

## Whole Genome Analysis of Mahsuri Rice and Its Blast-Resistant Mutant for Understanding Resistance Mechanisms

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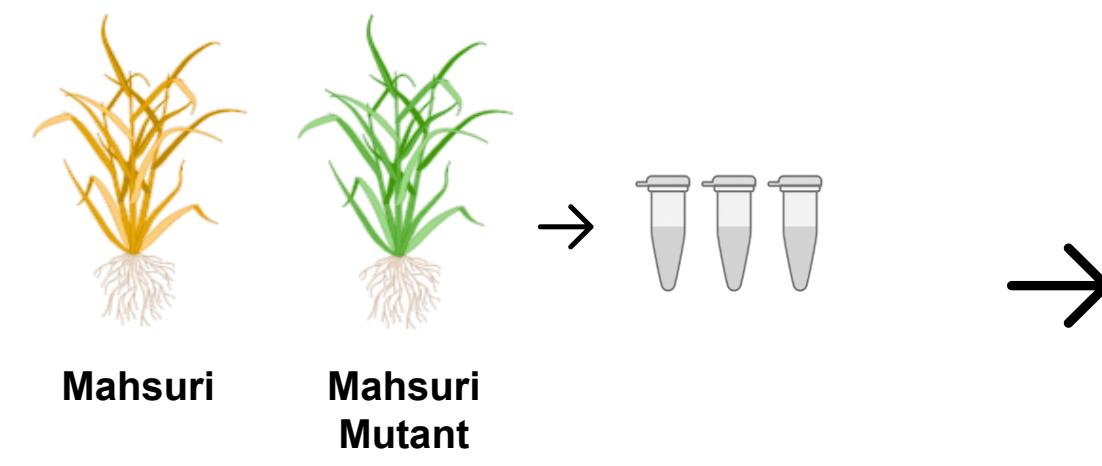
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### INTRODUCTION & AIM

Rice (*Oryza sativa* L.) is a staple food for over 40% of the global population, especially in Asia. The traditional high-yielding cultivar 'Mahsuri', developed by the Food and Agriculture Organization (FAO) through japonica-indica hybridization, is susceptible to blast disease. Blast disease can affect all above ground parts of the rice plants, with initial symptoms white to grey-green lesions with brown borders. To address this, the 'Mahsuri Mutant' was created via mutational breeding to enhance blast resistance while retaining desirable traits. However, the specific molecular mechanisms and genetic mutations driving this resistance remain unexplored as the lack of molecular markers found that associated with specific SNPs in mutant line. Therefore, this study aims to conduct a genomic profiling of the susceptible 'Mahsuri' and its blast-resistance mutant line against a high-quality reference genome to identify genetic variants underlying blast resistance. By developing these genomic tools, these research aims to accelerate the development of improved rice cultivars which directly contributing to achieving several United Nations Sustainable Development Goals (SDGs) by 2030.

### METHODOLOGY



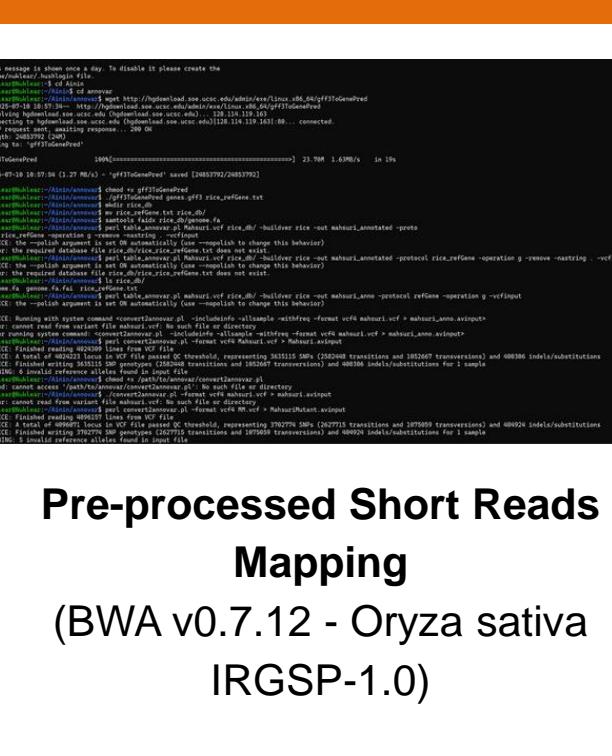
#### Sample Preparation and DNA Extraction

- Mahsuri seeds from Malaysian Agricultural Research and Development Institute (MARDI).
- Mahsuri Mutant seeds from Malaysian Nuclear Agency.
- Extract two weeks old of young leaves using QIAGEN DNAeasy Plant Extraction Kit.

