Special Issue

Applications of High Throughput Sequencing Technologies in Forest and Other Species

Message from the Guest Editor

Long-read sequencing technologies including PacBio and Oxford Nanopore sequencing provide unprecedented opportunities for forestry to overcome the disadvantage of short reads. At genome-wide level, PacBio or Nanopore has far superior contiguity for forestry genome assembly due to the long reads. At transcriptome level, both PacBio and Oxford Nanopore Technologies sequence single molecules can detect post-transcriptional regulation, which contributes to transcriptome diversity. In addition, direct RNA-Seq based on an Oxford Nanopore Technologies sequence provides valuable information about RNA modifications, which are lost during PCR amplification in other methods.

However, the analysis of PacBio and Oxford Nanopore long-read data comes with new technical challenges. Both new experimental and bioinformatics method are needed to fully utilize the advantage of long-read sequencing for forestry research. In this SI, we welcome the submission of reviews or original research that uses high throughput sequencing technology to address biological question in forestry, or bioinformatics methods/computational tools or database for sequence data analysis in forestry.

Guest Editor

Prof. Dr. Lianfeng Gu
Basic Forestry and Proteomics Research Center, College of Forestry,
Fujian Agriculture and Forestry University, Fuzhou 350002, China

---

Deadline for manuscript submissions

closed (25 November 2022)

G C A T
T A C G
G C A T

Genes

an Open Access Journal by MDPI

Impact Factor 2.8
CiteScore 5.5
Indexed in PubMed

mdpi.com/si/104566

Genes
Editorial Office
MDPI, Grosspeteranlage 5
4052 Basel, Switzerland
Tel: +41 61 683 77 34
genes@mdpi.com

mdpi.com/journal/genes

MDPI

G C A T
T A C G
G C A T

Genes

an Open Access Journal
by MDPI

Impact Factor 2.8
CiteScore 5.5
Indexed in PubMed

mdpi.com/journal/genes

MDPI

About the Journal

Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

Editor-in-Chief

Prof. Dr. Selvarangan Ponnazhagan
Department of Pathology, The University of Alabama at Birmingham,
1825 University Blvd, SHEL 814, Birmingham, AL 35294-2182, USA

Author Benefits

Open Access:

free for readers, with article processing charges (APC) paid by authors or their institutions.

High Visibility:

indexed within Scopus, SCIE (Web of Science), PubMed, MEDLINE, PMC, Embase, PubAg, and other databases.

Journal Rank:

JCR - Q2 (Genetics and Heredity) / CiteScore - Q2 (Genetics (clinical))