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Enhancing our shared platform for genomics research: an update from *Genomics Communications*

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Since its launch on August 19, 2024, *Genomics Communications* (*gComm*) has rapidly grown into an active, internationally shared platform for genomics research. Over the past two years, we have observed strong engagement from authors worldwide, with contributions originating from 11 countries, including China, the United States, Australia, France, Canada, the Netherlands, and Italy. Guided by a commitment to efficient academic exchanges, we have established streamlined peer-review processes that support a positive submission experience for authors. The average time of first decisions with external reviews after submission was 28 d, and the average time of final disposition was 53 d. The *gComm* journal is currently indexed in AGRIS, CABI, CAS, and DOAJ, with applications for ESCI and Scopus under review, indicating our growing visibility within the global genomics community. We are deeply grateful to our reviewers for their expert critiques, our Editorial Board members for their scholarly guidance, and all authors for entrusting us with their outstanding research.

To date, the journal has published 32 articles spanning major areas of genomics research, including genome assembly and annotation, studies of organellar and microbiome genomes, functional genomics investigations, epigenomics, and advances in computational and data-driven methodologies. For examples, Zhou & Zhou reviewed rice genomic resources constructed in recent years and new genomic technologies, highlighting applications of artificial intelligence (AI) in breeding[1]; Wang et al. revisited hypotheses regarding mutations in plant organellar genomes, emphasizing that mutations in plant mitochondrial genomes likely result from interactions among multiple factors rather than a single dominant factor[2]; Chen et al. compared high-quality genome assemblies of three species in Bruchinae and identified genomic structural variation related to sex-biased genes, highlighting the rapid evolution of sexual chromosomes through frequent acquisition of novel genes in seed beetles[3]; and an open-source bioinformatics package, Homotools, was published to facilitate functional genomic studies through homologous identification, comparison, and polymorphic annotation across genomes[4].

Our published articles on diverse genomic topics evidence our achievements and indicate areas where we should continue to focus our efforts. As a journal dedicated to genomics, we welcome high-quality manuscripts from a broad range of disciplines, including microorganism, plant, animal, and medical genomics. We particularly encourage studies that employ innovative experimental designs, integrative multi-omics approaches, or advanced computational and statistical methodologies to deepen genomic insights. In addition, we place special emphasis on the development and application of AI and machine learning techniques in genomics, recognizing their growing impact on data interpretation, predictive modeling, and biological discovery.

The year 2026 will mark the third anniversary of the launch of *gComm*. Our goal of establishing *gComm* as a leading platform for genomic research publications remains unchanged. In addition to assisting scientists in disseminating their research findings, we will work to increase the number of short perspective letters that highlight current trends and emerging directions in genomics. We also plan to summarize and share round-table discussions from genomics conferences to broaden community engagement. Through these efforts, *gComm* seeks to support a strong and connected genomics research community.

Conflict of interest

The authors declare that they have no conflict of interest.

Dates

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