Physiological genomics - where are we now?

Andrew S. Greene
Biotechnology and Bioengineering Center and Department of Physiology, Medical College of Wisconsin, Milwaukee, Wisconsin

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The first words of a new journal, published in 1999, promised us that we were “...in the midst of a revolution in biology and medicine: an information revolution” (1). The members of founding editorial group of Physiological Genomics wisely predicted that the merging of the fields of physiology, genomics, and medicine would capitalize on our ability to combine and analyze large datasets and communicate their meaning effectively. From their vantage point at the entry into the 21st century, they saw that “...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.” Together with the support of the American Physiological Society and an editorial board of outstanding breadth, they created a new journal that has been amazingly successful in solidifying a new field of study. As the journal completes its 11th year of publication, it seems worthwhile to see how the field and the journal have evolved together.

From its inception, prompted by the unveiling of the draft of the human genome, the field of physiological genomics has had at its core the task of assigning function to genes. With the advent of new technologies that have allowed collection of biological data at unprecedented scales, practitioners of physiological genomics have quickly realized that this task is extraordinarily complex. Interactions between genes, proteins, cells, tissues and organs and even organisms define function, and so it is very rare that we can understand physiology in the context of a single gene. As our thinking about “genes to function” has evolved, so too has our journal. Last year, we reorganized Physiological Genomics into nine separate sections acts as a mini-journal with a separate section editor and editorial group. With such diversity in our journal that represents a field that changes so rapidly, getting a handle on where we are is a challenge.

In 2014, four articles graced the electronic cover of Physiological Genomics. Even in these days of electronic publication, being selected by the reviewers and the editors as the “cover article” remains an honor. What better way, then, to see what the authors and the editors consider the best work submitted to the journal, than to review the articles that made it to the cover. Like the field, these articles spanned entirely different areas of focus and made use of model organisms that ranged from hibernating ground squirrels (4), to rats (2), to sheep (5), to humans (3). Two of the papers (2, 5) used microarray analysis, a technique that was embraced early in the journal’s history. As predicted, the tools available on the web now make deep mechanistic analysis of these data sets simple. Beyond that, databases of expression profiles now allow investigators to explore differences in gene expression across species, between tissues, and during the development of disease.

As if following a script laid out in those first words published in our journal, the two other cover articles (3, 4) used proteomic technologies that Victor Dzau and colleagues labeled “emerging” (1). This emerging technology, with its broad applicability to measure protein levels and their modifications, allowed new insight into the metabolic changes underlying hibernation and fasting in ground squirrels (4), as well as the discovery of novel mechanistic biomarkers for a devastating human cancer (3).

This year our journal will pass into the hands of a new editor and a new group of associate editors. As it does, I can report that the journal continues to propel the field of physiological genomics forward thanks to the scientists who contribute their best work, the editorial board members who contribute their expertise, and the APS, which continues to support this experiment.

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REFERENCES

Address for reprint requests and other correspondence: A. S. Greene, Biotechnology and Bioengineering Center and Dept. of Physiology, Medical College of Wisconsin, 8701 Watertown Plank Rd., Milwaukee, WI 53226 (e-mail agreene@mcw.edu).