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Editor's Foreword

Dear Scholars, Researchers, Clinicians, and Esteemed Readers,

Cancer is not a single disease, nor can it be understood through a single scale of observation. It arises through dynamic interactions among inherited susceptibility, acquired genomic alteration, epigenetic regulation, cellular state, tissue environment, immune response, and exposure over time. Tumors that share an anatomical diagnosis may differ profoundly in their molecular drivers, patterns of evolution, and response to therapy. This biological complexity is the central challenge of cancer research, but it is also the source of new opportunities for more precise diagnosis, prognosis, prevention, and treatment.

The development of high-throughput sequencing and computational analysis has transformed our ability to study that complexity. Whole-genome and transcriptome profiling, single-cell and spatial technologies, liquid biopsy, functional genomics, and integrative multi-omics now reveal tumor diversity at unprecedented resolution. At the same time, the expansion of clinically annotated cohorts and longitudinal data makes it possible to examine how genetic and genomic features shape therapeutic response and resistance. The task before us is not simply to generate more data, but to convert molecular information into knowledge that is reproducible, biologically meaningful, and capable of improving patient care.

The *Journal of Cancer Genetics and Genomics* (JCGG) is established to support this task. JCGG is an international, peer-reviewed, open-access journal devoted to the genetic and genomic mechanisms underlying cancer initiation, development, progression, and treatment response. The journal aims to bring together researchers and clinicians working across cancer biology, genetics, genomics, molecular oncology, bioinformatics, pathology, and precision medicine. By connecting mechanistic discovery with clinical investigation, we seek to promote research that explains disease and advances responsible translation.

Our scope includes germline cancer susceptibility, somatic mutation, structural variation, copy-number alteration, epigenomics, transcriptomics, noncoding regulation, tumor evolution, clonal heterogeneity, cancer predisposition, molecular classification, genomic biomarkers, pharmacogenomics, immunogenomics, and mechanisms of drug sensitivity and resistance. We welcome studies using bulk, single-cell, spatial, and multi-omic approaches, as well as functional experiments that establish the consequences of genomic findings. Research on circulating tumor DNA, minimal residual disease, molecular diagnostics, targeted therapy, and clinically relevant computational methods also lies at the heart of the journal.

JCGG places particular value on integration. Genomic association alone may identify a signal, but biological interpretation requires attention to mechanism, cellular context, and independent validation. Likewise, a promising biomarker must be assessed for analytical validity, clinical validity, and potential

utility before it can guide care. We encourage authors to connect computational inference with experimental evidence, molecular findings with phenotypic and clinical data, and discovery cohorts with appropriate validation. Studies that examine why a proposed marker or model fails to generalize are also important to the field.

Three principles will guide our editorial direction. First, rigor and reproducibility: study design, specimen handling, analytical pipelines, statistical methods, and validation strategies should be described with sufficient clarity to permit critical evaluation. Second, clinical relevance without overstatement: translational promise should be distinguished from demonstrated clinical benefit, and conclusions should remain proportionate to the evidence. Third, responsible data practice: genomic research requires careful attention to consent, privacy, data governance, population representation, and the ethical implications of findings for patients and families.

Representation is a scientific as well as an ethical priority. Many genomic datasets remain uneven in ancestry, geography, cancer type, and clinical setting. Such imbalance can limit discovery, distort risk estimates, and reduce the performance of diagnostic or predictive tools in underrepresented populations. JCGG welcomes research that broadens the evidentiary base of cancer genomics and examines population-specific as well as shared mechanisms. We also encourage transparent discussion of cohort composition and the limits it places on interpretation.

The journal will serve as a forum for original research, comprehensive reviews, methodological advances, translational studies, and critical perspectives. We are interested in emerging technologies, but novelty alone will not determine significance. A contribution may be important because it reveals a mechanism, validates a finding, improves measurement, challenges an assumption, or clarifies the path from laboratory observation to clinical application. Across article types, our standard will be whether the work strengthens understanding and can support further inquiry.

We warmly invite geneticists, genomic scientists, cancer biologists, clinicians, pathologists, bioinformaticians, data scientists, and other members of the oncology community to contribute to JCGG. We ask reviewers to combine exacting evaluation with constructive guidance, and we encourage readers to engage with the journal as an active scientific forum. Progress against cancer depends on shared standards, open exchange, and collaboration across specialties and institutions.

With the inaugural issue, JCGG begins with a clear purpose: to help turn the expanding language of cancer genomes into deeper biological understanding and better-informed care. We know that translation is neither immediate nor simple. It requires validation, humility, ethical responsibility, and sustained cooperation. On behalf of the editorial team, I thank our authors, reviewers, readers, and partners for joining this endeavor. We look forward to advancing cancer genetics and genomics together.

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Editor-in-Chief: Assoc. Prof. Peitao Wu