archaea use ADP rather than ATP to phosphorylate sugar metabolites in their glycolytic pathway (18, 19). [3] At least three different pathways are known for heme biosynthesis (20, 21). Zorzosopulos (22) proposed that the birth of each domain was an independent event consisting in the genetic isolation of a particular cell from a very diverse pool of “primitive cells”, and that within each domain, branching was a consequence of sporadic events of fusion between two cells of different phylogenetic lineages, followed by DNA recombination and
cell wall regeneration. This proposal has to be modified to allow some degree of DNA recombination among cells belonging to different domains for the coding system to be unified.

It is said that a diverse biomass exists in the deep-sea hydrothermal vents (23, 24). It may reveal there exist many more new pathways of metabolism.

On the “universal codon system” there are reports on the cases that do not agree with its universality. In addition to the discrepancy between codons between mammalian cells and their mitochondria, similar cases are found also in some species of yeasts (25, 26). The living things may be approaching to the universal codon system after 3.5 billion years of communication.

Selenocysteine, which uses codon UGA, one of the stop codons, may be now beginning to distribute as the 21st amino acid (27, 28). Tryptophan, which has the lowest average occurrence in proteins as compared to the other 19 amino acids (2, 29) and has only one codon (UGG), might have become distributed later than the other amino acids because of its complicated structure and indispensable character as a protein component. From the sequence comparison, Syvanen (30) concluded that tryptophan synthase gene was introduced after the three domains of living matter “diverged” from one another.

The difference in the conversation languages is a big problem we human beings are confronting. Living things might have nearly overcome the difficulty through 3.5 billion years of communication and they almost succeeded to construct the Tower of Babel. This is why we can synthesize human proteins, such as insulin and growth hormone (31, 32, 33) in the bacterial systems. There are, however, unsuccessful cases among yeast species due to the code difference (25, 26) The introduction of a new property is due to the variation in gene by mutation and other mechanisms. The tools we use for gene-engineering, namely vectors (i.e. phages, plasmids) and enzymes (i.e. restriction enzymes, ligases), may also work in nature for gene-transfer.

When one of the authors gave talk on the idea in an international meeting (34), one from the audience said that if living creatures exchanged information so widely, all of them would have become a homogeneous mess. This will never happen because the size of information, a living creature can carry, is limited: it cannot be very different from its direct vertical ancestor.

In conclusion, it is not necessary to think that all living things evolved from a common ancestor, which emerged only once. Instead, gene-exchange can explain most of the characteristics, which present organisms share in common.
The authors published essentially the same idea in 1985 (35). In the report the authors pointed out the discrepancy of the phylogenetic trees constructed based on different proteins of closely related species.

The authors are grateful to their late Professor Shiro Akabori for his continued encouragement by letters on the idea mentioned above.

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