IOCBI 2026 Conference

The 1st International Online Conference on Biology

10–12 February 2026 | Online

MDPI

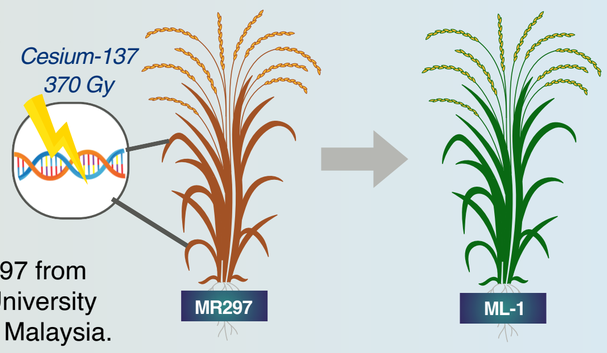
Identification of Candidate SNPs in Protein-coding Regions in Gamma-ray Irradiated Mutant Rice

Siti Amira Adilah Kamarudin[1], Nor'Aishah Hasan[1], Faiz Ahmad[2]

[1] Faculty of Applied Sciences, University of Technology MARA (UiTM), Branch Negeri Sembilan, Campus Kuala Pilah, 72000 Negeri Sembilan, Malaysia
[2]Agrotechnology and Biosciences Division, Malaysian Nuclear Agency, 43000 Kajang, Selangor, Malaysia

INTRODUCTION

- MR297 is a farmers' favourite rice variety **commercially** grown across Peninsular Malaysia for over a decade.
- However, this superior variety has become **less adaptable** to biotic and abiotic stresses causing economic distress.
- As an alternative, a promising mutant line, ML-1, was successfully developed through **acute gamma irradiation** of MR297 from the collaboration between University Technology MARA and Nuclear Malaysia.



- ML-1 has shown **improved** yield potential and enhanced resistance to bacterial diseases during field evaluation.
- Yet, the **causative mutations** that contribute to these genetic improvements are still unknown.

OBJECTIVES

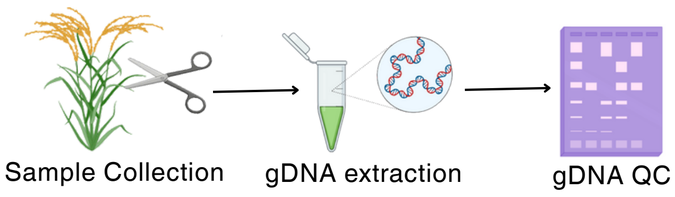
▶ To **characterise** the mutation profile in mutant ML-1 by comparing genome sequences to wild-type MR297.

▶ To **identify** candidate SNPs that are associated with agronomic traits and resistance to bacterial leaf blight (BLB) disease.

