Physiological Genomics: the next three years

I assume the stewardship of Physiological Genomics with appreciation for the contributions and leadership of our first Editor-in-Chief, Victor Dzau. The initial, defining years for any new journal are inevitably fraught with uncertainties and are never easy. For this journal, the task was particularly challenging, given the goal of bridging two distinct scientific cultures. Our ever-increasing submission rate and our continued publication of high-quality manuscripts, together with our rapidly rising impact factor (see the accompanying editorial by outgoing Editor-in-Chief, Victor Dzau; Ref. 1), all testify to the success of this now-established journal. As the new board of Editors now assume responsibility for moving this journal forward, we thank and congratulate the many individuals who have helped launch this important venture. We especially want to recognize the important contributions made by Susan Glueck, who has served as the Deputy Editor of Physiological Genomics since 2001.

Physiological Genomics was launched by the American Physiological Society in 1999 in anticipation of not only the challenges, but also the opportunities that researchers would face in the postgenome era. The term “genomics” emerged a decade ago to describe the innovative high-throughput sequencing technologies and computational approaches that enabled the study of an organism’s DNA in the full set of chromosomes, rather than the study of a single gene or a family of functionally or structurally related genes. “Genomics” was a term coined by T. H. Roderick of the Jackson Laboratory (2) to distinguish it from the field of genetics that it focused on the study of DNA from a broader standpoint, that of the entire complement of genetic material. Driven by the Human Genome Project, a number of new journals sprang up in the early 1990s to accommodate this burgeoning field. The ever-efficient parallel sequencing approaches were elucidating swiftly the genomic sequences of a myriad of complex organisms. Scientists from both the genomics and physiology research communities recognized that sooner, rather than later, they would be faced with the enormous task of attaching function to the seemingly endless genomic sequences that were being posted daily from the remarkable activities of the Human Genome Project and related model organism sequencing projects.

Physiologists began to recognize these needs and ask the critical questions. Who would do the work required to link nucleic acid sequence to protein, and proteins to the complex function of living organisms? What role should the physiology community play in this process? Could physiologists devise techniques to match the massive parallel approaches of genomics, or would they even be interested in doing so? Would high-throughput genomic data sources be able to produce an essential understanding of the inner workings of cellular and organismal function? The greatest challenge scientists faced was the existence of two very separate and distinct scientific cultures: the genomics community versus the traditional world of the biological sciences, biochemistry, and physiology. Clearly, both communities needed each other’s expertise, but how could they work together and would they?

When issues such as these were discussed by the APS Council in 1997, it was quickly recognized that genomics provided wonderful opportunities and challenges for physiologists and that ways could be found to foster collaborative research between these disparate fields of science. It was at this time that the APS made the bold decision to launch a vanguard journal to encourage and publish studies that would advance the new approaches required to bring function to the genome. It was, appropriately, an issue of considerable debate, for it was uncertain whether genomic scientists would be interested in publishing their work in a journal of a society representing a discipline that traditionally had little expertise or interest in either genetics or genomics. At the time, the idea of such a journal seemed premature in the sense that physiologists were only starting to engage in research in this arena. It was uncertain how long it would take for the physiology community to engage in productive collaborative studies with the genomics community, if ever. What would be the focus of the Journal in this vast arena of science with seemingly boundless horizons? How long could the APS afford to subsidize this venture, and how long would it take before sufficient manuscripts and subscriptions could be generated to independently sustain the journal?

It is a tribute to the forward thinking of the APS that approval and plans for Physiological Genomics were so quickly implemented. During the first four years since the Journal’s inception, it has indeed attracted strong interest and has successfully published a number of interesting and innovative studies. To the credit of its founders, in a remarkably short time, it has stimulated great interest within both the genomics and physiological communities and has become recognized as a journal of scientific excellence.

