Foreword: Propelling a Field Forward

PUBLICATION OF THIS THIRD EDITION of *Essentials of Glycobiology* inspires a look back as well as a look forward. Rarely has a textbook played such a dominant role in defining, reporting, and guiding progress in a field. From a global perspective, the importance of its subject matter is obvious: glycans are the most abundant organic polymers in our biosphere. However, the complexity of these molecules can be intimidating. Glycan biosynthesis occurs in a combinatorial, non-template-driven fashion, in contrast to DNA, RNA, and protein. Glycan biosynthesis and degradation are driven by myriad enzymes, many of whose substrate specificities and kinetic mechanisms remain poorly defined. In addition, glycans perform an immense range of biological functions, serving, for example, as nutrient substrates, as participants in signaling pathways, and as scaffolds for building multicellular "machines." Considering these realities, and the competing allure of many other scientific fields in this rapidly evolving era of genome-driven fundamental and applied science, it is not hard to understand why "glycobiologists" today have become an endangered species. On the other hand, the importance of their field has never been greater. Glycobiology is inherently interdisciplinary and radiates into, as well as being informed and "fertilized" by, so many other areas of biology.

We all need mentors, and in many ways this textbook has served that function for both nascent and established glycobiologists; it has provoked thinking and provided stewardship as a cogent, consistent, and accessible source of accrued knowledge over its two- (and now three-) edition life span.

This knowledge is also timely as we consider the present and the future. Like many fields, glycobiology has benefited from high-throughput genomics, which has allowed rapid identification of potential glycan-modifying enzymes as well as glycan-binding proteins. This explosion of information is illustrated by the outpouring of microbiome sequencing projects, which are emphasizing how richly endowed microbes are with glycoside hydrolases, polysaccharide lyases, and glycosyltransferases not encoded in the genome of their respective hosts. Moving forward, ongoing analyses of microbial community function will undoubtedly provide new insights into how glycans serve as foundations for nutrient-sharing relationships between primary and secondary consumers in the food webs that sustain these communities. These analyses should also continue to reveal new details about how glycans function as microbial "signposts" recognized and accommodated by the host immune system so that mutually beneficial host–microbial relationships can be established and maintained, whereas in other contexts they are attacked by the immune system or function to cloak pathogens from recognition.

Ongoing improvements in the analytic tools used for characterizing glycan-containing molecules will propel efforts seeking to comprehensively define "glycomes" that comprise all of the glycans that can be made by a cell, tissue, or organism as a function of its differentiation, development, or physiological state. CRISPR-based genome editing tools will provide unprecedented opportunities to precisely manipulate glycan biosynthetic and degradative pathways within cells and thus ascertain the functions of their products. New chemical tools that allow modification of specified glycans in living cells should also facilitate studies of glycan function in different physiological and pathologic contexts. At the same time, improvements in glycan synthetic chemistry are yielding high-diversity libraries that enable the targets of carbohydratebinding proteins to be determined. These improvements are also allowing specific glycans of interest to be produced in large quantities for a variety of purposes. For these and many other reasons, the readers and editors of this volume face an exciting future for glycobiology and, together, are poised to create that future.

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October 2016