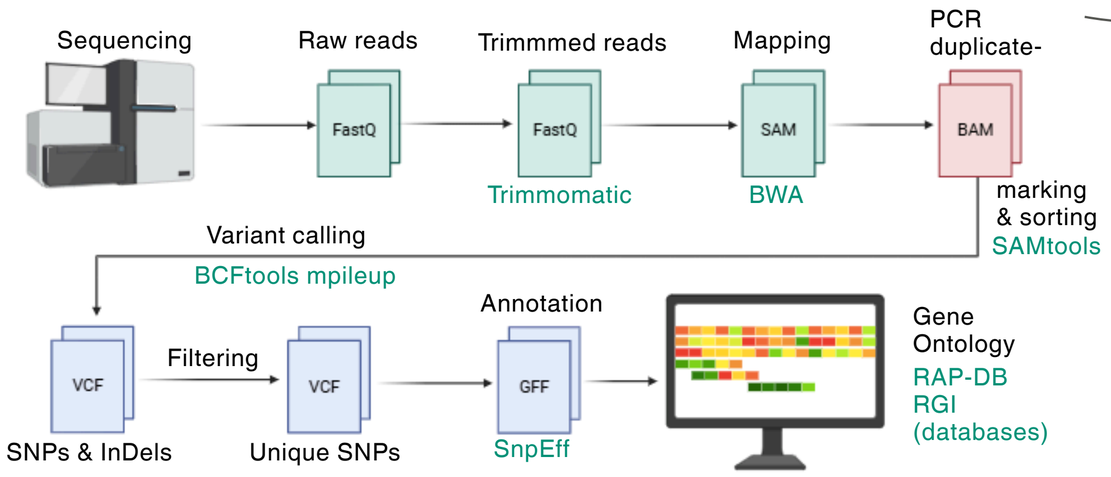
METHODOLOGY

PRESENT

Sample Preparation

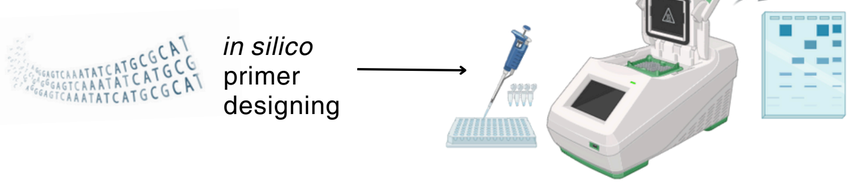


Bioinformatics Pipeline



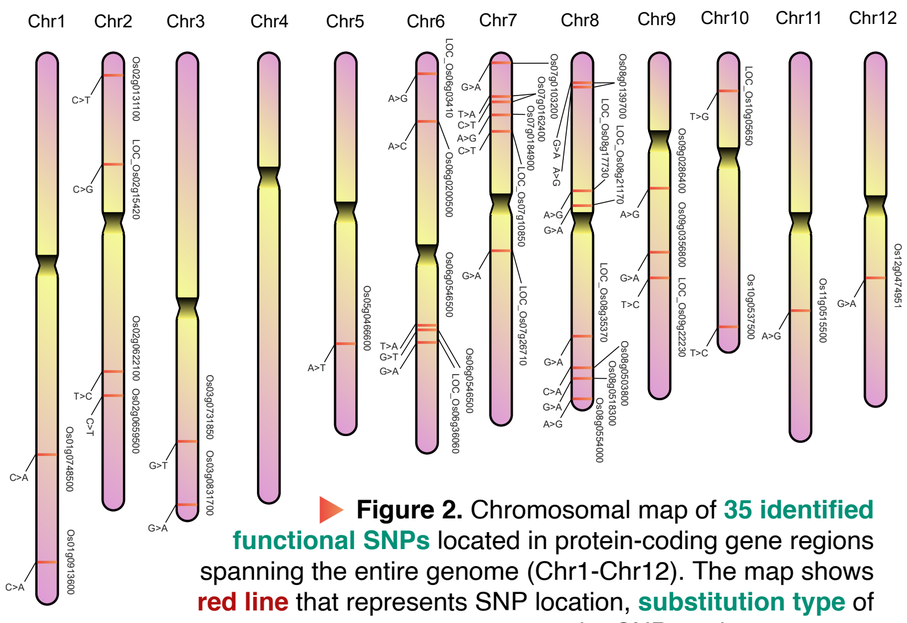
FUTURE

Allele-specific Primer Designing and Validation



FINDINGS

▶ **Figure 1.** Heatmap of variant distribution binned into 100kb windows across all 12 chromosomes in the genome of the mutant, ML-1. **(A) SNP density. (B) InDel density.** x-axis represents individual chromosomes, y-axis represents the genomic position along each chromosome in Megabases (Mb). Bin colours denote the ranges of SNP and InDel frequency. (**Darker colours** = Higher frequency, **Lighter colours** = lower frequency).



▶ **Figure 2.** Chromosomal map of **35 identified functional SNPs** located in protein-coding gene regions spanning the entire genome (Chr1-Chr12). The map shows **red line** that represents SNP location, **substitution type** of the SNP, and **gene name**.

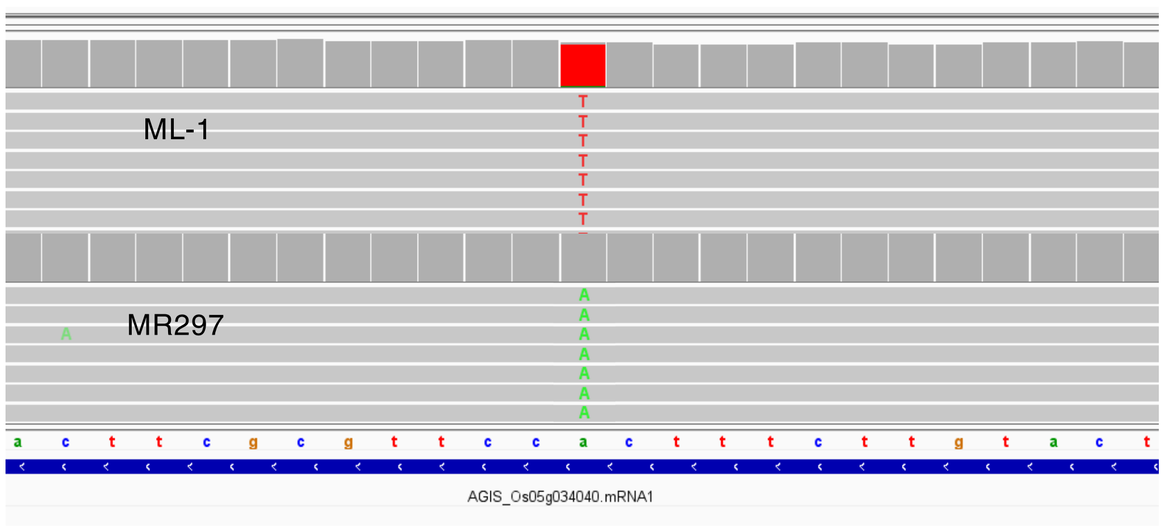


Figure 3. Sequence comparison between wild-type and mutant on IGV software showing **SNP (A > T)** mutation in a gene region on chromosome 5.

CONCLUSIONS

▶ We reported **35 SNPs** in protein-coding gene regions in the mutant genome spanning from chromosome 1 until chromosome 12, excluding chromosome 4.

▶ Among the putative candidate genes, **12** are associated to **immune response** towards pathogens, **9** encode for proteins related to **growth development**, **7** are related to tolerance to **abiotic stresses**, and **7** are **novel genes**.

What is next?

▶ The identified candidate SNPs will be further <u>developed and validated</u> as allele-specific molecular markers. These SNP markers will be further used in marker-assisted breeding and selection.

Acknowledgements:

Bioinformatics Lab Group

Reference:

Pariasca-Tanaka, J., Ueda, Y., Kondo, K., Prodhan, M. A., Rajonandraina, T., Ranaivo, H. N., Rakotondramanana, M. F., Saito, H., Lam, T. D., Wissuwa, M. (2025). Genome-wide sequence comparison and development of InDel and SNP markers to facilitate localized rice breeding. Current Plant Biology, 42(100469), https://doi.org/10.1016/j.cpb.2025.100469.

Contact me: