Preface

20 Years of *Genome Research*

The first issue of *Genome Research* published in August of 1995, from the need to understand and elaborate the first fruits of the Human Genome Project. The goal of the Editors has always been to capture the exciting advances and critical technology developments in genomics by publishing novel and insightful research into genome structure and function, and the genomic basis of human disease. *Genome Research* was necessarily about the future—one to be fueled by the genomes of many species and new creative tools enabling all biomedical researchers to answer previously intractable biological questions.

This issue of *Genome Research*, marking its 20th year of publication, remains focused on that future. We highlight the next generation of *Genome Research* with a series of Perspectives written by future leaders of genomics-based research and technology. We find the authors, all in the first few years of their independent faculty positions, to be at the right time and place to offer fresh viewpoints and critical insights into the future of our field. These stimulating contributions envision the next 20 years, spanning some of the most rapidly growing areas: mobile sequencing, biological data science, functional and disease genomics, genome editing, single-cell genomics, systems biology, and host-microbiome research.

We offer these unique Perspectives with sincere thanks to our authors, our reviewers, our Editorial Board members, and our readers—past and present—and with the expectation that the journal will continue to be about the increasing ability of genomics to elucidate previously opaque biological processes.

In this issue, we also include current primary research within some of these areas. Two articles in cancer genomics focus on cellular heterogeneity and the development of pathogenesis. There is also an article that points to the significance of the evolution of gene regulation in phenotypic diversification, and one that illustrates the importance of genetic background in microbiota composition. Finally, two advanced methods are offered that facilitate a more thorough exploration of the genome: One demonstrates accurate variant discovery within repeat regions of the genome, and another allows for genome-wide binding profiles where suitable antibodies are unavailable. Together, the authors of these Perspectives and Research articles offer their own exciting discoveries, represent the state of the art, and point toward the future of genomics, ripe and revealing.

Hillary E. Sussman, for the Editors of Genome Research

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