

UNIVERSITI TEKNOLOGI MARA

**AGRONOMIC PERFORMANCE
AND GENETIC ANALYSES
OF RESISTANCE AGAINST
Xanthomonas oryzae pv *oryzae*
IN RICE MUTANT LINES
(*Oryza sativa* L.)**

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ABSTRACT

Rice (*Oryza sativa* L.) is the third main staple food of the world. Over the years, the demands for rice are increasing but denied by the decrease in global and local production. The great fall of production is caused by multiple factors including the outbreak of bacterial leaf blight (BLB) disease which reduced the production by up to 60%. Mutagenesis is one method applied to develop a resistant line with great yield rate and better agronomic performances. In this study, a preliminary selection on six Malaysian rice varieties namely MR84, MR219, MR284, MR297, MR303 and MR307 was done based on twelve agronomic traits. MR297 was selected as the parental line for the development of rice mutant lines as it recorded the shortest days to flowering, shortest days to maturity, shortest plant height, highest number of tiller, highest number of panicle, highest weight of 1000 grains, lowest number of unfilled grains per panicle and highest yield rate per plant in parental screening. Post of preliminary selection, the seeds of MR297 were exposed to ten different treatments of acute gamma irradiation for identification of lethal dose (LD₅₀). A total of 10 000 seeds were irradiated at 450 Gy (lethal dose, LD₅₀) and developed as M₁ generation. Throughout the observation on M₁ generation, only one trait (day of maturity) showed a positive improvement among other traits as compared to parental line, MR297. In M₂ generation, all twelve traits illustrated a better agronomic performance including days to maturity (104.23 days ± 0.52), plant height (95.23 cm ± 0.52) yield rate (81.97 % ± 2.61) as compared to parental line, MR297. Phenotypic screening against pathotype of *Xanthomonas oryzae* pv *oryzae* revealed that 1370 M₂ plants were identified as resistant with lesion score between 1 and 3 whereas most of the plants in MR 297 were classified as susceptible with lesion score > 5. Chi-square test (χ^2) for a single gene model in M₂ generation did not show a good fit on the test cross of 3R:1S (3 resistant: 1 susceptible) ratio at ($\chi^2=7.46$; p= 0.063). In the M₃ generation, 391 out of 500 plants were found to be resistant by producing lesion scores 1 to 3 whereas parental plant, MR297 exhibited susceptible reaction with lesion scores between 5 and 7. Phenotypic selection on bacterial leaf blight occurrence in M₃ population segregated in 3R:1S ratio. Genotype analysis among 30 selected M₃ plants revealed that all of the potential plants were identified with recessive *Xa5* gene whereas seven of them were carrying a combination of dominant *Xa21* gene and recessive *Xa5* gene viz., ML-1, ML-3, ML-9, ML-16, ML-17, ML-28 and ML-29. Based on the UPGMA dendrogram, these seven potential mutant lines were grouped together in Cluster II at 0.78 similarity coefficient. They carried two *Xa* genes (*Xa21* and *Xa5*), illustrated high resistance against *Xanthomonas oryzae* pv *oryzae* based on lesion scoring, good yield rate and wise performance of all agronomic traits. Hence, they were suitable for further cultivation in M₄ – M₆ generation to develop a new high yielding variety with durable resistance against bacterial leaf blight (BLB) disease.

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