Biomarker science: on a theme of personalized medicine

Richard C. Becker · Susan Smyth

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Imagine a scenario where drug development and its rational application to patient care begins with a platform of biomarkers derived from phenotypic screening [1]—an

approach associated with 50 % more FDA-approved first-in-class drugs than target-based drug screening [2]. Now envision an academic community-industry collaborative

Fig. 1 Drug discovery and development is an iterative process that includes systems-based biology, pathophenomics, systems-based pharmacology and biomarker science employed as a continuum of biomedicine across multiple points of interface

R. C. Becker (✉)
Divisions of Cardiology and Hematology, Duke University
School of Medicine, Pratt Street, Durham, NC 27705, USA
e-mail: richard.becker@duke.edu

S. Smyth
The Gill Heart Institute, Lexington VA Medical Center,
Lexington, KY, USA
e-mail: ssmyt2@email.uky.edu

relationship where-in systems-based biology, driven by the rapidly evolving technologies of genetics, genomics, transcriptomics, proteomics and metabolomics is integrated, employing complex informatic algorithms and biological networks (interactome) with systems pharmacology, an in-depth understanding of the molecular basis of disease and large-scale clinical data sets (pathophenomics) [3]. The end-result? A comprehensive, flexible and translatable systems-based model for rational drug development formulated to restore human biological homeostasis and preemptively identify undesirable adverse effects. The model also provides a direct pathway and iterative means to develop diagnostic tools that both reflect and capture drug properties, the phenotypic expression of disease and non-homeostatic maintaining drug and disease responses (Fig. 1).

This special issue of the journal highlights biomarker science and its pivotal role in changing the dated landscape of a reductionist mentality of one drug, one target and one disease as being applicable to a highly complex universe. The special issue also heralds a new section of the journal that is dedicated to Biomarker Science.

Fellows Forum section, a recurring element of the journal that recognizes scholarly activities in trainees participating in the continuum of cardiovascular science, follows the Biomarker theme of the issue with two original articles on biomarkers in thrombotic disorders. The first paper by Kim et al. [4] shows that activated thrombin-activatable fibrinolysis inhibitor accumulates in baboons during *E. coli* sepsis, positioning it to influence fibrinolysis

and inflammation. In the second paper, Rios et al. [5] examine the association between end-stage kidney disease requiring dialysis, vascular-access thrombosis, and plasma levels of von Willebrand factor and its cleaving enzyme, ADAMTS13. Both articles fulfill the intent of the Forum, which is to provide trainees with an avenue for publication of meritorious original work devoted to fundamental science in the areas of cardiovascular disease, preclinical and clinical research, global health, and epidemiology.

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