Physiological genomics in PG and beyond: October to December 2005

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Submitted 7 November 2005; accepted in final form 7 November 2005

PHYSIOLOGICAL GENOMICS (PG) publishes, on a quarterly basis, brief editorial perspectives entitled “Physiological genomics in PG and beyond.” These editorial perspectives provide brief, accessible highlights of the studies published in PG in the most recent quarter, and relate those studies to aspects of physiological genomics that are being emphasized in PG and other leading journals.

DNA MICROARRAY: BEYOND A LIST OF GENES

PG recognizes the value of comprehensive profiles of gene expression and has been at the forefront of publishing studies utilizing DNA microarrays and other high-throughput molecular profiling techniques. A typical expression profiling study compares two or more conditions using DNA microarrays and generates a list of genes considered “differentially expressed” between different conditions according to some criteria. As the fields of expression profiling and physiological genomics evolve, many investigators are exploring new ways to utilize these powerful techniques to generate valuable information beyond a list of differentially expressed genes.

Several examples can be seen this quarter in PG. These studies use gene expression profiling to:

1) identify subpopulations of cells (29a);
2) generate integrative models (30);
3) identify potential pharmacological agents with desired effects (11);
4) annotate new genes and reveal cross-species conservation (26); and
5) nominate candidate genes within a specific genomic region (20).

In studies previously published in PG, microarray technology and expression profiles have also been used to integrate transcriptomes with other levels of biological control (15, 18, 49, 59), to identify molecular signatures of disease (8, 17), to analyze specific subsets of mRNA (63), to study carbohydrates (55), and to assess the reliability of popular research tools (33, 40). Recent studies published by other leading journals have demonstrated the usefulness of these microarray techniques for determining expression profiles of microRNA (1, 57), positioning patterns of nucleosome (65), DNA methylation (56), RNA alternative splicing (51), potential new exons (16), histone H3.3 variant replacement (35), histone acetylation and methylation (39), protein fingerprinting (42), genomic binding patterns of estrogen receptor (5), and carbohydrate specificity (3) as well as disease molecular signature (2).

The conventional use of DNA microarrays to identify differentially expressed genes will continue to provide new biological insights. Meanwhile, it is evident from the studies published in PG and other leading journals that the power of high-throughput molecular profiling, exemplified by DNA microarray, is multifaceted.

HYPERTENSION AND DIABETES

PG has recently published a number of studies investigating hypertension, diabetes, and related disorders (7, 10, 12–14, 19, 21, 23–25, 29, 31, 35, 36, 45, 52–54, 58, 60, 62, 64). Studies in this quarter of PG reported

1) gene expression profiling in diabetic rats with erectile dysfunction (47);
2) metabolic and blood pressure phenotypes during aging in transgenic rats with altered brain renin-angiotensin systems (22);
3) autoimmune process and bone in diabetes (23a); and
4) gene expression profile associated with a blood pressure quantitative trait locus in Dahl salt-sensitive rats (20).

A quantitative assessment of the impact of erectile dysfunction on diabetic patients’ quality of life (9) and a possible causal role of specific glycosylation of endothelial nitric oxide synthase in this disorder were recently reported (37).

NEW TOOLS AND APPROACHES OF PHYSIOLOGICAL GENOMICS

In this quarter, PG published a number of articles describing new tools or new approaches for performing physiological genomics studies, including

1) the Rat Genome Database (50);
2) combining sequence analysis and chromatin immunoprecipitation to screen for gene regulatory elements (41); and
3) noninvasive ultrasound screening of cardiovascular phenotypes of fetal mice with ethynitrosourea (ENU) mutations (44).

These studies have extended the collection of new tools for physiological genomics published in PG over the past six years, which range from whole animal and molecular techniques, genomic resources, to new software tools (4, 6, 27, 28, 32, 38, 43, 46, 48, 61, 66).

REFERENCES