The Evolution and Content of Physiological Genomics

The content of Physiological Genomics reflects the evolution of the various technologies that have emerged to move beyond the laborious hunts for single disease genes that dominated the field of genetics during the early 1980s and 1990s. However, in light of a number of other new journals that were spawned by the novel technologies involved in the sequencing, annotating, quantifying, and modifying multiple genes, there has been a continuing effort to define a broad but clear focus for this journal. Rather than focusing on “genomics” per se, the goal of the Journal from its
inception was, and continues to be, the publication of research directed toward an understanding of the relationship of genes to complex physiological functions. Four areas of research have been at the forefront of these efforts in the immediate postgenome period. These include research on gene expression and profiling utilizing microarrays; complex functional cell or system studies utilizing yeast, *Escherichia coli*, rats, mice, *Drosophila*, and zebrafish; research directed at the mapping of complex traits; and the emerging work in proteomics as applied to the understanding of complex systems biology and medicine.

**Where Do We Go From Here?**

Appropriately, much of what has been published in this journal until this time reflects the underlying heritable component of observed physiological responses generally with large-scale data sets, the essence of genomics. However, physiological genomics is a constantly evolving field, so it is to be expected that the nature of the publications will change as they have during the past four years, driven by the changing technologies and directions of research. Accordingly, any studies related to the broad aim of linking genomics and physiology will be considered for publication in this journal, with scientific excellence being the sole criterion for acceptance. Particularly, we will place greater emphasis upon research that merges high-throughput data sources and hypothesis-driven research into a cohesive picture of cellular, tissue-level, and whole organismal function. Toward this end, the Journal will encourage the publication of the following.

1) Research that aims to distill independent discoveries contained in journals and from high-throughput data sources into an interpretable computational form that advances our understanding of complex living systems. As we are attaining an understanding of gene network structure, we must now be able to investigate network dynamics. Quantitative computational approaches applied to these areas of research will also undoubtedly lead to an increased emphasis on hypothesis-driven research in physiological genomics. For example, a DNA microarray study would be of greater relevance if the profiling was carried out using an extensive experimental design and the results were analyzed in a greater depth to provide novel, well-formulated insights into biological processes. The significance of such studies could be further enhanced by performing hypothesis-driven studies aimed to experimentally validate some or all of the new biological mechanisms suggested by the profiling results.

2) Research that utilizes established or novel approaches such as gene targeting and RNA interference for hypothesis-driven studies designed to determine the role of gene(s) within the context of complex functional pathways. Applications of these approaches in a genomic or large scale would be particularly encouraged.

3) Research that utilizes the comparative analysis of nucleic acid sequences from species at varying evolutionary distances for identifying both coding and functional noncoding sequences, as well as sequences that are unique for a given organism.

4) Research that begins to utilize emerging proteomic technologies to understand the relationship of genes to complex physiological functions. Although proteomics remains in a formative state, as capabilities to measure function and interactions in a high-throughput manner become available, we will encourage publication of this work in *Physiological Genomics*. This includes efforts to characterize the many ways in which a gene can be expressed and the proteins sorted, modified, and interact, with an emphasis on linking such biochemical phenomena to physiological significance.

5) Research that interfaces between the environment and genetic processes such as diet/nutrition, toxins, drugs, etc., is a subject of great interest to the readers of this journal, and manuscripts in this area are welcome.

6) As reflected by the interests and expertise of the Associate Editorship of this journal, we encourage submission of translational research in the fields of cardiovascular, kidney, neurobiology, cancer, endocrinology/metabolism/diabetes/obesity, inflammation, bone/joint/arthritis, connective tissue and matrix molecules.

7) We will continue to solicit high-quality brief reviews written in a manner that will best serve the interests of scientists participating in the emerging field of physiological genomics.

In closing, I thank and look forward to working with the outstanding group of Associate Editors, Consulting Editors, and the Editorial Board, who have volunteered their time and considerable talents to help the continued forward expansion of the Journal. These individuals reflect the wide range of genomic and physiological expertise required to provide appropriate peer review of the diverse science that is published in *Physiological Genomics*.

*Allen W. Cowley, Jr.*

**Editor-in-Chief**

**REFERENCES**
