

Editorial

The Day after Genomic and Proteomic Era

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This day inevitably will come once in the near future, although today it is difficult to predict when it will happen. Suddenly, all the sequencing robots and sophisticated mass spectrometers and protein analyzers will stop because there will be no samples to be loaded. The disks of supercomputers with megabyte capacities will be clogged with sequences of genomes and proteins of all organisms living on the Earth, and perhaps, also of many extinct organisms, and the kinship to their successor will be determined. We will understand the causes and consequences of all genetically inherited diseases at the genomic and protein levels and, probably, any individual case of appearance of somatic mutation will be routinely detected from the drop of blood, if not from the amniotic fluid, and cured at the embryonic stage. Every citizen will possess identity passport based on the gene and protein polymorphism maps. Many genetically modified organisms and enzymes will increase the efficacy of all fields of technology. Not least, it is feasible that many companies will appear which will be able to synthesize any gene and/or protein so that the successful recipient of a research grant will be able to order the synthesis of all cellular genes and proteins (the low-molecular-weight cell constituents are, perhaps, available even today).

This day will come as a consequence of both past and present (and probably also future) tremendous input of intellectual and laboratory work, and money, which brought already exciting and admirable results. The end of genomic and proteomic era certainly will offer the scientists enormous possibilities to study the number of scientific problems concerning the functioning of cells and their constituents under various conditions. It is clear now that this development has been a consequence of epochal discoveries in biochemistry and genetics of molecular basis of enzymic catalysis, metabolism, the nature of genetic information, and the nature of signalling between and inside living cells, which qualitatively changed our understanding of life, and which will, finally, lead to the complete description of all cellular constituents.

Nevertheless, due to the perpetual evolution of science one can ask (or guess) what will be the next breakthrough in life sciences of similar impact and significance for the mankind?

Certainly, the answers could be dependent on the taste, profession, etc., of the asking person. Let me present a personal opinion and emphasize another fundamental aspect of life, that is its dynamic character.

Let us imagine that an experimental scientist has on his/her laboratory table a complete set of cellular constituents and, naturally, raises the question: How can we organize all of them in order to obtain a "synthetic" cell, or at least a part of it, e.g., a "synthetic" organelle? How could we put the nutrient consumption, turnover of metabolites or proteins, ion homeostasis, etc., into motion? Is it achievable at all? Of course, we feel that it is impossible at the cellular level of complexity. Surprisingly (without claiming to be exhaustive in searching), I did not find any attempt in the literature where authors tried to create even a simplest cell-like sustaining and thermodynamically open system (dissipative structures) from the biological components experimentally. (Coacervates of Oparin and of his successors are not stable and are not dissipative structures.)

If we analyze the reasons of this failure, probably, we may come to the conclusion that such experiments should not be only extremely difficult to design but also difficult to evaluate, not speaking about their expenses. In general, a prerequisite for experiments of this kind should obligatorily be a sustained energy source, sink of reaction products, an autocatalytic step, and elements creating boundaries between phases or at least diffusion barriers like those known in Belousov-Zhabotinsky reaction. This reaction, however, tends to equilibrium because the substrate is consumed and not all products are eliminated from the reaction mixture. The elaboration of such experimental systems will speed up the progress in analysis of the very basic properties of living cells.

Perhaps, there is also another barrier which prevents scientists from experimental activity in creation and analysis of dissipative structures based on biomolecules. This is probably the way of thinking. A living cell manages to process an immense number of variables simultaneously in order to survive, but we analyse the phenomena step by step, or variable by variable. Speaking metaphorically, we think in terms of equilibrium thermodynamics and organize experiments as if the cells were closed or isolated thermodynamic systems, so that the products of our activities should be also described in similar terms. I hope that viewing the cell as an open thermodynamical system combined with analysis of dynamic processes in cells based on creation of corresponding analytical tools could open new horizons in understanding the properties of living matter.

P.S. The text above has been inspired by the article "Is a human proteome project next?" by Douglas Steinberg published in *The Scientist* (2001) 15, 1-8.