#### Whole-Genome Resequencing

- Illumina Novaseq 6000 with a depth 30x coverage, 150 bp paired end.
- Data NCBI: SRR24388814 (Mahsuri) and SRR22952097 (Mahsuri Mutant).

#### Bioinformatics Analysis



### CONCLUSION

The whole-genome sequencing of 'Mahsuri' and its blast-resistant mutant, were successfully sequenced to the *Oryza sativa* Japonica reference genome. By identifying genome-wide Single Nucleotide Polymorphisms (SNPs) and Insertions/Deletions (InDels), this study highlight the key genetic variants potentially linked to important agronomic traits, including disease resistance. These findings have resulted in findings the specific molecular markers to Mahsuri and Mahsuri Mutant, and will provide valuable insights for Malaysian rice varieties. In the future, functional validation will be emphasized to validate the particular functions of discovered blast resistance (R) genes using targeted gene expression analysis and transgenic research, providing a foundation for developing climate-resilient rice cultivars that support global food security goals.

### REFERENCES

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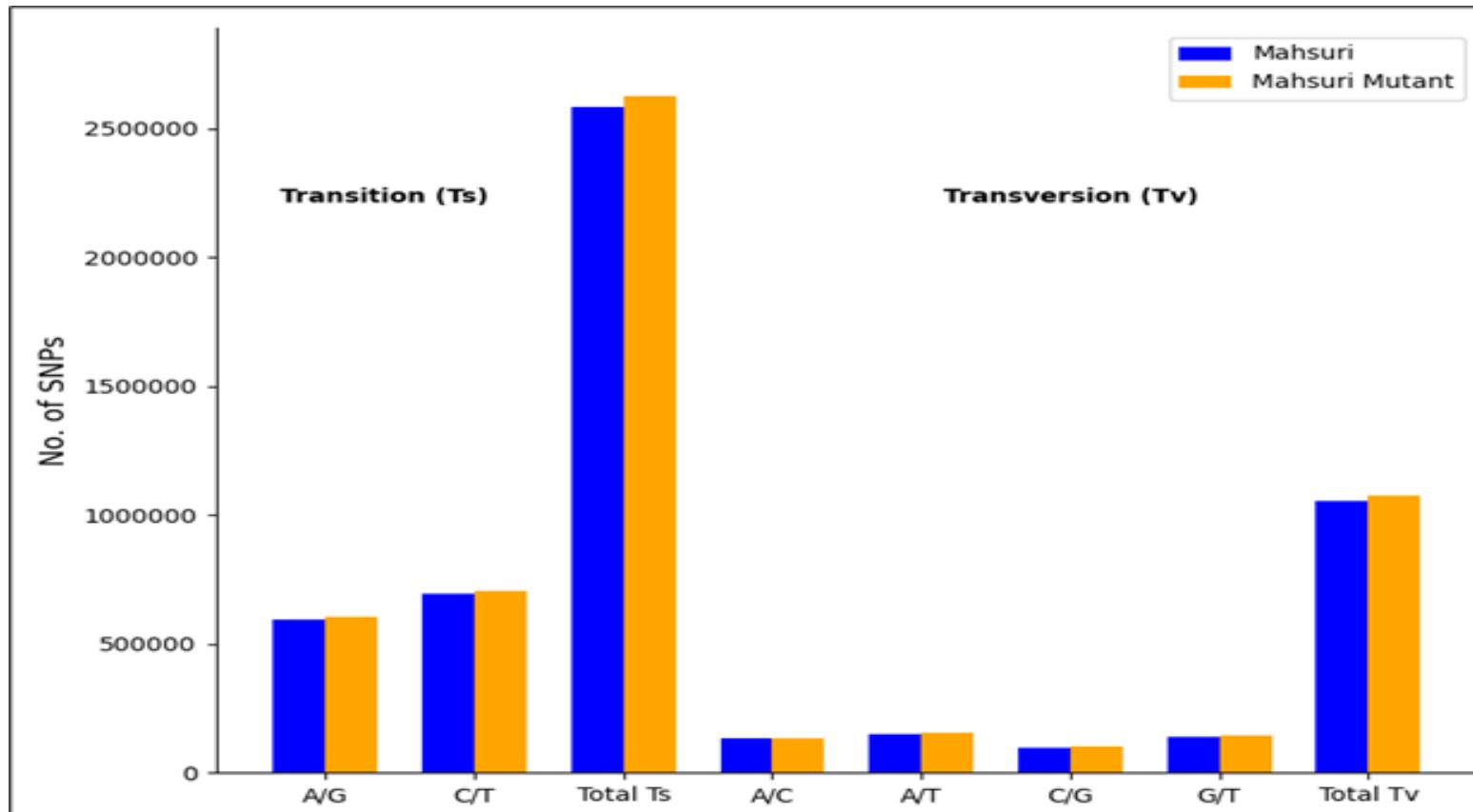
### RESULTS & DISCUSSION

