Revolution and renaissance

We are in the midst of a revolution in biology and medicine: an information revolution. Many will herald the completion of the human genome sequence, the revealing of our most fundamental biological information, as this era's greatest scientific/technological achievement. We would argue, however, that the information technology revolution that has enabled this feat deserves top honor. Not only has it enabled large-scale genome sequencing and analysis, but it has revolutionized, renewed, and reinvented many biological fields. The development of large data sets that can readily be manipulated and algorithms to reveal known information about similar unknowns has reached far beyond the disciplines of genetics and genomics. From this information generation and management boom, numerous fields, including physiology, are being redefined, new ones such as proteomics are emerging, and others (e.g., structural biology) are poised to contribute significantly to defining gene function on a large scale.

The existing and forthcoming DNA sequences of model organisms and human are proceeding at an expedient pace, and the enormous task of linking genes to function has now begun. New genetic knowledge coupled with existing and emerging molecular genetic, bioinformatic, and other biological techniques have paved the way for the next great challenge and opportunity for physiology and medicine: a more complete understanding of whole organism functioning.

We now can study biological processes from the initial actions of genes within the nucleus through cellular processes to the functions of tissues and organs and ultimately to the workings of the organism. Within this gestalt we can begin to tease out the effects and interactions of our internal environment with our external environment. We will soon have the opportunity to assess individual variation in normal and disease phenotypes. Understanding the variation in these processes will elucidate how small yet different perturbations can produce the same overt disease in two individuals who have dramatically different responses to treatment. This knowledge will ultimately lead to new therapies, diagnostic tools, and better overall health management.

Physiological Genomics is created in response to the perceived need of the scientific community for a rapid conduit of information, the transmission of information. Timely advances in research depend on the rapid communication of information. Therefore, the Journal is committed to enhancing the understanding of the scientific approaches and concepts that link genetics and physiology.

Our goal is to publish the results of a wide variety of studies from human and informative model systems with techniques linking genes and pathways to physiology, from prokaryotes to eukaryotes. The Journal encourages the submission of research that links genes to cell replication, development, metabolic function, cell signal transduction and intracellular signaling pathways, tissue and organ function, and whole organism function. Physiological Genomics encourages the utilization of approaches ranging from expression profiling, assays for molecular interactions, protein mapping, functional predictions from structural assignments, natural and directed gene alteration, selective breeding studies, gene identification, and the assessment of gene-environment interaction. The Journal welcomes important new technologies and concepts that enhance the study of physiological genomics. The Journal encourages publication of new computational approaches, integrative models, and image analysis predictive of gene function. Physiological Genomics will also feature invited reviews and perspectives that contribute to enhancing the understanding of the scientific approaches and concepts that link genetics and physiology.

Science is the systematic acquisition of knowledge, and knowledge is derived from information. Communication is the transmission of information. Timely advances in research depend on the rapid communication of information. Therefore, the Journal is committed to rapid peer review to ensure the timely publication of high-quality papers. To achieve this result, Physiological Genomics will utilize the most important change the information technology and computing revolution has produced: the way we communicate through the World
Wide Web. This new publishing medium creates the opportunity to submit, review, and publish manuscripts more rapidly. We will take full advantage of this and employ an on-line submission and review process, as well as publishing as rapidly as possible—on-line prior to print.

The Web not only makes the dissemination of information more easily accessible globally, but it also allows the reader to interact with and manipulate the information to create new knowledge beyond that contained in the published item. Through this medium authors will be able to bring the reader large data sets and results in dynamic formats that would be impossible to produce in print. Web publishing will allow researchers to present their data, results, and ideas in ways that the readers can more readily apply to their research. One’s creativity can be extended beyond the design of elegant experiments into the elegant presentation of results.

The “new biology” has created a renaissance in physiology. Through this new journal and method of publishing, our goal is to enable, foster, and lead this renewal. In March of 1997, Daniel Tosteson, then dean of the Harvard Medical School, summed up the current change in how we do biology: “In the past we have had functions in search of sequences. In the future, pathology and physiology will become functionators for the sequences.”

We welcome you to the future and to Physiological Genomics.

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