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EDITED AND REVIEWED BY
Gulnihal Ozbay,
Delaware State University, United States

*CORRESPONDENCE
Md. Anwar Hossain
✉ mahossain95@hotmail.com

RECEIVED 19 July 2023
ACCEPTED 18 August 2023
PUBLISHED 24 August 2023

CITATION
Hossain MA and Roslan HA (2023) Editorial:
Emerging genomic technologies for
agricultural biotechnology: current trends
and future prospects.
Front. Plant Sci. 14:1263289.
doi: 10.3389/fpls.2023.1263289

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Editorial: Emerging genomic technologies for agricultural biotechnology: current trends and future prospects

Md. Anwar Hossain^{1*} and Hairul Azman Roslan²

¹Department of Biochemistry and Molecular Biology, University of Rajshahi, Rajshahi, Bangladesh,

²Faculty of Resource Science and Technology, Universiti Malaysia Sarawak, Kota Samarahan, Sarawak, Malaysia

KEYWORDS

CRISPR/Cas9, RNA-sequencing, quantitative trait loci, genome editing, marker assisted selection (MAS)

Editorial on the Research Topic

[Emerging genomic technologies for agricultural biotechnology: current trends and future prospects](#)

The current earth's population of 7.6 billion is expected to reach 8.6 billion by 2030. The increased population will need more food than it can currently produce. However, world agriculture is facing severe challenges such as global climate change, exhausted resources, reduction of arable lands and various pathogens. Advances in genomic technologies may offer potential solutions to these agricultural problems. New genomic technologies such as, Next generation sequencing (NGS), Ribonucleic acid sequencing (RNA-Seq), Clustered Regularly Interspaced Short Palindromic Repeat-Cas9 (CRISPR/Cas9), Transcription activator-like effector nucleases (TALENs) and Oligonucleotide-directed mutagenesis (ODM) as well as doubled haploids, molecular markers and mapping populations have been developed and utilized for increasing the crop production. Together with the rapidly expanding availability of genome sequence data, these technologies have the potential to transform plant breeding.

In this Research Topic we aim at the collection of articles on application of cutting-edge genomic technologies to improve various crops, vegetables and fruits which includes two reviews and seven original articles.

In first review, [Aziz et al.](#) explored the deployment of GM crops and their effects on sustainable food production systems which provided a comprehensive overview of the cultivation of GM crops and the issues preventing their widespread adoption, with appropriate strategies to overcome them. They also presented new tools for genome editing technology with special reference of CRISPR/Cas9 platform. They outlined the role of crops developed through CRISPR/Cas9 for sustainable development goals by 2030.

Nowadays in the post genomic era, transcriptomic or RNA-Seq technology focuses on functional studies of transcriptomes. It is a high-resolution, sensitive and high-throughput NGS approach used to study non-model plants and other organisms. RNA-Seq is an important technique for predictions and functional analysis of genes that improves gene ontology biological processes, molecular functions, and cellular components, but still now