**Table 1** Mapping statistics data of short reads from Mahsuri and Mahsuri Mutant rice variety.

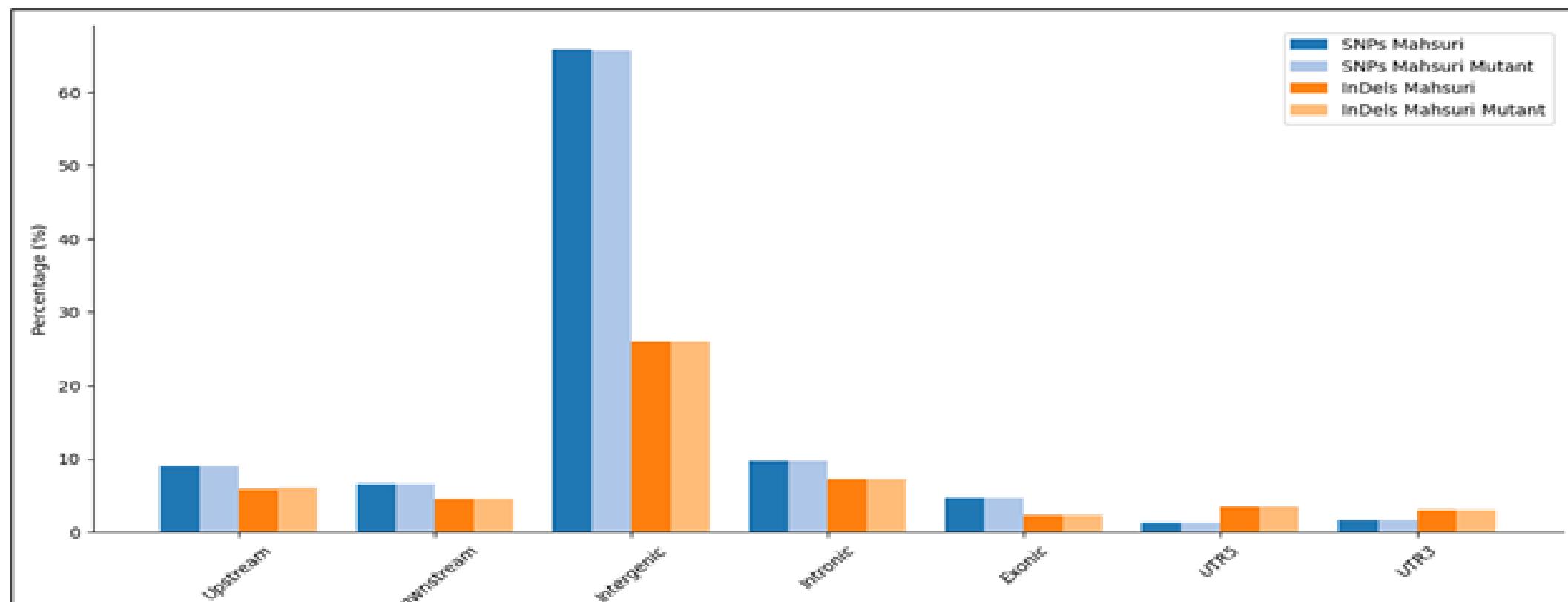
Variant	Mahsuri	Mahsuri Mutant
<b>Total reads</b>	55,510,645	60,907,677
<b>Mapped reads</b>	54,976,618 (99.04%)	60,365,342 (99.11%)
<b>Properly paired</b>	51,784,952	57,173,975
<b>Singleton</b>	534,027 (0.96%)	542,335 (0.89%)
<b>Sequencing coverage</b>	21.76	23.91

