

Biology's next revolution*

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The interpretation of recent environmental genomics data exposes the far-reaching influence of horizontal gene transfer, and is changing our basic concepts of organism, species and evolution itself.

One of the most fundamental patterns of scientific discovery is the revolution in thought that accompanies the acquisition of an entirely new body of data. The new window on the Universe opened up by satellite-based astronomy has in the last decade overthrown our most cherished notions of Cosmology, especially related to the size, dynamics and composition of the Universe. Similarly, the convergence of new theoretical ideas in evolution together with the coming avalanche of environmental genomic data, especially from marine microbes and viruses, will fundamentally alter our understanding of the global biosphere, and is likely to cause a revision of such basic and widely-held notions as species, organism and evolution. Here's why we foresee such a dramatic transformation on the horizon, and how biologists will need to join forces with quantitative scientists, such as physicists, to create a biology that embraces collective phenomena and supersedes the molecular reductionism of the twentieth century.

The place to start is the notion of horizontal gene transfer (HGT)[1], sometimes touted as the “spoiler” in molecular phylogeny[2] because of the deviations it implies from a perfectly structured picture of Darwinian, vertical, evolution. At the microbial level, HGT is a pervasive and incredibly strong force[1], famously accelerating the spread of antibiotic resistance for example[3, 4]. The widespread occurrence of HGT means that it is not a good approximation (except perhaps within the sterile confines of a laboratory) to regard microbes as organisms that are dominated by individual characteristics[5]. In fact, their communications at both the genetic and signal response levels (think quorum sensing) indicate that microbial behavior must be understood as predominantly cooperative. In the wild—and recall that perhaps only about one percent of microbes can currently be cultured—microbes form communities, invade biochemical niches, and partake in biogeochemical cycles on a global scale. The available studies strongly indicate that microbes absorb and discard genes as needed[6], and

in response to their environment[7, 8, 9, 10]. Rather than a discrete spectrum, we see a continuum of genomic possibilities, casting doubt on the validity of the fundamental concept of species, extended into the microbial realm[11]. The lack of usefulness of the species concept[12] is inherent in the recent exciting forays into metagenomics[13, 14]; for example, studies of the spatial distribution of rhodopsin genes observed in marine microbes are in accord with the concept of “cosmopolitan genes”, wandering among bacteria, or archaea, as environmental pressures dictate[9].

Equally exciting is the growing realization that the virosphere plays an absolutely fundamental role in the biosphere on both immediate and long-term evolutionary senses[15, 16]. Recent work, including our own unpublished work, suggests that viruses may play an important role as a repository and memory of a community's genetic information, contributing to the evolutionary dynamics[17, 18] and the stability of the system. This is hinted at, for example, by environmental triggering of prophage induction[19], in which viruses latent in cells can become activated by environmental influences. The ensuing destruction of the cell and viral replication is a potent mechanism for dispersal of host and viral genes.

What is becoming clear is that microorganisms have a remarkable ability to reconstruct their genomes in the face of dire environmental stresses[20], and that in some cases at least[21], their collective interactions with the virosphere (and perhaps other gene transfer agents) may be crucial to this. In such a situation, how valid is the very concept of an organism in isolation? It seems that there is a continuity of energy flux, communication, informational transfer from the genome up through cells, community, virosphere, and environment. If the interactions are strong, and collective effects dominant, then an organism cannot even be considered in isolation. Indeed, we would go so far as to suggest that a defining characteristic of life is the strong dependency on flux from the environment, be it energy-giving, chemical-giving, metabolism-giving, or genetically-giving. This inherently biocomplex perspective renders academic such debates as “is a virus dead or alive?”.

Nowhere are the implications of collective phenomena, mediated by HGT, so pervasive and important as in evolution itself. A computer scientist might term the cells

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translational apparatus (used to convert genetic information to proteins) an operating system, by which all innovation is communicated and realized. The fundamental role played by translation, represented in particular by the genetic code, is shown by the clearly-documented optimization of the code[22]. Its special role in any form of life leads inexorably to the rather striking prediction that early life must have evolved in an inherently Lamarckian way, with vertical descent marginalised by the more powerful early forms of HGT[23]. Such gradual refinement through the horizontal sharing of genetic innovations would have led to the generation of a combinatorial explosion of genetic novelty, until the level of complexity, as exemplified perhaps by the multiple levels of regulation, required a transition to the present era of vertical evolution. Thus, we regard as rather regrettable the conventional concatenation of Darwin's name with evolution, because there are other modalities that must be entertained and which we regard as mandatory during the course of evolutionary time.

This is an extraordinary time for biology, because the perspective we have indicated places biology within a context that must necessarily engage other disciplines (such as statistical physics) that are more strongly aware of the importance of collective phenomena than biology has been until now.

Questions suggested by the generic energy, information and gene flows to which we have alluded will probably require resolution in the spirit of statistical mechanics and dynamical systems theory. In time, the current approach of post-hoc modelling will be replaced by interplay between quantitative prediction and experimental test, nowadays more characteristic of the physical sciences.

Sometimes, language expresses ignorance rather than knowledge, as in the case of the nomenclature "prokaryote" now superseded by the terms Archaea and Bacteria, deriving from detailed and well-founded molecular phylogeny. We foresee that in biology, new concepts will require a new language, one that is grounded in the discoveries emerging from the new data we have highlighted in this essay. At the time of an earlier revolution, Lavoisier[24] observed that scientific progress, just like evolution itself, must overcome a challenge of communication:

"...we cannot improve the language of any science without at the same time improving the science itself; neither can we, on the other hand, improve a science, without improving the language or nomenclature which belongs to it."

Biology is about to meet this challenge.

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