Preface

Recent progress in stem cell research has begun to transform concepts and applications in biology and medicine. Beyond instilling hope and high expectations with respect to cell therapeutic measures, personalized medicine, cancer eradication, and human cellular model systems in the near future, this rapidly developing field has begun to unveil the intricacies of phenotypic plasticity in development, tissue homeostasis, and disease.

In the context of our own research in neural stem cell biology and neuroregeneration, a major obstacle to translational progress has been the inability to precisely mimic in the dish the faithful development of cells exclusively toward the phenotype of interest: the equivalent of a particular physiological cell type in need of being replaced or of being studied in biomedical in vitro assays and screens. To eliminate confounding contaminants of unwanted cells and to isolate specific subsets of cells, stem cell scientists have begun to revert to flow cytometric and other cell isolation methods based on neural surface antigens. Along with that has come a quest for novel markers and marker combinations to better define the target population.

Parts of these efforts may yield a surface antigen marker "tree" for neuropoiesis, a definition of neural developmental stages and phenotypes by neural surface antigens, analogous to the well-established hematopoietic lineage analysis. As opposed to the "fishing approaches" of earlier times, today's high-throughput screening approaches imply an exhaustive, comprehensive analysis of surface molecules expressed on neural cell populations. In that context it becomes humbling to be made aware of the sheer complexity of possibilities that biology provides by the dynamics of posttranslational modifications, membrane trafficking, and conformational changes of these molecules and the introduction of numerous splice variants—features that may not only correlate with, but also contribute to explaining the complexity of the nervous system.

Beyond description, the real fun starts with the functional implications and effects of such differential surface antigen expression. While the implications are immediately apparent in fundamental neural cell biology, neural development, and neuro-oncology alike, what determines an individual cell's decision to develop in a microcontext appropriate manner has remained unanswered. Which mechanisms govern a cell's decision to grow or to differentiate? The improved understanding of surface antigens and their signaling pathways lies at the heart of this exciting and important challenge. "All" inputs to a particular cell are mediated by the molecules presented on its surface. A cell senses its position in the world via the differential composition of molecules expressed on its outer membrane. Surface molecules comprise growth factor receptors, adhesion molecules and cell–cell interaction proteins. Biochemically, they include glycoproteins and glycolipids, channels, and immunoglobulin superfamily members. They can be membrane-spanning, GPI-anchored or extrinsic and may themselves be cleaved off, secreted, and act as long-range signaling molecules. Some may be more prominent on different subsets of neurons, others on glia, and/or on transformed cells of either lineage. The selected expert contributions from leading authorities working on neural surface antigens in the fields of neural stem cell biology, neurodevelopment and cancer presented in this volume for the first time explore and cover this topic for the neural lineage. It is targeting researchers ranging from student-level to experienced investigators in cellular neurobiology and biomedicine.

The book is divided into three parts. The first (Chapters 1 and 2) covering fundamentals that may prepare the readership from various backgrounds and fields of specialization for the remainder of the volume. The second section (Chapters 3–13) dealing with particular subsets of surface antigens and family of molecules largely from a fundamental biological perspective. And the final part (Chapters 14–18) focusing in on biomedical applications when exploiting surface molecules as markers. The concluding Chapter 19 represents an attempt to synthesize and integrate these components and to provide an outlook on future challenges and opportunities in exploring neural surface antigens in basic biology and biomedical applications.

Unique to this book is its intention to serve as an integrator at multiple levels, across particular surface molecule families, encouraging to explore and to identify commonalities in between researchers working in disparate fields. It also demands and provides justification for an overview, bird's eye view perspective of neural surface antigens (transcriptome, proteome, "surfaceome"), and the development of analogous analytical tools for computational, large-scale readout of presence and cellular effects of neural surface antigens.

As the editor, I am indebted and thankful to all contributors, and I am incredibly pleased to witness such a diverse project come to fruition. I thank Christine Minihane and Shannon Stanton at Elsevier for proposing the book and for their overall editorial support from the publisher's side throughout the project. Together with my coauthors, I thank the readers for using this book, for applying its concepts and approaches to their own particular research questions and for continuous discourse toward refinement of an integrated functional understanding of neural surface antigen dynamics and signaling.

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