

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

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Deadline for manuscript submissions

closed (25 November 2022)

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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

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