Preface

This Special Issue was born out of conversations within the Editorial Board about the need to refocus the Journal to better reflect the expanding field of genomic and postgenomic studies of kidney function in health and disease. This issue represents a launching pad for this new dimension in renal research and should stimulate our readership to support this shift in focus of the Journal with appropriate scientific contributions.

Functional genomics can be defined as a tool-kit consisting of a variety of molecular, cellular, and whole-animal approaches, all directed toward elucidation of the role played by genes and their encoded products in maintaining physiological performance or triggering pathologic events. This is not to say that the subject of functional genomics is monochromatically split into thousands of finite topics, each dealing with an individual gene. The problem at hand is much more complex. On the one hand, while harboring 30,000–40,000 genes, the human genome, in reality, encodes for hundreds of thousands of proteins. Each of these may exhibit a different function, depending on the cellular context, and each may serve different purposes in different cell types. On the other hand, the integrated functions of an organ are supported by ensembles of genes and their products. Understanding the ‘wholeness’ of these ensembles represents a major challenge for functional genomics. What are the outcomes of the lack or addition of components of ensembles? What is

the time course of turning the elements of ensemble on and off? Where are the points of least resistance, and what kind of interventions may facilitate the recovery of function? These types of questions outline the application of functional genomics to the problems of health and disease. It is the spatial and temporal mapping of these processes that constitutes the ultimate goal of biomedical research.

It may be whispered softly that the renal research community is near the bottom of the ladder leading toward this goal. This Special Issue is intended to facilitate the recognition of the challenge ahead to provide the tools to address the special requirements of kidney research. Toward this end, several reviews describe technical approaches to gene screening (S. Gullans, J. Elalouf, J. Sedor, E. Bottinger), other reviews offer examples of the complexities of gene function in various disease states or their models (J. Davies, M. Gerritsen, H. Brady, Y. Kanwar, R. Falk, S. Ylä-Herttuala, H. Li). It is our hope that thoughts and experimental examples shared by the specialists and gathered in this issue will facilitate the ascent to the first rung of the ladder leading to the deeper understanding of renal function in health and disease.

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