**Table 2** Number of SNPs and InDels identified in Mahsuri and Mahsuri Mutant rice varieties.

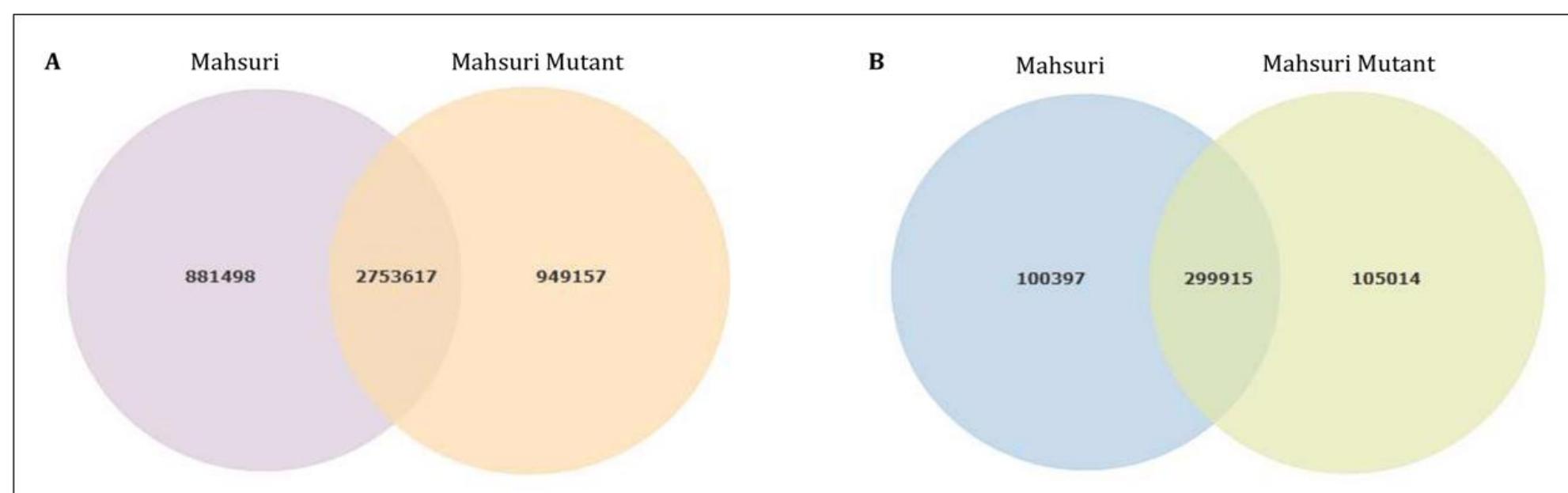
Variant	Mahsuri	Mahsuri Mutant
<b>SNPs</b>	3,629,220	3,696,685
<b>InDels</b>	395,003	399,386
<b>Total</b>	4,024,223	4,096,071



**Figure 1** Transition (Ts) and transversion (Tv) substitutions in SNPs in Mahsuri and Mahsuri Mutant rice varieties.



**Figure 2** Distribution of SNPs and InDels in different genomic regions for Mahsuri and Mahsuri Mutant rice variety.



**Figure 3** Number of shared and unique SNPs (A) and InDels (B) among Mahsuri and Mahsuri Mutant rice variety.

- The increased SNPs frequency suggested that 'Mahsuri Mutant' received new point mutations during mutagenesis, which may alter or disrupt the existing genes' functions (Abdelhameed et al., 2024).
- The 'Mahsuri Mutant' showed a higher count of unique SNPs (949,157) and InDels (105,014), are strong candidates for the genetic basis of improved traits (Bohy et al., 2021).

**Table 3** Summary of the identified blast resistance gene and its location in Mahsuri Mutant.

Gene ID	Gene Name	Chromosome	Gene Length	Location Number
Os01g0149500	<i>Pyricularia oryzae resistance T</i>	1	4,937	2,681,220 – 2,686,364
Os01g0781200	<i>Pyricularia oryzae resistance 64</i>	1	4,411	33,098,082 – 33,103,904
Os01g0782100	<i>Pyricularia oryzae resistance SH</i>	1	4,636	33,136,846 – 33,136,846
Os04g0401000	<i>Pyricularia oryzae resistance 21</i>	4	1,183	19,835,206 – 19,836,892
Os06g0286700	<i>Pyricularia oryzae resistance Z</i>	6	2,673	10,387,793 – 10,390,465
Os11g0689100	<i>Pyricularia oryzae resistance KM</i>	11	3,777	27,984,697 – 27,989,128
Os12g0281300	<i>Pyricularia oryzae resistance TA</i>	12	4,094	10,606,359 – 10,611,917

Unique SNPs within these loci can be used as molecular markers for Marker-Assisted Selection (MAS).